

Thu Apr 17 08:21:55 2003

us-09-424-686b-1del.rn1

Page 1

GenCore version 5.1.4.P5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: April 16, 2003, 19:47:50 ; Search time 131 Seconds
(Without alignments)
9378.222 Million cell updates/sec

Title: US-09-424-686B-1DEL

Perfect score: 4006
Sequence: 1 gttctagcagcgcgtcgtc.....aaaaaaaaaaaaaaaa 4006

Scoring table: IDENTITY, NUC
Gapop 10.0 , Gapext 0.0

Searched: 441362 seqs, 15333831 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents, NA: *
2: /cgn2_6/prodata/1/jna/5A.COMB.seq: *
3: /cgn2_6/prodata/1/jna/5B.COMB.seq: *
4: /cgn2_6/prodata/1/jna/5A.COMB.seq: *
5: /cgn2_6/prodata/1/jna/5B.COMB.seq: *
6: /cgn2_6/prodata/1/jna/backfile1.seq: *

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3982.6	99.4	4037	4	US-08-974-549A-343 Sequence 343, App
2	3969	99.1	4015	3	US-08-851-843A-224 Sequence 224, App
3	3969	99.1	4015	4	US-08-974-549A-1 Sequence 1, Appl1
4	3969	99.1	4015	4	US-08-854-050-224 Sequence 224, App
5	3969	99.1	4015	4	US-09-430-323-224 Sequence 3, Appl1
6	3969	99.1	4015	4	US-09-572-423B-3 Sequence 1, Appl1
7	3969	99.1	4015	4	US-09-128-354-1 Sequence 1, Appl1
8	3969	99.1	4015	4	US-09-675-321-1 Sequence 1, Appl1
9	3969	99.1	4015	4	US-09-052-919-1 Sequence 1, Appl1
10	3932.6	95.7	4029	3	US-08-851-843A-173 Sequence 173, App
11	3932.6	95.7	4029	4	US-08-974-549A-292 Sequence 292, App
12	3932.6	95.7	4029	4	US-08-854-050-173 Sequence 173, App
13	3932.6	95.7	4029	4	US-09-430-323-173 Sequence 173, App
14	3797	54.2	3855	4	US-08-974-549A-4 Sequence 4, Appl1
15	2170.4	54.2	3451	4	US-08-974-549A-721 Sequence 721, App
16	2160.2	53.6	3396	4	US-08-974-549A-639 Sequence 639, App
17	2160.2	53.6	3396	4	US-08-974-549A-638 Sequence 638, App
18	2116.4	52.8	2176	4	US-08-974-549A-3 Sequence 3, Appl1
19	2039.2	50.9	2171	3	US-08-851-843A-100 Sequence 100, App
20	2039.2	50.9	2171	4	US-08-974-549A-266 Sequence 266, App
21	2039.2	50.9	2171	4	US-08-854-050-100 Sequence 100, App
22	1830.6	45.7	2171	4	US-09-430-323-100 Sequence 100, App
23	1830.6	45.7	2171	4	US-08-974-549A-642 Sequence 642, App
24	1724.4	43.0	3356	4	US-08-974-549A-641 Sequence 641, App
25	1635.2	40.8	4335	4	US-08-974-549A-6 Sequence 6, Appl1
26	1512.2	37.7	3396	4	US-08-974-549A-640 Sequence 640, App
27	427.2	10.7	44377	2	US-08-804-227C-7 Sequence 7, Appl1

28	427.2	10.7	44377	2	US-08-804-198-1 Sequence 1, Appl1
29	423.6	10.6	68750	3	US-09-335-409-1 Sequence 1, Appl1
30	423.6	10.6	68750	4	US-09-568-102-1 Sequence 1, Appl1
31	423.6	10.6	68750	4	US-09-567-969-1 Sequence 1, Appl1
32	423.6	10.6	68750	4	US-09-568-480-1 Sequence 1, Appl1
33	423.6	10.6	68750	4	US-09-568-486-1 Sequence 1, Appl1
34	423.6	10.6	68750	4	US-09-567-472-1 Sequence 1, Appl1
35	423.6	10.6	68750	4	US-09-567-899-1 Sequence 1, Appl1
36	425.6	10.6	71989	4	US-09-443-501A-2 Sequence 2, Appl1
37	414.8	10.4	71989	4	US-09-443-501A-2 Sequence 2, Appl1
38	412	10.3	36506	3	US-08-804-227C-1 Sequence 1, Appl1
39	410.8	10.3	43280	2	US-08-658-136-2 Sequence 2, Appl1
40	410.6	10.2	53526	3	US-08-658-136-1 Sequence 1, Appl1
41	410.6	10.2	53577	3	US-08-804-227C-7 Sequence 7, Appl1
42	399.8	10.0	44377	2	US-08-804-198-1 Sequence 1, Appl1
43	399.8	10.0	44377	2	US-08-105-537-5 Sequence 5, Appl1
44	399.4	10.0	36778	4	US-08-804-227C-1 Sequence 1, Appl1
45	397.6	9.9	43280	2	US-08-804-227C-1 Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-974-549A-343
Sequence 343, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morlin, Gregg B.
APPLICANT: Hartley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56...3454
OTHER INFORMATION: /note= "refined sequence of hprt cDNA"
US-08-974-549A-343

Query Match 99.4%; Score 3982.6; DB 4; Length 4037;
Best Local Similarity 98.9%; Pred. No. 1.2e-235;
Matches 3992; Conservative 4; Mismatches 3; Indels 36; Gaps 1;

QY 8 GCACGCGTCTCTGTCGCGCAGCTGGAGCCCTGGCCCCGACACCCCGGATGCC 67
Db 1 GCACGCGTCTCTGTCGCGCAGCTGGAGCCCTGGCCCCGACACCCCGGATGCC 60
QY 68 GCGGCGTCCCGCTGCGCAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGAGTGTCT 127
Db 61 GCGGCGTCCCGCTGCGCAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGAGTGTCT 120
QY 128 GCGGCGTCCCGCTGCGCAGCGCTGCGCTCCCTGCTGCGCAGCGCTGCGCAGCGCG 187
Db 121 GCGGCGTCCCGCTGCGCAGCGCTGCGCTCCCTGCTGCGCAGCGCTGCGCAGCGCG 180
QY 188 GGACGCGCGCTTCCGCGCGCTGCTGCGCAGCGCTGCTGCGCAGCGCTGCGCAGCGCG 247
Db 181 GGACGCGCGCTTCCGCGCGCTGCTGCGCAGCGCTGCTGCGCAGCGCTGCGCAGCGCG 240
QY 248 AGGCGCGCGCTTCCGCGCGCTGCTGCGCAGCGCTGCTGCGCAGCGCTGCGCAGCGCG 307
Db 241 AGGCGCGCGCTTCCGCGCGCTGCTGCGCAGCGCTGCTGCGCAGCGCTGCGCAGCGCG 300
QY 308 CCGAGTGTGAGAGCGCTGCTGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
Db 301 CCGAGTGTGAGAGCGCTGCTGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 368 GCTGTCGAGCG 427
Db 361 GCTGTCGAGCG 420
QY 428 CCG 487
Db 421 CCG 480
QY 488 CCGCGTGGCG 547
Db 481 CCGCGTGGCG 540
QY 548 GCGTCG 607
Db 541 GCGTCG 600

QY 608 TCAGGCG 667
Db 601 TCAGGCG 660
QY 668 CTGAGACCATAGCTCAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
Db 661 CTGAGACCATAGCTCAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 728 GAGGCG 787
Db 721 GAGGCG 780
QY 788 TGCCCTGAGCG 847
Db 781 TGCCCTGAGCG 840
QY 848 GCGTGAACCGAGTACCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 907
Db 841 GCGTGAACCGAGTACCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 908 CACCTCTTGGAGGAGTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 967
Db 901 CACCTCTTGGAGGAGTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 968 GCACCG 1027
Db 961 GCACCG 1020
QY 1028 CCGGCTGAGCG 1087
Db 1021 CCGGCTGAGCG 1080
QY 1088 GCGCTCTCTCTACTAGCTCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1147
Db 1081 GCGCTCTCTCTACTAGCTCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
QY 1148 GACCATCTTCTGAGGCTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1207
Db 1141 GACCATCTTCTGAGGCTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1200
QY 1208 GCGCGAGCGCTACG 1267
Db 1201 GCGCGAGCGCTACG 1260
QY 1268 GTGCGCGCTACG 1327
Db 1261 GTGCGCGCTACG 1320
QY 1328 AGCGGCTGTCTGCG 1387
Db 1321 AGCGGCTGTCTGCG 1380
QY 1388 CACAGACCG 1447
Db 1381 CACAGACCG 1440
QY 1448 GCGCTGTCG 1507
Db 1441 GCGCTGTCG 1500
QY 1508 CAACGACCGCGCTTCTCAGAGAACACCAAGAGTTCATCTCTGCGGGAAGCATGCCAA 1567
Db 1501 CAACGACCGCGCTTCTCAGAGAACACCAAGAGTTCATCTCTGCGGGAAGCATGCCAA 1560
QY 1568 GCTCTGCTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1627
Db 1561 GCTCTGCTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1620
QY 1628 GAGCCAGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1687
Db 1621 GAGCCAGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680

Page 4

Query Match	Best Local Similarity	Score	DB 3:	Length	4015:
Matches 3979;	Conservative	0;	Mismatches	0;	Indels 36; Gaps
99.1%;	99.1%;	Score 3969;	DB 3:	Length 4015;	
99.1%;	99.1%;	Pred. No. 8e-235;			
LOCATION: 56..3454	OTHER INFORMATION: /product- "hrrt"				
OTHER INFORMATION: /note- "human telomerase reverse					
OTHER INFORMATION: transcriptase (hrrt) catalytic protein					
OTHER INFORMATION: component"					
US-08-851-843A-224					
8	GCAGCGCTGCTCTCTCTGCGACGTGGAAAGCCCTGCGCCCGCCACCCCGCGATGCC	67			
1	GCAGCGCTGCTCTCTCTGCGACGTGGAAAGCCCTGCGCCCGCCACCCCGCGATGCC	60			
68	GCAGCGCTCTCCGCTGCGACGCGTCTGCTCTCTGCGACGACACTACCGCGAGTGT	127			
61	GCAGCGCTCTCCGCTGCGACGCGTCTGCTCTCTGCGACGACACTACCGCGAGTGT	120			
128	GCAGCGCTGCGACGCTGCGCGCGCTGCGCGCCCGCGAGGCTGCGCGCTGCGCGCG	187			
121	GCAGCGCTGCGACGCTGCGCGCGCTGCGCGCCCGCGAGGCTGCGCGCTGCGCGCG	180			
188	GCAGCGCGCGCTGCTCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	247			
181	GCAGCGCGCGCTGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	240			
248	ACG	307			
241	ACG	300			
308	CCGAGTGTGCGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	367			
301	CCGAGTGTGCGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	360			
368	GCTCTGTGAGCG	427			
361	GCTCTGTGAGCG	420			
428	CGTCCCAACAGGCTGACCGACGACACTGCGCGCGCGCGCGCGCGCGCGCGCGCG	487			
421	CGTCCCAACAGGCTGACCGACGACACTGCGCGCGCGCGCGCGCGCGCGCGCGCG	480			
488	CCGCGTGGGAGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	547			
481	CCGCGTGGGAGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	540			
548	GCTCTGTGAGCG	607			
541	GCTCTGTGAGCG	600			
608	TCAGGCG	667			
601	TCAGGCG	660			
668	CTGGAACCATGACGCTGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	727			
661	CTGGAACCATGACGCTGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	720			
728	GAGGCGCGGAGGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	787			
721	GAGGCGCGGAGGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	780			
788	TCGCGCTGAGCGCGGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	847			
781	TCGCGCTGAGCGCGGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	840			
848	CGGTGAGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	907			
841	CGGTGAGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	900			
908	CACCTCTTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG				

[illegible]

us-09-424-686b-1del.rn

Page 6

RESULT 3
US-08-974-549A-1
Sequence 1, Application US/08974549A
Patent No. 6165178
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
APPLICANT: Linnner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.

```

1 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
2
3 NUMBER OF SEQUENCES: 727
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: Townsend and Townsend and Crew LLP
6 STREET: Two Embarcadero Center, Eighth Floor
7 CITY: San Francisco
8 STATE: California
9 COUNTRY: USA
10 ZIP: 94111-3834
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: PatentIn Release #1.0, Version #1.30
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/974,549A
19 FILING DATE: 19-NOV-1997
20 CLASSIFICATION: 536
21
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 08/724,643
24 FILING DATE: 01-OCT-1996
25
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 08/844,419
28 FILING DATE: 18-APR-1997
29
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 08/846,017
32 FILING DATE: 25-APR-1997
33
34 PRIOR APPLICATION DATA:
35 APPLICATION NUMBER: US 08/851,843
36 FILING DATE: 06-MAY-1997
37
38 PRIOR APPLICATION DATA:
39 APPLICATION NUMBER: US 08/854,050
40 FILING DATE: 09-MAY-1997
41
42 PRIOR APPLICATION DATA:
43 APPLICATION NUMBER: US 08/911,312
44 FILING DATE: 14-AUG-1997
45
46 PRIOR APPLICATION DATA:
47 APPLICATION NUMBER: US 08/912,951
48 FILING DATE: 14-AUG-1997
49
50 PRIOR APPLICATION DATA:
51 APPLICATION NUMBER: US 08/915,503
52 FILING DATE: 14-AUG-1997
53
54 PRIOR APPLICATION DATA:
55 APPLICATION NUMBER: WO PCT/US97/17618
56 FILING DATE: 01-OCT-1997
57
58 PRIOR APPLICATION DATA:
59 APPLICATION NUMBER: WO PCT/US97/17885
60 FILING DATE: 01-OCT-1997
61
62 ATTORNEY/AGENT INFORMATION:
63 NAME: Apple, Randolph Ted
64 REGISTRATION NUMBER: 36,429
65 REFERENCE/DOCKET NUMBER: 015389-002610US
66 TELECOMMUNICATION INFORMATION:
67 TELEPHONE: (415) 576-0200
68 TELEFAX: (415) 576-0300
69
70 INFORMATION FOR SEQ ID NO: 1:
71 SEQUENCE CHARACTERISTICS:
72 LENGTH: 4015 base pairs
73 TYPE: nucleic acid
74 STRANDEDNESS: single
75 TOPOLOGY: linear
76 MOLECULE TYPE: CDNA
77 FEATURE:
78 NAME/KEY: CDS
79 LOCATION: 56..3454
80 OTHER INFORMATION: /product="hTERT"
81 OTHER INFORMATION: /note="human telomerase reverse
82 transcriptase (hTERT) catalytic protein
83 component"
84
85 US-08-974-549A-1

```

Query Match	99.1%;	Score 3969;	DB 4;	Length 4015;
Best Local Similarity	99.1%;	Pred. No. 8e-235;		

QY	2168	GCGCCCTGACTGTA	-----CATCCCCA	2191
Db	2161	GCGCCCTGACTGTA	CTTTGTCAAGGTGATGACGGGCGGTACACACCATCCCCA	2220
QY	2192	GCACAGGCTCACGAGGTATCGCCAGCATCATCAAA	CCCCGAAACAGTACTGCTGCG	2251
Db	2221	GGACAGGCTCACGAGGTATCATCCCGACATCATCAAA	CCCCCGAAACAGTACTGCTGCG	2280
QY	2252	TCGGTATGCGGTGTCAGAAAGGCGCCCATGAGGAC	CGTCCGACAGGCTTCAGAGCA	2311
Db	2281	TCGGTATGCGGTGTCAGAAAGGCGCCCATGAGGAC	CGTCCGACAGGCTTCAGAGCA	2340
QY	2312	CGTCTACCTTGACAGACCTCCAGCCGATACATGCGAC	AGTTGCTGAGCTCACTTCAGCA	2341
Db	2341	CGTCTACCTTGACAGACCTCCAGCCGATACATGCGAC	AGTTGCTGAGCTCACTTCAGCA	2400
QY	2372	GACACAGCCCGCTAGAGGATATCCGTCATCGACAGAG	CTCTCTCGATGAGCCAG	2431
Db	2401	GACACAGCCCGCTAGAGGATATCCGTCATCGACAGAG	CTCTCTCGATGAGCCAG	2460
QY	2432	CAGTGGCCTCTTGAGAGCTCTTCTAGCGTTCAATGTC	CCACAGCCGTCGATCAGAGG	2491
Db	2461	CAGTGGCCTCTTGAGAGCTCTTCTAGCGTTCAATGTC	CCACAGCCGTCGATCAGAGG	2520
QY	2492	CAAGTCTTACGTCCAGTGCAGGGGATCCCGAGGGCTC	ATCTCTCCACGCTGCTG	2551
Db	2521	CAAGTCTTACGTCCAGTGCAGGGGATCCCGAGGGCTC	ATCTCTCCACGCTGCTG	2580
QY	2552	CAGCTCTGTGACGGGACATGTGAGAAAGAGTGTTGG	GGGGATTTGGCGGGAGCGGCT	2611
Db	2581	CAGCTCTGTGACGGGACATGTGAGAAAGAGTGTTGG	GGGGATTTGGCGGGAGCGGCT	2640
QY	2612	GCTCTCTGTTGGTGATGATTCTTGTGTGACACCTCA	CTCACCTCACGCGAAGAC	2671
Db	2641	GCTCTCTGTTGGTGATGATTCTTGTGTGACACCTCA	CTCACCTCACGCGAAGAC	2700
QY	2672	CTTCTCTAGAGACCTGGTCCGAGGTCCTCATGATG	GTGCTGCGGTGAATTCGGGA	2731
Db	2701	CTTCTCTAGAGACCTGGTCCGAGGTCCTCATGATG	GTGCTGCGGTGAATTCGGGA	2760
QY	2732	GACAGTGTGAACCTTCCCTGTAGAAAGACGAGCCCT	GGTGGACAGGCTTTTGTTCAGAT	2791
Db	2761	GACAGTGTGAACCTTCCCTGTAGAAAGACGAGCCCT	GGTGGACAGGCTTTTGTTCAGAT	2820
QY	2792	GGCGGCCACAGGCGCTATTTCCCGTGGTGGCGCC	CGTGTGTGATATCCCGAGTGGAGGT	2851
Db	2821	GGCGGCCACAGGCGCTATTTCCCGTGGTGGCGCC	CGTGTGTGATATCCCGAGTGGAGGT	2880
QY	2852	GCAGAGGAGTACTCCAGCTATCTCCCGAGACCTTC	ATCATAAGGACAGTCTACCTTCACACG	2911
Db	2881	GCAGAGGAGTACTCCAGCTATCTCCCGAGACCTTC	ATCATAAGGACAGTCTACCTTCACACG	2940
QY	2912	CGGCTTCAAGGCTGGGAGAACATGCGTGGCAAACT	CTTTGGGGCTTGGCGGTGAATG	2971
Db	2941	CGGCTTCAAGGCTGGGAGAACATGCGTGGCAAACT	CTTTGGGGCTTGGCGGTGAATG	3000
QY	2972	TCACAGGCTGTTTCTGGATTTTGGAGGTGAACAGCC	TCAGAGGAGTGGACCAACATCTA	3031
Db	3001	TCACAGGCTGTTTCTGGATTTTGGAGGTGAACAGCC	TCAGAGGAGTGGACCAACATCTA	3060
QY	3032	CAGAGTCTCTCTGCTGACAGGCTGACAGGTTTAC	AGCGATGTGCTGACAGCTCCATTTTCA	3091
Db	3061	CAGAGTCTCTCTGCTGACAGGCTGACAGGTTTAC	AGCGATGTGCTGACAGCTCCATTTTCA	3120
QY	3092	TCACAGATTTTGGAAAGAACCCCATTTTTTCTGCG	CGCTATCTCTGACAGGCTCCCT	3151
Db	3121	TCACAGATTTTGGAAAGAACCCCATTTTTTCTGCG	CGCTATCTCTGACAGGCTCCCT	3180
QY	3152	CTGTACTTCATCCTTAAACCAAGAACAGAGGATGT	CGCTGGGGCCCAAGGGCGCGC	3211
Db	3181	CTGTACTTCATCCTTAAACCAAGAACAGAGGATGT	CGCTGGGGCCCAAGGGCGCGC	3240
QY	3212	CGGCGCTCTGCGCTCCGAGGCGGTGACAGTGTGCT	CCACCAAGCATTTCTGCTCAAGCT	3271

Db	3241	CGGCCCTCTGCTCCCTCGAGGGCCGTGCAGTGGGTGGCCACCAGCATTTCTGTCTCAAGCT	3300
Qy	3272	GACTCGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAGAGCGA	3331
Db	3301	GACTCGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAGAGCGA	3360
Qy	3332	GCTCAGTCGGAGACCTCCCGGGGAGCAGACGCTGACTGCGCTGGAGGGCCGAGCCAGCCGGC	3391
Db	3361	GCTCAGTCGGAGACCTCCCGGGGAGCAGACGCTGACTGCGCTGGAGGGCCGAGCCAGCCGGC	3420
Qy	3392	ACTGCCCCAGACTTCAAGACCACTCTGTGACACTGATGGCCACCCGCCACAGCCAGCGCGA	3451
Db	3421	ACTGCCCCAGACTTCAAGACCACTCTGTGACACTGATGGCCACCCGCCACAGCCAGCGCGA	3480
Qy	3452	GAGCAGACACCCAGACAGCCCTGTACGCCGGGCTCTACGTCCAGGAGGAGGGGGCGCC	3511
Db	3481	GAGCAGACACCCAGACAGCCCTGTACGCCGGGCTCTACGTCCAGGAGGAGGGGGCGCC	3540
Qy	3512	CACACCCAGGCCCCGACCCGCTGGGAGTCTGAGGCCCTGATGATGTTTGGCCGAGAGCGCTG	3571
Db	3541	CACACCCAGGCCCCGACCCGCTGGGAGTCTGAGGCCCTGATGATGTTTGGCCGAGAGCGCTG	3600
Qy	3572	CATGTCCGGGTGAAGGCTGTAGTGTCCGGCTGAGGGCTGAGCGAGTGTCCAGCCAGAGGCT	3631
Db	3601	CATGTCCGGGTGAAGGCTGTAGTGTCCGGCTGAGGGCTGAGCGAGTGTCCAGCCAGAGGCT	3660
Qy	3632	GAGTGTCCAGACACACCTGGCCGTCTTACATTCCCAACAGGCTGGGCTGCCACCCCA	3691
Db	3661	GAGTGTCCAGACACACCTGGCCGTCTTACATTCCCAACAGGCTGGGCTGCCACCCCA	3720
Qy	3692	GGGCGACACTTTTCTCAACAGAGAGCCGGCTTCACATCCCAATAGGAATAGTCCATCC	3751
Db	3721	GGGCGACACTTTTCTCAACAGAGAGCCGGCTTCACATCCCAATAGGAATAGTCCATCC	3780
Qy	3752	CCGAGTTGCCATTGTTCACACCTCGCCCTGGCCCTCTTGGCTTCCACCCCAACATCC	3811
Db	3781	CCGAGTTGCCATTGTTCACACCTCGCCCTGGCCCTCTTGGCTTCCACCCCAACATCC	3840
Qy	3812	AGGTGAGACACCTTGAGAGAGACCTGGAGACTCTGGGAATTTGGAGTATACCAAAAGTGTG	3871
Db	3841	AGGTGAGACACCTTGAGAGAGACCTGGAGACTCTGGGAATTTGGAGTATACCAAAAGTGTG	3900
Qy	3872	CCCTGTACACAGGCGAGAGACCTGTCACTGTGATGGGGTCCCTGTGGGCTCAAAATTTGGGG	3921
Db	3901	CCCTGTACACAGGCGAGAGACCTGTCACTGTGATGGGGTCCCTGTGGGCTCAAAATTTGGGG	3960
Qy	3932	GAGTGTGTTGGGAGATTAATTAAGTAATTAAGTATTTTCAAGTTTGAATAAAAAA	3986
Db	3961	GAGTGTGTTGGGAGATTAATTAAGTAATTAAGTATTTTCAAGTTTGAATAAAAAA	4015

RESULT 4
 US-08-554-050-224
 Sequence 224, Application US/08854050
 Patent No. 6261836
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 APPLICANT: Linger, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: No. 6261836el Telomerase
 TITLE OF INVENTION: No. 6261836el Telomerase
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/854,050
 FILING DATE: 09-MAY-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0300
 TELEFAX: (415) 576-0200
 INFORMATION FOR SEQ ID NO: 224:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4015 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 56..3454
 OTHER INFORMATION: /product="hprt"
 OTHER INFORMATION: /note="human telomerase reverse
 transcriptase (hprt) catalytic protein
 OTHER INFORMATION: component"
 US-08-854-050-224

Query Match 99.1%; Score 3969; DB 4; Length 4015;
 Best Local Similarity 99.1%; Pred. No. 8e-235;
 Matches 3979; conservative 0; Mismatches 0; Indels 36; Gaps 1;

DB 8 GCAGCGTGGTCTGCTGCGACAGTGGAGACCCCTGCCCCGCGCCATCGCC 67
 1 GCAGCGTGGTCTGCTGCGACAGTGGAGACCCCTGCCCCGCGCCATCGCC 60
 QY 68 GCGCGCTCCCGCTGCGAGCGCTGCGCTGCTGCGAGCCACTACCGGAGTGC 127
 DB 61 GCGCGCTCCCGCTGCGAGCGCTGCGCTGCTGCGAGCCACTACCGGAGTGC 120
 QY 128 GCGCGTGGCCAGCTGCTGCGAGCGCTGCGAGCGCCAGAGGCTGCGCTGCGAGCCG 187
 DB 121 GCGCGTGGCCAGCTGCTGCGAGCGCTGCGAGCGCCAGAGGCTGCGCTGCGAGCCG 180
 QY 188 GAGCCGCGCGCTTCCGCGCGCTGCGAGCGCCAGTGCCTGCTGCTGCGAGCCG 247
 DB 181 GAGCCGCGCGCTTCCGCGCGCTGCGAGCGCCAGTGCCTGCTGCTGCGAGCCG 240
 QY 248 ACGGCGCGCGCGCGCGCGCGCTTCCGCGCGAGGTGCTGCTGCTGCGAGGAGCTG 307
 DB 241 ACGGCGCGCGCGCGCGCGCGCTTCCGCGCGAGGTGCTGCTGCTGCGAGGAGCTG 300
 QY 308 CCGAGTGTGAGAGCTGTGCGAGCGCGCGCGAGAGAGTGTGCTGCGCTTGC 367

DB 301 CCGAGTGTGAGAGCTGTGCGAGCGCGCGCGAGAGAGAGTGTGCTGCGCTTGC 360
 QY 368 GCTGCTGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 427
 DB 361 GCTGCTGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
 QY 428 CTTGCGCGAGAGGTGAGCGAGCGAGCTGCGAGCGCGCGCGCGCGCGCGCGCGCG 487
 DB 421 CTTGCGCGAGAGGTGAGCGAGCGAGCTGCGAGCGCGCGCGCGCGCGCGCGCGCG 480
 QY 488 CCGCGTGGCGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
 DB 481 CCGCGTGGCGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 548 GGTCTCCAGCTGCGCGCTTACAGAGTGTGCGAGCGCGCGCGCGCGCGCGCGCGCG 600
 DB 541 GGTCTCCAGCTGCGCGCTTACAGAGTGTGCGAGCGCGCGCGCGCGCGCGCGCGCG 600
 QY 608 TCAGGCG 667
 DB 601 TCAGGCG 660
 QY 668 CTGGAACATAGAGCTGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
 DB 661 CTGGAACATAGAGCTGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
 QY 728 GAGGCG 787
 DB 721 GAGGCG 780
 QY 788 TGCCCGTGAAGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
 DB 781 TGCCCGTGAAGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
 QY 848 GCGTGGAGCGAGTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 907
 DB 841 GCGTGGAGCGAGTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 QY 908 CACCTCTTGGAGAGTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 967
 DB 901 CACCTCTTGGAGAGTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 QY 968 GAGCAGCG 1027
 DB 961 GAGCAGCG 1020
 QY 1028 CCGCGTGGAGCGAGAGCAAGCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1087
 DB 1021 CCGCGTGGAGCGAGAGCAAGCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
 QY 1088 GCGCTCTTCT 1147
 DB 1081 GCGCTCTTCT 1140
 QY 1148 GACCATCTTCT 1207
 DB 1141 GACCATCTTCT 1200
 QY 1208 GCGCGAGCTACTGAGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1267
 DB 1201 GCGCGAGCTACTGAGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
 QY 1268 GTGCGCTTCT 1327
 DB 1261 GTGCGCTTCT 1320
 QY 1328 ACGCGTGTCTGTGCGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1387
 DB 1321 ACGCGTGTCTGTGCGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
 QY 1388 CAGAGAGCG 1447

Db	2881	GCACAGGAGCTACCTCCAGCTATTGCCCGAGCTCCATCAGAGCGCATCTCACCCTTGAACGC	2940
Oy	2912	CGGGCTTCAGAGCTGGGAGAGACATGCTGGCAAACTCTTTGGGGGCTTTGGGGGTGAATG	2971
Db	2941	CGGGCTTCAGAGCTGGGAGAGACATGCTGGCAAACTCTTTGGGGGCTTTGGGGGTGAATG	3000
Oy	2972	TGCACAGCCTGTTTCTGATTTGCAGAGTAACAGCTCTCAACGGGTGTGCACCAACATCTA	3031
Db	3001	TGCACAGCCTGTTTCTGATTTGCAGAGTAACAGCTCTCAACGGGTGTGCACCAACATCTA	3060
Oy	3032	CAGATCCTCTGCTGTGAGGCGTACAGAGTTTCAACGATGTGTCTGTACAGTCCCATTTCA	3091
Db	3061	CAGATCCTCTGCTGTGAGGCGTACAGAGTTTCAACGATGTGTCTGTACAGTCCCATTTCA	3120
Oy	3092	TCAGCAGTTTGGAGAAACCCCAATTTTTCGCGCGTCACTGTGAACGGCTTCCT	3151
Db	3121	TCAGCAGTTTGGAGAAACCCCAATTTTTCGCGCGTCACTGTGAACGGCTTCCT	3180
Oy	3152	CTGTCTACCTCACTCTGAAAGCAAGCAAGGAGATGTGCTGTGGGGGCCAAGGGCGCCG	3240
Db	3181	CTGTCTACCTCACTCTGAAAGCAAGCAAGGAGATGTGCTGTGGGGGCCAAGGGCGCCG	3240
Oy	3212	CGGGCTTCGCTCTCCGAGGCGCGGAGGAGTGTGTGCACCAAACTTCCTCTCAAGCT	3271
Db	3241	CGGGCTTCGCTCTCCGAGGCGCGGAGGAGTGTGTGCACCAAACTTCCTCTCAAGCT	3300
Oy	3272	GACTGCACACCTGTGTACTATACGTGTGCATCTCTGGGTATCTACAGAGCCCAAGACGA	3331
Db	3301	GACTGCACACCTGTGTACTATACGTGTGCATCTCTGGGTATCTACAGAGCCCAAGACGA	3360
Oy	3332	GCTGAGTGGAGCTCCGGGGGAGAGAGAGGTGATCTGTGGGAGGCGCCAGACCCAGC	3391
Db	3361	GCTGAGTGGAGAGCTCCGGGGGAGAGAGAGGTGATCTGTGGGAGGCGCCAGACCCAGC	3420
Oy	3392	ACTGCTCTCAAGCTTCAAAACATCTCTGAGACGTAAAGGCCACCGCGCCAGACGGCGGA	3451
Db	3421	ACTGCTCTCAAGCTTCAAAACATCTCTGAGACGTAAAGGCCACCGCGCCAGACGGCGGA	3480
Oy	3452	GAGCAGACACAGCAGCCCTCTGTACAGCGCGGGGTCTTAAGTCCCAAGGAGAGAGGGCGCC	3511
Db	3481	GAGCAGACACAGCAGCCCTCTGTACAGCGCGGGGTCTTAAGTCCCAAGGAGAGAGGGCGCC	3540
Oy	3512	CACACCCAGGCGCCGACCCGTGGAGATCTTAGAGCCTTAGATGTTGGTGGCCAGGCGTG	3571
Db	3541	CACACCCAGGCGCCGACCCGTGGAGATCTTAGAGCCTTAGATGTTGGTGGCCAGGCGTG	3600
Oy	3572	CATGTCCGAGTAAGGCTGATGTCCGCTGTAGAGCCCTGAAGAGATGTCCACCAAGGGCT	3631
Db	3601	CATGTCCGAGTAAGGCTGATGTCCGCTGTAGAGCCCTGAAGAGATGTCCACCAAGGGCT	3660
Oy	3632	GAGTCTCCAGACACACTCCGCTTCACTTCCCAACAGGCTGTGGGTGTCCACCCCA	3691
Db	3661	GAGTCTCCAGACACACTCCGCTTCACTTCCCAACAGGCTGTGGGTGTCCACCCCA	3720
Oy	3692	GGGCGAGCTTTCCTACACAGAGAGCCGAGTCTCACTCCCAATATAGAAATGTGCATCC	3751
Db	3721	GGGCGAGCTTTCCTACACAGAGAGCCGAGTCTCACTCCCAATATAGAAATGTGCATCC	3780
Oy	3752	CCAGATATGGCATATGTTCAACCCCTCCGCTCCCTCCCTCTTGGCTTCAACCCCACTATCC	3811
Db	3781	CCAGATATGGCATATGTTCAACCCCTCCGCTCCCTCCCTCTTGGCTTCAACCCCACTATCC	3840
Oy	3812	AGGTGGAGACCTGTGAAGAGACCTCTGGAGCTCTGGAAATTTGGAGTGAACAAAGTGTG	3871
Db	3841	AGGTGGAGACCTGTGAAGAGACCTCTGGAGCTCTGGAAATTTGGAGTGAACAAAGTGTG	3900
Oy	3872	CCCTGTACACAGGGAGAGACCTCTCAACGTATGGGGGTCCCTGTGGTCAATTTGGGGG	3931
Db	3901	CCCTGTACACAGGGAGAGACCTCTCAACGTATGGGGGTCCCTGTGGTCAATTTGGGGG	3960
Oy	3932	GAGGTCTGTGGAGTAAATATCTGATATATAGATTTTCAAGTTTGAATAAAAA	3986
Db	3961	GAGGTCTGTGGAGTAAATATCTGATATATAGATTTTCAAGTTTGAATAAAAA	4015

RESULT 57-423B-3

US-09-572-423B-3

Sequence 3, Application US/09572423B

Patent No. 6331399

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: William A. Gaarde

APPLICANT: Edward Mancewicz

TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION

FILE REFERENCE: ISPH-0462

CURRENT APPLICATION NUMBER: US/09/572.423B

CURRENT FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 3

LENGTH: 4015

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (56) ... (3454)

US-09-572-423B-3

Query Match

Best Local Similarity 99.18% Pred. No. 8e-235; Mismatches 0; Indels 36; Gaps 1.

Matches 3979; Conservative

Oy	8	GCAGCCCTGCGTCTGCTGCGACGATGGGAACCCCTGGGCCCCGGGACACCCCGCGATGCG	67
Db	1	GCAGCCCTGCGTCTGCTGCGACGATGGGAACCCCTGGGCCCCGGGACACCCCGCGATGCG	60
Oy	68	GCAGCGTCCCGCGTGCAGAACCCGTGCGTCCCTGCTGCGACGACATACCGCGAGGTC	127
Db	61	GCAGCGTCCCGCGTGCAGAACCCGTGCGTCCCTGCTGCGACGACATACCGCGAGGTC	120
Oy	128	GCCCGTGGGACGATGCTGCGGCGCGCTGGGAGCCCGACAGGCGGCGCTGTGTGACGGCGG	187
Db	121	GCCCGTGGGACGATGCTGCGGCGCGCTGGGAGCCCGACAGGCGGCGCTGTGTGACGGCGG	180
Oy	188	GGACCGCGGCGGCTTTCGCGCGCGTGTGTGGGCCAGTCCCTGTGTGCGTCCCTGGAGCCG	247
Db	181	GGACCGCGGCGGCTTTCGCGCGCGTGTGTGGGCCAGTCCCTGTGTGCGTCCCTGGAGCCG	240
Oy	248	ACGGCGCGCCCCCGCGCGCCCTCTCTCCGACAGTGTCTGTGCTGAAAGACTGTGTGCG	307
Db	241	ACGGCGCGCCCCCGCGCGCCCTCTCTCTCCGACAGTGTCTGTGCTGAAAGACTGTGTGCG	300
Oy	308	CCGAGTCTGCGAAGGCTGTGCGAGCGGCGCGAAGAACGTGCTGCGCTTTCGCTTTCG	367
Db	301	CCGAGTCTGCGAAGGCTGTGCGAGCGGCGCGAAGAACGTGCTGCGCTTTCGCTTTCG	360
Oy	368	GCTGCTGAGGGGGCGCGCGGGGGGCCCCCGGAGGCTTTCACACACAGCTGTGGAGCTA	427
Db	361	GCTGCTGAGGGGGCGCGCGGGGGGCCCCCGGAGGCTTTCACACACAGCTGTGGAGCTA	420
Oy	428	CTGCGCAACAGGTGACGACGACGTCGGGGGGAGGGGGGCTGTGGGGGTGTGCTGCG	487
Db	421	CTGCGCAACAGGTGACGACGACGTCGGGGGGAGGGGGGCTGTGGGGGTGTGCTGCG	480
Oy	488	CCGCGTGGGCGAGAGCTGTGCTTCACTGCTGGACAGGTGTGGCGCTTTCGCTGCTGT	547
Db	481	CCGCGTGGGCGAGAGCTGTGCTTCACTGCTGGACAGGTGTGGCGCTTTCGCTGCTGT	540
Oy	548	GGCTCCCAAGCTGCGCTTACAGAGTGTGGGGGCGCGCTGTACACAGCTGGGCGCTGCAC	607
Db	541	GGCTCCCAAGCTGCGCTTACAGAGTGTGGGGGCGCGCTGTACACAGCTGGGCGCTGCAC	600
Oy	608	TCAGGCGCGCGCGCGCGACAGCTAGTGGACCCCGAAGCGTGTGGATGCGAAGGGCG	667
Db	601	TCAGGCGCGCGCGCGCGACAGCTAGTGGACCCCGAAGCGTGTGGATGCGAAGGGCG	660
Oy	668	CTGGAACATACGCTCAGGGAGGCGGGGGTCCCTCGGAGCTGCGACGCCCGGGTGTGAG	727

|||||
Db 661 CTGGAACCTATAGCTGACGGAGGCGGGGTCCTCCCTGGGCTGACACGCCGGGTGGAG 720
Qy 728 GAGCGCGGGGAGAGTGCACAGCCGAACTTCCTCCCTCCCAAGAGGCCCAAGGCTGGCGC 787
Db 721 GAGCGCGGGGAGAGTGCACAGCCGAACTTCCTCCCTCCCAAGAGGCCCAAGGCTGGCGC 780
Qy 788 TGCCCTGAGCCGAGGAGCGCCGTTGGGACAGGGTCTCTGGGCCCAACCCGGGACAGAC 847
Db 781 TGCCCTGAGCCGAGGAGCGCCGTTGGGACAGGGTCTCTGGGCCCAACCCGGGACAGAC 840
Qy 848 GCGTGACCCGAGTACCGTGGTTCTGTCGTGTCACCTGCGACGCCCGGGAAGAAC 907
Db 841 GCGTGACCCGAGTACCGTGGTTCTGTCGTGTCACCTGCGACGCCCGGGAAGAAC 900
Qy 908 CACTCTTTGGAGGGTGCAGCTCTCTGGACAGCGCACCTCCACCCATCCGTGGGCCGCA 967
Db 901 CACTCTTTGGAGGGTGCAGCTCTCTGGACAGCGCACCTCCACCCATCCGTGGGCCGCA 960
Qy 968 GCACACGCGGGGCCCCCATTACATCGGGCACACAGTCCCTGGGACAGCGCTGTCC 1027
Db 961 GCACACGCGGGGCCCCCATTACATCGGGCACACAGTCCCTGGGACAGCGCTGTCC 1020
Qy 1028 CCGCGGTGAGCCCGAGACAGCACTTCTCTACTCTCTCAGGCGCAAGAGAGAGCTGCG 1087
Db 1021 CCGCGGTGAGCCCGAGACAGCACTTCTCTACTCTCTCAGGCGCAAGAGAGAGCTGCG 1080
Qy 1088 GCCCTCTCTCTACTCTCTGAGGCGCCAGCTGACCTGGCGCTCGAGAGCTGTGA 1147
Db 1081 GCCCTCTCTCTACTCTCTGAGGCGCCAGCTGACCTGGCGCTCGAGAGCTGTGA 1140
Qy 1148 GACCATCTTCTGAGGTTCCAGGCGCTGGAGTCCAGGGACTCCCGCAGGTGGCCCGCT 1207
Db 1141 GACCATCTTCTGAGGTTCCAGGCGCTGGAGTCCAGGGACTCCCGCAGGTGGCCCGCT 1200
Qy 1208 GCCCAGCGCTACAGCAAAATGCGGCCCTTCTGAGAGTGTGGGAACACAGCGCA 1267
Db 1201 GCCCAGCGCTACAGCAAAATGCGGCCCTTCTGAGAGTGTGGGAACACAGCGCA 1260
Qy 1268 GTGCCCCACAGGGGTGCTCTCAAGACGACATGCCCGCTGAGAGTGGGTACACCCAGC 1327
Db 1261 GTGCCCCACAGGGGTGCTCTCAAGACGACATGCCCGCTGAGAGTGGGTACACCCAGC 1320
Qy 1328 AGCCGGTGTGTGCGCGGGGAAGCCCGAGGCTGTGCGCGGCCCGGAGAGAGAGA 1387
Db 1321 AGCCGGTGTGTGCGCGGGGAAGCCCGAGGCTGTGCGCGGCCCGGAGAGAGAGA 1380
Qy 1388 CACAGACCCCGGTGCGGTGAGCTGCTCGGACGACAGAGCCGCTGGAGAGTGA 1447
Db 1381 CACAGACCCCGGTGCGGTGAGCTGCTCGGACGACAGAGCCGCTGGAGAGTGA 1440
Qy 1448 CGGCTTCTGCGGGGCTGCTGCGCGCGGCTGTGCGGCCCTCTGGGCTCCAGGCA 1507
Db 1441 CGGCTTCTGCGGGGCTGCTGCGCGCGGCTGTGCGGCCCTCTGGGCTCCAGGCA 1500
Qy 1508 CACAGACCGCGCTTCTCTCAGAGAACACCAAGTTCATCTCCCTGGGGAAGATGCCAA 1567
Db 1501 CACAGACCGCGCTTCTCTCAGAGAACACCAAGTTCATCTCCCTGGGGAAGATGCCAA 1560
Qy 1568 GCTCTGCTGAGAGAGTGAAGATGAGCTGCGGGGAGCTGCGCTGGCTCGGAG 1627
Db 1561 GCTCTGCTGAGAGAGTGAAGATGAGCTGCGGGGAGCTGCGCTGGCTCGGAG 1620
Qy 1628 GAGCCCAAGGGTGTGCTGTCCGCGCAGAGACCGCTGTGCTGAGAGATCTGGC 1687
Db 1621 GAGCCCAAGGGTGTGCTGTCCGCGCAGAGACCGCTGTGCTGAGAGATCTGGC 1680
Qy 1688 CAAGTCTCTGACATGCTGATGATGTGTAGTCTCTGAGCTGCTCAGGTCTTTTATA 1747
Db 1681 CAAGTCTCTGACATGCTGATGATGTGTAGTCTCTGAGCTGCTCAGGTCTTTTATA 1740
Qy 1748 TGTACGAGAGACCACTTTTCAAAAGACAGGCTTTTCTACCGGAAGAGTGTGGAG 1807
|||||

Db 1741 TGTACGAGAGACCACTTTTCAAAAGACAGGCTTTTCTACCGGAAGAGTGTGGAG 1800
Qy 1808 CAAGTCTCAAAAGCATTTGGATCAGACAGCACTTGAAGAGGTGCACTGCGGGAGCTGTG 1867
Db 1801 CAAGTCTCAAAAGCATTTGGATCAGACAGCACTTGAAGAGGTGCACTGCGGGAGCTGTG 1860
Qy 1868 GGAAGCAGAGTCAAGGAGCATGTGGGAAGCGAGGCCCGCCCTGCTGAGAGTCAAGACTCG 1927
Db 1861 GGAAGCAGAGTCAAGGAGCATGTGGGAAGCGAGGCCCGCCCTGCTGAGAGTCAAGACTCG 1920
Qy 1928 CTTATCCCCCAAGCCTGACGGGCTGCGCGCATTTGTGAACATGAGACTACGTGAGAGC 1987
Db 1921 CTTATCCCCCAAGCCTGACGGGCTGCGCGCATTTGTGAACATGAGACTACGTGAGAGC 1980
Qy 1988 CAGAACGTTCCGACAGAGAAAGAGGCCGAGCGTCTACCTCTGAGAGGTGAAGCACTGTT 2047
Db 1981 CAGAACGTTCCGACAGAGAAAGAGGCCGAGCGTCTACCTCTGAGAGGTGAAGCACTGTT 2040
Qy 2048 CAGCGTCTCAACTACGAGGGGGGGGGCGCCCGCGCTCTGGGGCGCTGTGCTGGG 2107
Db 2041 CAGCGTCTCAACTACGAGGGGGGGGGCGCCCGCGCTCTGGGGCGCTGTGCTGGG 2100
Qy 2108 CCTGAGCATATCCACAGAGGCTGCGCACCTTGTGCTGCTGCTGCGGGGCCAGAGACC 2167
Db 2101 CCTGAGCATATCCACAGAGGCTGCGCACCTTGTGCTGCTGCTGCGGGGCCAGAGACC 2160
Qy 2168 GCCGCTGAGCTGA-----CATCCCCA 2191
Db 2161 GCCGCTGAGCTGATCTTGTCAAGGTGATGTACGGGCGCTGACGACACATGCCCA 2220
Qy 2192 GGACAGGCTCACAGAGGTCATCGCAGATCATCAACCCCGAGAACATGATCGGTGCG 2251
Db 2221 GGACAGGCTCACAGAGGTCATCGCAGATCATCAACCCCGAGAACATGATCGGTGCG 2280
Qy 2252 TCGGATGCGCTGCTCAGAAAGGCCGCCATGAGGACATGCCGCAAGGCTTCAAGAGCA 2311
Db 2281 TCGGATGCGCTGCTCAGAAAGGCCGCCATGAGGACATGCCGCAAGGCTTCAAGAGCA 2340
Qy 2312 GGTCTTACCTTGACAGACCTCCAGCGCTACATGCGAGACATTTGCTGCTCACTGCAAGA 2371
Db 2341 GGTCTTACCTTGACAGACCTCCAGCGCTACATGCGAGAGACTCTCTGAAATGAGGCCAG 2400
Qy 2372 GACCAAGCCCGTGAAGGATGCGCGTGCATGAGAGAGCTCTCCCTGAATGAGGCCAG 2431
Db 2401 GACCAAGCCCGTGAAGGATGCGCGTGCATGAGAGAGCTCTCTGAAATGAGGCCAG 2460
Qy 2432 CAGTGGCTTCTGACAGCTCTTCTACGCTTATGTGCCACCAAGCGGCTGCCATCAGGG 2491
Db 2461 CAGTGGCTTCTGACAGCTCTTCTACGCTTATGTGCCACCAAGCGGCTGCCATCAGGG 2520
Qy 2492 CAAGTCTTACGCTCAGTGCACAGGGGATCCCGAGGGCTTCATCTCTGCAAGCTGCTGTG 2551
Db 2521 CAAGTCTTACGCTCAGTGCACAGGGGATCCCGAGGGCTTCATCTCTGCAAGCTGCTGTG 2580
Qy 2552 CAGCCTGCTTACAGCGCATGAGGAGAACAGTGTTCGGGGATTCGGGGAGCGGCT 2611
Db 2581 CAGCCTGCTTACAGCGCATGAGGAGAACAGTGTTCGGGGATTCGGGGAGCGGCT 2640
Qy 2612 GCTCTGCGTGTGTGATGATTTCTGTGTGACACCTCACTACCCACGCGAAAC 2671
Db 2641 GCTCTGCGTGTGTGATGATTTCTGTGTGACACCTCACTACCCACGCGAAAC 2700
Qy 2672 CTTCTCAGAGACCTGCTGTCGAGGTGTCCTCTGATGATGATGTCCTGAGTGAAGTCTGGAA 2731
Db 2701 CTTCTCAGAGACCTGCTGTCGAGGTGTCCTCTGATGATGATGTCCTGAGTGAAGTCTGGAA 2760
Qy 2732 GACAGTGGGAACCTCCCTGTGAGAGAGAGGCTCTGGGTGAGAGGCTTTTGTTCAGAT 2791
Db 2761 GACAGTGGGAACCTCCCTGTGAGAGAGAGGCTCTGGGTGAGAGGCTTTTGTTCAGAT 2820
Qy 2792 GCCGGCCCAAGGCTATTCCCTGCTGCTGCTGCTGATACCGGAGACCTGGAGT 2851
Db 2821 GCCGGCCCAAGGCTATTCCCTGCTGCTGCTGCTGATACCGGAGACCTGGAGT 2880
|||||

Qy	2857	GCACAGCACTACTCAGGCTATTGCCCGGACGCTCATCAGAGAGAGTCAACCTTCAACG	2911
Qy	2881	GCAGAGGAGCTACTCAGCACTATGCCCCGAGGACTCTCATAGAGCCAGTCTCACTTCAACG	2940
Qy	2912	CGGGCTTCAAGGCTGGGAGAACATCGCTCCGAACACTCTTTGGGCTCTGGCGTGAAGT	2971
Db	2941	CGGGCTTCAAGGCTGGGAGAACATCGCTCCGAACACTCTTTGGGCTCTGGCGTGAAGT	3000
Qy	2972	TCACAGGCTGTTTTCTGAGATTGTGAGGTGAACAGCTCCAGACGGTGTGACCAACATCTA	3031
Db	3001	TCACAGGCTGTTTTCTGAGATTGTGAGGTGAACAGCTCCAGACGGTGTGACCAACATCTA	3060
Qy	3032	CAGATGCTCTGCTGCGACAGGCGTAGAGGTTTCAAGCATGTGTGTCTCAGTCTCCATTTC	3091
Db	3061	CAGATGCTCTGCTGCGACAGGCGTAGAGGTTTCAAGCATGTGTGTCTCAGTCTCCATTTC	3120
Qy	3092	TCAGCAGTTTGGAGAACCCCACTTTTTCTGCGCGCTCATCTGTACAGCGCTCTCCT	3151
Db	3121	TCAGCAGTTTGGAGAACCCCACTTTTTCTGCGCGCTCATCTGTACAGCGCTCTCCT	3180
Qy	3152	CTGCTACTCCATCTGAGAAAGCAAGAACGACAGGAGATGTGCGCTGGGGGCCAAGGGCGCG	3211
Db	3181	CTGCTACTCCATCTGAGAAAGCAAGAACGACAGGAGATGTGCGCTGGGGGCCAAGGGCGCG	3240
Qy	3212	CGGGCTCTGCGCTCGAGGGCCGTGAGTGCTGTCCACCAACATCTCTCTCAAGCT	3271
Db	3241	CGGGCTCTGCGCTCGAGGGCCGTGAGTGCTGTCCACCAACATCTCTCTCAAGCT	3300
Qy	3272	GATCGAACCGTGTACTACTACGTGCACATGCTCTGGGTACTACAGCAAGCCCAAGACGA	3331
Db	3301	GATCGAACCGTGTACTACTACGTGCACATGCTCTGGGTACTACAGCAAGCCCAAGACGA	3360
Qy	3332	GCTGAGTGGAGAACCTCCGGGGAGAGACGCTGACGTGCGCTGGAGGCCCAAGCAACCGCG	3391
Db	3361	GCTGAGTGGAGAACCTCCGGGGAGAGACGCTGACGTGCGCTGGAGGCCCAAGCAACCGCG	3420
Qy	3392	ACTGCGCTAAGCTCAAGACATCTCCGGAGCTGATGAGGCCAACCGCCACAGCGACGGCGA	3451
Db	3421	ACTGCGCTAAGCTCAAGACATCTCCGGAGCTGATGAGGCCAACCGCCACAGCGACGGCGA	3480
Qy	3452	GAGCAGACACCAAGCAGCGCTGTCAACCGCGGTGTACGTCCCAAGGAGAGGAGGGGGCGCC	3511
Db	3481	GAGCAGACACCAAGCAGCGCTGTCAACCGCGGTGTACGTCCCAAGGAGAGGAGGGGGCGCC	3540
Qy	3512	CACACCAAGGCCGACACCGCTGGAGTCTGAGGCTGTAGTGAATGTTTGGCGSAGGCGTG	3571
Db	3541	CACACCAAGGCCGACACCGCTGGAGTCTGAGGCTGTAGTGAATGTTTGGCGSAGGCGTG	3600
Qy	3572	CATGTCGGGCTGAGAGGCTGAGTGTGCGGCTGAGGCTAGCGAGTGTCCAGCCAAAGGCT	3631
Db	3601	CATGTCGGGCTGAGAGGCTGAGTGTGCGGCTGAGGCTAGCGAGTGTCCAGCCAAAGGCT	3660
Qy	3632	GAGTGTCCAGACACATCGCGCTTTCACCTTCCCAAGGCTGGCGCTGAGCTCCACCCCA	3691
Db	3661	GAGTGTCCAGACACATCGCGCTTTCACCTTCCCAAGGCTGGCGCTGAGCTCCACCCCA	3720
Qy	3692	GGGGCAGCTTTTCCACACAGGAGCCGGGTTTCCACTCCCAATAGGAATAGTCCATCC	3751
Db	3721	GGGGCAGCTTTTCCACACAGGAGCCGGGTTTCCACTCCCAATAGGAATAGTCCATCC	3780
Qy	3752	CCAGATTGCGCAATTTTCAACCCCTGGCCGCGCTCTTTTCCCTTCAACCCCAACATCC	3811
Db	3781	CCAGATTGCGCAATTTTCAACCCCTGGCCGCGCTCTTTTCCCTTCAACCCCAACATCC	3840
Qy	3812	AGGTGAGACCCGAGAGGAGCCGTGGAGAGTGTGGAAATTTGGATGACCAAGAGTGTG	3871
Db	3841	AGGTGAGACCCGAGAGGAGCCGTGGAGAGTGTGGAAATTTGGATGACCAAGAGTGTG	3900
Qy	3872	CCCTGTACAGGCGAGACACCTGTGACCGGTGAGGGGGTCCCTGTGGGTCAAAATTGGGGG	3931
Db	3901	CCCTGTACAGGCGAGACACCTGTGACCGGTGAGGGGGTCCCTGTGGGTCAAAATTGGGGG	3960

[illegible]

Db	301	CCGAGTCTCTGAGAGGCTGTGTCCAGCCGCGCGGAAACAGTCTGCTTCCTGGCTTCGC	360
Qy	368	GCCTGCTGACGGGGCCCCGCGGGGGCCCCCGGAGGCTTTCACACACAGCTGGGCAAGTA	427
Db	361	GTCTGTGAGAGGGGCCCGCGGGGGCCCCCGGAGGCTTTCACACACAGCTGGGCAAGTA	420
Qy	428	CTGTGCCAAACAGGATGACGACGACACTGCGGGGGGAGCGGGGGCTGTGGGCTGTGCG	487
Db	421	CTGTGCCAAACAGGATGACGACGACACTGCGGGGGGAGCGGGGGCTGTGGGCTGTGCG	480
Qy	488	CCCGCTGTGGGAGACGACGTGCTGTTCACCTGTGTGACGCTGTGCGGCTGTGCTGTGCT	547
Db	481	CCCGCTGTGGGAGACGACGTGCTGTTCACCTGTGTGACGCTGTGCGGCTGTGCTGTGCT	540
Qy	548	GGGTCCACACTGGGCTTACCAAGGTGTGGGGGCGCGCGCTGTACCAAGCTTGGGCTGCCAC	607
Db	541	GGGTCCACACTGGGCTTACCAAGGTGTGGGGGCGCGCGCTGTACCAAGCTTGGGCTGCCAC	600
Qy	608	TCAAGCCCGGGCCCCCGCCACACGCTAGTGGACCCCGGAAGGCGTGGGATGGGAACGGGC	667
Db	601	TCAAGCCCGGGCCCCCGCCACACGCTAGTGGACCCCGGAAGGCGTGGGATGGGAACGGGC	660
Qy	668	CTGGAACCATTAACGTTCAGGAGAGCGGGGGTCCCTGTGGGCTGCCAGCCCGGGTGCAG	727
Db	661	CTGGAACCATTAACGTTCAGGAGAGCGGGGGTCCCTGTGGGCTGCCAGCCCGGGTGCAG	720
Qy	728	GAGGCGCGGGGGCACTGTCACCCGGAAGTCTGCGCTTGGCCGAAGAGCCCGAGGCTGGCG	787
Db	721	GAGGCGCGGGGGCACTGTCACCCGGAAGTCTGCGCTTGGCCGAAGAGCCCGAGGCTGGCG	780
Qy	788	TGCCCTGTAGCGCGGAGCGGACCGCCGTTGGGCAAGGGTCTCGGGCCACCGCGGCAAGAC	847
Db	781	TGCCCTGTAGCGCGGAGCGGAGCGCCGTTGGGCAAGGGTCTCGGGCCACCGCGGCAAGAC	840
Qy	848	GCGTGGACCGAGTACCGTGGTTTCTGTGTGTGTACCTGACCTGTGCAGACCGCGCGGAAGC	907
Db	841	GCGTGGACCGAGTACCGTGGTTTCTGTGTGTGTACCTGACCTGTGCAGACCGCGCGGAAGC	900
Qy	908	CACCTCTTTGGAGGGTGCCTCTGTGTGCACGCGCACTGCCACCATCCGTGGGCGCGCA	967
Db	901	CACCTCTTTGGAGGGTGCCTCTGTGTGCACGCGCACTGCCACCATCCGTGGGCGCGCA	960
Qy	968	GCACACAGCGGGCCCCCATATCAATATGCGGGCCACACAGTCCCTGGGACACGCTTGTCC	1027
Db	961	GCACACAGCGGGCCCCCATATCAATATGCGGGCCACACAGTCCCTGGGACACGCTTGTCC	1020
Qy	1028	CCGGGTGTAGCGCGGAGACCAAGACATTCTTACTCTTAGGCGACAAAGAGAGCTGTGC	1087
Db	1021	CCGGGTGTAGCGCGGAGACCAAGACATTCTTACTCTTAGGCGACAAAGAGAGCTGTGC	1080
Qy	1088	GCCCTCTTCTTACTAGCTCTGTGAGGCGCAAGCCGACTGTGGCGCTGTGAGCTGTGGA	1147
Db	1081	GCCCTCTTCTTACTAGCTCTGTGAGGCGCAAGCCGACTGTGGCGCTGTGAGCTGTGGA	1140
Qy	1148	GACCACTTTTGTGGTTTCCAGGCGCTGTATGTCAGAGGACTTCCCGCAGTTGCTCCGCGCT	1207
Db	1141	GACCACTTTTGTGGTTTCCAGGCGCTGTATGTCAGAGGACTTCCCGCAGTTGCTCCGCGCT	1200
Qy	1208	GCCCGAGCGCTACTGTGGCAAAATGCGGCGCTGTGTTCTGAGCTGCTTGGGAACAGCGCA	1267
Db	1201	GCCCGAGCGCTACTGTGGCAAAATGCGGCGCTGTGTTCTGAGCTGCTTGGGAACAGCGCA	1260
Qy	1268	GTGCGCTTACGGGGGTGCTCTTCAAAACGACATGCGCGGTGGAGGTGTGGGTACCCGAGC	1327
Db	1261	GTGCGCTTACGGGGGTGCTCTTCAAAACGACATGCGCGGTGGAGGTGTGGGTACCCGAGC	1320
Qy	1328	AGCGGTGTCTGTGCGCGGAGAAAGCCCAAGGCTGTGTGGCGGCCCCCGAGAGAGAGA	1387
Db	1321	AGCGGTGTCTGTGCGCGGAGAAAGCCCAAGGCTGTGTGGCGGCCCCCGAGAGAGAGA	1380
Qy	1388	CACAGACCCCGCTGTGCTGTGAGAGCTCTCGGACAGACAGCCCTGTGACGTTGTA	1447

Db	1381	CACGAGACCCCGTCGCTGCTGTCAGCTGCTCCGCCAGACACACAGACCCCTTG6CAGTGTGA	1440
QY	1448	CGGTTTCGTGCGGGGCTGCTGCTGCGCCGCGCTGGTGGCCCCAGGCTCTG6GGGCTCCAGCA	1507
Db	1441	CGGCTTCGTGCGGGGCTGCTGCTGCGCCGCGCTGGTGGCCCCAGGCTCTG6GGGCTCCAGCA	1500
QY	1508	CAACGAAGCGCGCTTGGCTCAGGAAACCAAGAATTCACTTCCTG6GGGAAGCATGCCAA	1567
Db	1501	CAACGAAGCGCGCTTGGCTCAGGAAACCAAGAAGTTCACTTCCTG6GGGAAGCATGCCAA	1560
QY	1568	GCTCTGCTGCAGAGAGACTGAGAAAGTGAAGTGCSTGTGGGAGACTGGCTTGGGCTGGCCAG	1627
Db	1561	GCTCTGCTGCAGAGAGACTGAGAAAGTGAAGTGCSTGTGGGAGACTGGCTTGGGCTGGCCAG	1620
QY	1628	GAGCCCCAGGGGGTTGGCTGTGTTCCGGCCGACAGACACCCTGTGCTGAGAGAGATCCGCGC	1687
Db	1621	GAGCCCCAGGGGGTTGGCTGTGTTCCGGCCGACAGACACCCTGTGCTGAGAGAGATCCGCGC	1680
QY	1688	CAAGTTCCTGCATCGCTGCTGATGAGTGTACGTGTGAGAGTGGTCAAGGCTTTCTTTTA	1747
Db	1681	CAAGTTCCTGCATCGCTGCTGATGAGTGTACGTGTGAGAGTGGTCAAGGCTTTCTTTTA	1740
QY	1748	TGTCACGAGACACACGTTTCAAAAAGACAGGCTTTTTCCTACCGGAAGATGTCTGGAG	1807
Db	1741	TGTCACGAGACACACGTTTCAAAAAGACAGGCTTTTTCCTACCGGAAGATGTCTGGAG	1800
QY	1808	CAAGTTCGAAAGCATTTGGAAATCACAAGCACTTGAAGAGGTCACCTGGCGGAGCTGTC	1867
Db	1801	CAAGTTCGAAAGCATTTGGAAATCACAAGCACTTGAAGAGGTCACCTGGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGCCGCGCTGCTACGCTCCAGACTCGC	1927
Db	1861	GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGCCGCGCTGCTACGCTCCAGACTCGC	1920
QY	1928	CTTATATCCCCAAGCGCTGACGGGGTGGCGCGGATTGTGAACATGAGACTACGTGTTGGAGC	1987
Db	1921	CTTATATCCCCAAGCGCTGACGGGGTGGCGCGGATTGTGAACATGAGACTACGTGTTGGAGC	1980
QY	1988	CAGAACCTTCGCGAGAAAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT	2047
Db	1981	CAGAACCTTCGCGAGAAAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT	2040
QY	2048	CAGCGTCTCAACTACGAGAGGGGGCGGGGGCCCGGCGCTCTG6GGCGCTGTGCTGGG	2107
Db	2041	CAGCGTCTCAACTACGAGAGGGGGCGGGGGCCCGGCGCTCTG6GGCGCTGTGCTGGG	2100
QY	2108	CTTGAGCATATCCACAGGGGCTTGCGGCACCTCTGTGTGGGTGCGGGGCCAGAGACC	2167
Db	2101	CTTGAGCATATCCACAGGGGCTTGCGGCACCTCTGTGTGGGTGCGGGGCCAGAGACC	2160
QY	2168	GCCGCGTGAAGCTGA-----CATCCCCA	2191
Db	2161	GCCGCGTGAAGCTGTACTTTGTCAAGGTGAGTGTACGGGCGCTGACAGACACATCCCCCA	2220
QY	2192	GGACAGGCTACAGGAGGTATCGCCAGCATATCAAAACCCAGAAACAGTACTGGCGG	2251
Db	2221	GGACAGGCTACAGGAGGTATCGCCAGCATATCAAAACCCAGAAACAGTACTGGCGG	2280
QY	2252	TGGGATATGCGGTGTGCCAAGAGCGCGCCATGGGCACGTCCGCAAGGCGCTTCAAGAGCCA	2311
Db	2281	TGGGATATGCGGTGTGCCAAGAGCGCGCCATGGGCACGTCCGCAAGGCGCTTCAAGAGCCA	2340
QY	2312	CGTCTCTACCTTGAACAGACCTCCAGCGGTATCATCCGACCACTTGTGGCTCACTGCAGGA	2371
Db	2341	CGTCTCTACCTTGAACAGACCTCCAGCGGTATCATCCGACCACTTGTGGCTCACTGCAGGA	2400
QY	2372	GACCAAGCCGCTGAGAGATGCCGTGATCATGAGCAGAGCTCTCCCTGAATATAGGCCAG	2431
Db	2401	GACCAAGCCGCTGAGAGATGCCGTGATCATGAGCAGAGCTCTCCCTGAATATAGGCCAG	2460
QY	2432	CAGTGGCGCTTTCGACAGCTTCCACACCTTCAATGTGCACACAGCGCTGCGCATAGGGG	2491
Db	2461	CAGTGGCGCTTTCGACAGCTTCCACACCTTCAATGTGCACACAGCGCTGCGCATAGGGG	2520

Qy	2492	CAAGCTCTAGCTCAGATGACGAGGGAATCCCGAGAGGCTCCCTCCCTCAACGCTGCTG	2513
Db	2521	CAGGCTCTAGCTCAGATGACGAGGGAATCCCGAGAGGCTCCCTCCCTCAACGCTGCTG	2580
Qy	2552	CAGCCTGTGTATCGGCGACATGGAGAAACAAGTGTGTGGGGGATTCGGCGGACGGCT	2611
Db	2581	CAGCCTGTGTATCGGCGACATGGAGAAACAAGTGTGTGGGGGATTCGGCGGAGGGCT	2640
Qy	2612	GCTCCTGCGTTTGTGTGATGATTTCTTTGTGTGACACCTCACTCAACCCACGCGAAAC	2671
Db	2641	GCTCCTGCGTTTGTGTGATGATTTCTTTGTGTGACACCTCACTCAACCCACGCGAAAC	2700
Qy	2672	CTTCTCTAGGACCTCTGTGCGAGGTGCTCTGTAGATGATGCTGTGCGTGTGAACCTTCGGA	2731
Db	2701	CTTCTCTAGGACCTCTGTGCGAGGTGCTCTGTAGATGATGCTGTGCGTGTGAACCTTCGGA	2760
Qy	2732	GACAGTGTGAACCTTCCCTGTAGAAAGACGAGGCTCGTGGTGTGACGGCTTTTGTTCAGT	2791
Db	2761	GACAGTGTGAACCTTCCCTGTAGAAAGACGAGGCTCGTGGTGTGACGGCTTTTGTTCAGT	2820
Qy	2792	GCGGCGCCACGAGGCTATTCCCTGTGCGGCGCTGCTCTGTGATACCGGACCCGTGAGGT	2851
Db	2821	GCGGCGCCACGAGGCTATTCCCTGTGCGGCGCTGCTCTGTGATACCGGACCCGTGAGGT	2880
Qy	2852	GCAAGAGCACTATCTCAGCTATGCGCGGACCTCCATAGAGCACTCAGCTTCACCTCAACG	2911
Db	2881	GCAGAGCACTATCTCAGCTATGCGCGGACCTCCATAGAGCACTCAGCTTCACCTCAACG	2940
Qy	2912	GCGCTCAAGGCGGGGAGAAACATGCTGTGCAACTCTTGTGGGTCCTTGGCGCTGAAGG	2971
Db	2941	GCGCTCAAGGCGGGGAGAAACATGCTGTGCAACTCTTGTGGGTCCTTGGCGCTGAAGG	3000
Qy	2972	TCAGAGGCTGTTCGTGATTTGCAGGTGAACAGCTCTCAAGCGGTGTGCACCAACTCA	3031
Db	3001	TCAGAGGCTGTTCGTGATTTGCAGGTGAACAGCTCTCAAGCGGTGTGCACCAACTCA	3060
Qy	3032	CAGATCTCTCTGTGTGCAAGGCTTACGCAATGTGTGTCTGAGCTCCCAATTTCA	3091
Db	3061	CAGATCTCTCTGTGTGCAAGGCTTACGCAATGTGTGTCTGAGCTCCCAATTTCA	3120
Qy	3092	TCAGCAAGTTTGGAGAAACCCCAATTTTTCTCGCGGTATCTGTGACAGGCTCCCT	3151
Db	3121	TCAGCAAGTTTGGAGAAACCCCAATTTTTCTCGCGGTATCTGTGACAGGCTCCCT	3180
Qy	3152	CTGCTACTCCATCTCGAAAGCGCAAGACGACAGGANTCTCCTGTGGGGCGCAAGGCGCCGC	3211
Db	3181	CTGCTACTCCATCTCGAAAGCGCAAGACGACAGGANTCTCCTGTGGGGCGCAAGGCGCCGC	3240
Qy	3212	CGGCGCTCTCCCTCGAGGCGCTGTGAGTGGCTGTGCACAAGAATTCCTGCTCAAGCT	3271
Db	3241	CGGCGCTCTCCCTCGAGGCGCTGTGAGTGGCTGTGCACAAGAATTCCTGCTCAAGCT	3300
Qy	3272	GACTGTGACACCGGTGACCTTACGCGCACTCTCGTGGGGTCACTAGAGACAGCCAGACGA	3331
Db	3301	GACTGTGACACCGGTGACCTTACGCGCACTCTCGTGGGGTCACTAGAGACAGCCAGACGA	3360
Qy	3332	GCTGAGTGTGGAAGCTCCGCGGGAGACAGCTGATCTGCTGTGGAGGCGCGAGCAACCGCGC	3391
Db	3361	GCTGAGTGTGGAAGCTCCGCGGGAGACAGCTGATCTGCTGTGGAGGCGCGAGCAACCGCGC	3420
Qy	3392	ACTGCTCTGAGCTTCAAGACATCTGTGACTGATGCGCACCCGCCACAGCTAGCGGCGA	3451
Db	3421	ACTGCTCTGAGCTTCAAGACATCTGTGACTGATGCGCACCCGCCACAGCTAGCGGCGA	3480
Qy	3452	GAGCAGACACAGACGCTGTCTACCGCGGGCTCTACGTCCAGGAGAGGAGGGGCGGCT	3511
Db	3481	GAGCAGACACACAGCCTGTCTACCGCGGGCTCTACGTCCAGGAGAGGAGGGGCGGCT	3540
Qy	3512	CACACCCAGGCGCGACGCTGTGAGTCTGAGGCTTGAAGTGTGTGTGGCGAGGCGCTG	3571
Db	3541	CACACCCAGGCGCGACGCTGTGAGTCTGAGGCTTGAAGTGTGTGTGGCGAGGCGCTG	3600

QY	3572	CATGCGCGCTGAAGCTGATGTGCGCGCTGAGGCGCTGACGAGTGTACCACTGAAGGCT	3613
Dp	3601	CATGCGCGCTGAAGCTGATGTGCGCGCTGAGGCGCTGACGAGTGTACCACTGAAGGCT	3660
QY	3632	GAGGTGCACACACCTGCGCTTTCACCTTCCCAACAGGTGGCGTGGGTCCACCCCA	3691
Dp	3661	GAGGTGCACACACCTGCGCTTTCACCTTCCCAACAGGTGGCGTGGGTCCACCCCA	3720
QY	3692	GGGCGACGTTTCTCTACACAGAGACCGGCGTTCCACGTCCCAATGAGATATGTCATC	3751
Dp	3721	GGGCGACGTTTCTCTACACAGAGACCGGCGTTCCACGTCCCAATGAGATATGTCATC	3780
QY	3752	CCAGTTTCGGCATTTGTTCACCCCTGGCCCTCTTGGCTTCACACCCCACTCC	3811
Dp	3781	CCAGTTTCGGCATTTGTTCACCCCTGGCCCTCTTGGCTTCACACCCCACTCC	3840
QY	3812	ACGTGAGACCCGAGAGAGACCTGGGAGCTGTGGAAATTTGATGATACCAAGGTG	3871
Dp	3841	ACGTGAGACCCGAGAGAGACCTGGGAGCTGTGGAAATTTGATGATACCAAGGTG	3900
QY	3872	CCCTGTACACAGGCGAGGACCTGTGCACCTGTGATGGGGGTCCGTGGGTCAAAATTTGGGG	3933
Dp	3901	CCCTGTACACAGGCGAGGACCTGTGCACCTGTGATGGGGGTCCGTGGGTCAAAATTTGGGG	3960
QY	3932	GAGGTGCTGTGGGAGTAAATTACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA	3986
Dp	3961	GAGGTGCTGTGGGAGTAAATTACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA	4015

```

RESULT 8
US-09-675-321-1
Sequence 1, Application US/09675321
Patent No. 6440735
GENERAL INFORMATION:
Applicant: Gaeta, Federico C.A.
Applicant: Genon Corporation
TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
Response to a Telomerase Antigen
FILE REFERENCE: 015389-003500pc
CURRENT APPLICATION NUMBER: US/09/675,321
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/112,006
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: WO PCT/US99/06898
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (56)..(3454)
OTHER INFORMATION: human telomerase reverse transcriptase (hTRT)
US-09-675-321-1

```

Query Match	Similarity	99.1%	Score	3969	DB 4	Length	4015
Best Local	Similarity	99.1%	Pred. No	8e-225			
Matches	3979	Conservative	0	Mismatches	0	Indels	36
						Gaps	1
QY	8	GCACGCTGCTCTCTCTGTCGCACTGGGAAAGCCCTGACCCCGGCACACCCCGATGCC	67				
Db	1	GCACGCTGCTCTCTCTGTCGCACTGGGAAAGCCCTGACCCCGGCACACCCCGATGCC	60				
QY	68	GCAGCTCCCGCGTCCGCGAGCCGCTGCTCTCTGTCGCGACGCCACTACCGCGAGTGCT	127				
Db	61	GCAGCTCCCGCGTCCGCGAGCCGCTGCTCTCTGTCGCGACGCCACTACCGCGAGTGCT	120				
QY	128	GCCGCTGACCACTGTCGTGGTGGGACCTGAGGGACCTCGAGGAGCTGTGTGACAGCGG	187				
Db	121	GCCGCTGACCACTGTCGTGGTGGGACCTCGAGGGACCTCGAGGAGCTGTGTGACAGCGG	180				

QY 188 GACCCGCGGCTTCCGCGCGCTGTGGCCAGTGCCTGTGTGCTGCTGCGTGCCTGGAGCG 247
Db 181 GGACCCGCGGCTTCCGCGCGCTGTGGCCAGTGCCTGTGTGCTGCTGCGTGCCTGGAGCG 240
QY 248 ACGGCCGCGGCTTCCGCGCGCTGTGGCCAGTGCCTGTGTGCTGCTGCGTGCCTGGAGCG 240
Db 241 ACGGCCGCGGCTTCCGCGCGCTGTGGCCAGTGCCTGTGTGCTGCTGCGTGCCTGGAGCG 307
QY 308 CCGAGTCTCAGAGGCTGTGGAGCGCGCGCGAGAAAGTGTGCTGCTGCGTGCCTGGAGCG 307
Db 301 CCGAGTCTCAGAGGCTGTGGAGCGCGCGCGAGAAAGTGTGCTGCTGCGTGCCTGGAGCG 360
QY 368 GCTGCTGGAGCG 427
Db 361 GCTGCTGGAGCG 427
QY 428 CCGCCCAACACAGTGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 487
Db 421 CCGCCCAACACAGTGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 488 CCGCTGGAGCG 547
Db 481 CCGCTGGAGCG 540
QY 548 GCGTCCACAGTGTGGAGCG 607
Db 541 GCGTCCACAGTGTGGAGCG 600
QY 608 TCAGCCG 667
Db 601 TCAGCCG 660
QY 668 CTGGAACCATAGAGTGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
Db 661 CTGGAACCATAGAGTGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 728 GAGGCG 787
Db 721 GAGGCG 780
QY 788 TGCCCTGAGCG 847
Db 781 TGCCCTGAGCG 840
QY 848 GCGTGGAGCG 907
Db 841 GCGTGGAGCG 900
QY 908 CACCTCTTGGAGGCTGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 967
Db 901 CACCTCTTGGAGGCTGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
QY 968 GCGACACG 1027
Db 961 GCGACACG 1020
QY 1028 CCGGCTGTACG 1087
Db 1021 CCGGCTGTACG 1080
QY 1088 GCGCT 1147
Db 1081 GCGCT 1140
QY 1148 GACCATCTTCT 1207
Db 1141 GACCATCTTCT 1200
QY 1208 GCGCCAGCGCTGTGGAGCG 1267
Db 1201 GCGCCAGCGCTGTGGAGCG 1260
QY 1268 GTGGCGCTTACGCGCGCTGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1327

Db 1261 GTGGCGCTTACGCGCGCTGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
QY 1328 AGCCGCTGTGTGCG 1387
Db 1321 AGCCGCTGTGTGCG 1380
QY 1388 CACAGACCG 1447
Db 1381 CACAGACCG 1440
QY 1448 CCGCTGTGTGCG 1507
Db 1441 CCGCTGTGTGCG 1500
QY 1508 CAAGCAAGCGCGCTTCT 1567
Db 1501 CAAGCAAGCGCGCTTCT 1560
QY 1568 GCTCTGCTGTGCG 1627
Db 1561 GCTCTGCTGTGCG 1620
QY 1628 GACCCGCGGCTGTGTGCG 1687
Db 1621 GACCCGCGGCTGTGTGCG 1680
QY 1688 CAAGTCTGTGCG 1747
Db 1681 CAAGTCTGTGCG 1740
QY 1748 TGTCACGCGGAGCG 1807
Db 1741 TGTCACGCGGAGCG 1800
QY 1808 CAAGTCTGTGCG 1867
Db 1801 CAAGTCTGTGCG 1860
QY 1868 GGAACCAAGGCTGTGCG 1927
Db 1861 GGAACCAAGGCTGTGCG 1920
QY 1928 CTTCATCCCAAGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1987
Db 1921 CTTCATCCCAAGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1980
QY 1988 CAGAAGCG 2047
Db 1981 CAGAAGCG 2040
QY 2048 CAGCGTCTCACTACGAGCG 2107
Db 2041 CAGCGTCTCACTACGAGCG 2100
QY 2108 CTTGGAGATATCAACAGCG 2167
Db 2101 CTTGGAGATATCAACAGCG 2160
QY 2168 GCGCGCTGAGCTGTGCG 2191
Db 2161 GCGCGCTGAGCTGTGCG 2190
QY 2192 GCGACAGCTGTGCG 2251
Db 2221 GCGACAGCTGTGCG 2280
QY 2252 TCGGTATGCG 2311
Db 2281 TCGGTATGCG 2340
QY 2312 GCTCTACCTGTGAGAGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2371

Db 2341 GCTCTTACCTTACAGACCTTCACAGCCGCTACATGAGACATGTCGGCTCAGCTGACAGA 2400
QY 2372 GACACAGCCCGCTAGAGGATGCCCTGCTACATGAGAGAGAGCTCCCTCCATATGAGAGCA 2431
Db 2401 GACACAGCCCGCTAGAGGATGCCCTGCTACATGAGAGAGAGCTCCCTCCATATGAGAGCA 2460
QY 2432 GAGTGGCCCTTTCAGAGCTTTCCTTACAGCTTCATGTCACACAGCCGCTGAGCATAGAGG 2491
Db 2461 GAGTGGCCCTTTCAGAGCTTTCCTTACAGCTTCATGTCACACAGCCGCTGAGCATAGAGG 2520
QY 2492 CAAGTCTACCTCCAGTGGCCAGAGGATCCGCAAGGCTCATCTCTCCACAGCTCTCTG 2551
Db 2521 CAAGTCTACCTCCAGTGGCCAGAGGATCCGCAAGGCTCATCTCTCCACAGCTCTCTG 2580
QY 2552 GAGCTGTCTACAGGAGCATGAGAGACAGCTGTTTGGGGGATTTGGGGGAGGCT 2611
Db 2581 GAGCTGTCTACAGGAGCATGAGAGACAGCTGTTTGGGGGATTTGGGGGAGGCT 2640
QY 2612 GCTCTGAGCTTTCAGAGCTTTCCTTACAGCTTCATGTCACACAGCTCAGCCAGCAAC 2671
Db 2641 GCTCTGAGCTTTCAGAGCTTTCCTTACAGCTTCATGTCACACAGCTCAGCCAGCAAC 2700
QY 2672 CTCTCTACAGACCTTCAGTGGAGGCTCCCTGATGATGCTGCTGATGATGCTGATGATG 2731
Db 2701 CTCTCTACAGACCTTCAGTGGAGGCTCCCTGATGATGCTGCTGATGATGCTGATGATG 2760
QY 2732 GACAGTGTACACTTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2791
Db 2761 GACAGTGTACACTTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2820
QY 2792 GCGGAGCCAGGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTAC 2851
Db 2821 GCGGAGCCAGGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTAC 2880
QY 2852 GCAGAGGAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAG 2911
Db 2881 GCAGAGGAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAG 2940
QY 2912 CGGCTTCAAGGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTAC 2971
Db 2941 CGGCTTCAAGGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTAC 3000
QY 2972 TCACAGCCGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTAC 3031
Db 3001 TCACAGCCGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTAC 3060
QY 3032 CAAGATCTCTCTGCTGAGGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAG 3091
Db 3061 CAAGATCTCTCTGCTGAGGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAG 3120
QY 3092 TCAGCAAGTTTGAAGAACCCCAATTTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 3151
Db 3121 TCAGCAAGTTTGAAGAACCCCAATTTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 3180
QY 3152 CTGCTACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3211
Db 3181 CTGCTACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3240
QY 3212 CGGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3271
Db 3241 CGGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
QY 3272 GAGTGTACAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTAC 3331
Db 3301 GAGTGTACAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTAC 3360
QY 3332 GGTGTGTGAGAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTAC 3391
Db 3361 GGTGTGTGAGAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTAC 3420
QY 3392 ACTGCTCTGAGACTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTAC 3451
Db 3421 ACTGCTCTGAGACTTTCCTTACAGCTTTCCTTACAGCTTTCCTTACAGCTTTCCTTAC 3480

QY 3452 GAGCAGACACAGAGCCCTGCTACAGCCGCTCTACGTCAGAGGAGAGGAGGAGGAGGAGG 3511
Db 3481 GAGCAGACACAGAGCCCTGCTACAGCCGCTCTACGTCAGAGGAGAGGAGGAGGAGGAGG 3540
QY 3512 CACACAGAGCCCGAGAGCCGCTGAGAGCTTACAGCTTACAGCTTACAGCTTACAGCTT 3571
Db 3541 CACACAGAGCCCGAGAGCCGCTGAGAGCTTACAGCTTACAGCTTACAGCTTACAGCTT 3600
QY 3572 CATGTCGCTGAGAGCTTACAGCTTACAGCTTACAGCTTACAGCTTACAGCTTACAG 3631
Db 3601 CATGTCGCTGAGAGCTTACAGCTTACAGCTTACAGCTTACAGCTTACAGCTTACAG 3660
QY 3632 GAGTGTACAGACCTGCTGCTTACAGCTTACAGCTTACAGCTTACAGCTTACAGCTT 3691
Db 3661 GAGTGTACAGACCTGCTGCTTACAGCTTACAGCTTACAGCTTACAGCTTACAGCTT 3720
QY 3692 GGGCCAGCTTTCCTACAGAGAGCCGCTGCTTACAGCTTACAGCTTACAGCTTACAG 3751
Db 3721 GGGCCAGCTTTCCTACAGAGAGCCGCTGCTTACAGCTTACAGCTTACAGCTTACAG 3780
QY 3752 CCAGATTCGCTTTCCTACAGAGAGCCGCTGCTTACAGCTTACAGCTTACAGCTTAC 3811
Db 3781 CCAGATTCGCTTTCCTACAGAGAGCCGCTGCTTACAGCTTACAGCTTACAGCTTAC 3840
QY 3812 AGGTGTACAGCTTACAGAGAGCCGCTGCTTACAGCTTACAGCTTACAGCTTACAG 3871
Db 3841 AGGTGTACAGCTTACAGAGAGCCGCTGCTTACAGCTTACAGCTTACAGCTTACAG 3900
QY 3872 CCCGTACACAGAGAGAGCCGCTGCTTACAGCTTACAGCTTACAGCTTACAGCTTACAG 3931
Db 3901 CCCGTACACAGAGAGAGCCGCTGCTTACAGCTTACAGCTTACAGCTTACAGCTTACAG 3960
QY 3932 GAGTGTGTGAGAGTAAATACGATATATGATGATGATGATGATGATGATGATGATG 3986
Db 3961 GAGTGTGTGAGAGTAAATACGATATATGATGATGATGATGATGATGATGATGATG 4015

RESULT 9
US-09-052-919-1
Sequence 1, Application US/09052919
Patent No. 6444650
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hailey, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Inhibiting Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,919
FILING DATE: 31-MAR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:

Db 2813 GATGCGGCGCCAGCGCTATTCCCTGTGGGGCTGTCTGTGATACCGCGACCTTGA 2872
Qy 2849 GGTGACAGAGGACACTACCCAGCTATGCCCCGAGCTCATAGAGCCAGTCTCACTTCA 2908
Db 2873 GGTGACAGAGGACACTACCCAGCTATGCCCCGAGCTCATAGAGCCAGTCTCACTTCA 2932
Qy 2909 CCGGGGCTTCAAGGCTGGGAGAAACATGCTGCGAAACCTTTGGGGCTGTGGGGCTGA 2968
Db 2933 CCGGGGCTTCAAGGCTGGGAGAAACATGCTGCGAAACCTTTGGGGCTGTGGGGCTGA 2992
Qy 2969 GTGTACAGCGCTTTTCTGTGATTTGCAAGTGAACAGCTTCCAGAGCGTGTGACCAACAT 3028
Db 2993 GTGTACAGCGCTTTTCTGTGATTTGCAAGTGAACAGCTTCCAGAGCGTGTGACCAACAT 3052
Qy 3029 CTACAGATCTCTCTGTGAGGCTACAGAGTTTACGATGTGCTGAGTCTGAGTCTCAT 3088
Db 3053 CTACAGATCTCTCTGTGAGGCTACAGAGTTTACGATGTGCTGAGTCTGAGTCTCAT 3112
Qy 3089 TCATCAGCAAGTTTGGAGAAACCCACATTTTCTGCGGTACATCTGTGACAGGCTTC 3148
Db 3113 TCATCAGCAAGTTTGGAGAAACCCACATTTTCTGCGGTACATCTGTGACAGGCTTC 3172
Qy 3149 CCTCTGCTACTCTCATCTTAAAGCCAGAGAGGATGTGCTGGGGCCAGAGGCGC 3208
Db 3173 CCTCTGCTACTCTCATCTTAAAGCCAGAGAGGATGTGCTGGGGCCAGAGGCGC 3232
Qy 3209 CCGCGGCTCTGCGCTCCGAGGCGGTGAGTGTGCTGTGACCAAGATTTCTGCTCA 3268
Db 3233 CCGCGGCTCTGCGCTCCGAGGCGGTGAGTGTGCTGTGACCAAGATTTCTGCTCA 3292
Qy 3269 GCTGACTGACACGCTGTACACTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3328
Db 3293 GCTGACTGACACGCTGTACACTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3352
Qy 3329 GAGCTGAGTGGAAAGTCTCCGGGAGACGCTGACTGCTGAGAGCGCGCAACCC 3388
Db 3353 GAGCTGAGTGGAAAGTCTCCGGGAGACGCTGACTGCTGAGAGCGCGCAACCC 3412
Qy 3389 GAGCTGAGTGGAAAGTCTCCGGGAGACGCTGACTGCTGAGAGCGCGCAACCC 3448
Db 3413 GAGCTGAGTGGAAAGTCTCCGGGAGACGCTGACTGCTGAGAGCGCGCAACCC 3472
Qy 3449 CGAGAGCAGACACAGAGCCCTGTACAGCGCGCTGTACGTCTCCAGAGAGGAGGCG 3508
Db 3473 CGAGAGCAGACACAGAGCCCTGTACAGCGCGCTGTACGTCTCCAGAGAGGAGGCG 3532
Qy 3509 GCGCCACACCCAGCGCGCGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAG 3568
Db 3533 GCGCCACACCCAGCGCGCGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAG 3592
Qy 3569 CTGATCTCCGGCTGAAGGCTGAGTGTGCGGCTGAGAGCTGTGAGAGCTGTGAGAG 3628
Db 3593 CTGATCTCCGGCTGAAGGCTGAGTGTGCGGCTGAGAGCTGTGAGAGCTGTGAGAG 3652
Qy 3629 GCTGAGTGTCCAGACACCGCGCTGTACCTTCCACAGGCTGTGAGAGCTGTGAGAG 3688
Db 3653 GCTGAGTGTCCAGACACCGCGCTGTACCTTCCACAGGCTGTGAGAGCTGTGAGAG 3712
Qy 3689 CCAAGGCGAGCTTTCTTCCACAGAGCGGCTTCCACTCCCAATGGAATATCTCA 3748
Db 3713 CCAAGGCGAGCTTTCTTCCACAGAGCGGCTTCCACTCCCAATGGAATATCTCA 3772
Qy 3749 TCCCGAGATTTCCGATTTTACCTTCCCTGCTGCTTGTGCTTCCACCCACCA 3808
Db 3773 TCCCGAGATTTCCGATTTTACCTTCCCTGCTGCTTGTGCTTCCACCCACCA 3832
Qy 3809 TCCAGTGGAGACCTGTGAGAGAGCCCTGGAGCTGTGAGATTTGGAATGACCAAGT 3868
Db 3833 TCCAGTGGAGACCTGTGAGAGAGCCCTGGAGCTGTGAGATTTGGAATGACCAAGT 3892
Qy 3869 GTGCGCTGTACACAGGCGAGGACCTGTGACCTGATGAGGAGTCTGCTGTGCTCAATGG 3928
Db 3893 GTGCGCTGTACACAGGCGAGGACCTGTGACCTGATGAGGAGTCTGCTGTGCTCAATGG 3952

Qy 3929 GGGAGGCTGCTGGAGTAAATATGATATATGACTTTTTCAGTTTGA 3988
Db 3953 GGGAGGCTGCTGGAGTAAATATGATATATGACTTTTTCAGTTTGA 4012
Qy 3989 AAAAAAAAAAAAAA 4005
Db 4013 AAAAAAAAAAAAAA 4029

RESULT 11
US-08-974-549A-292
Sequence 292, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cecb, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429


```
QY 1865 GTCCGAGACAGAGGTCAGGACGATCCGGAGAACAGGCGCCCTGCTGAGCTCCAGACT 1924
    |||||
Db 1853 GTCCGAGACAGAGGTCAGGACGATCCGGAGAACAGGCGCCCTGCTGAGCTCCAGACT 1912
QY 1925 CCGCTTCATCCCAAGGCTGACGGGCTGCGGCCGATTGTGAACATGAGACTACGTCGTGGG 1984
    |||||
Db 1913 CCGCTTCATCCCAAGGCTGACGGGCTGCGGCCGATTGTGAACATGAGACTACGTCGTGGG 1972
QY 1985 AGCCAGAACGTTCCGAGAGAGAGAGAGAGGCGCCGAGCGTCTACCTCGAGGGTGAAGGACT 2044
    |||||
Db 1973 AGCCAGAACGTTCCGAGAGAGAGAGAGAGGCGCCGAGCGTCTACCTCGAGGGTGAAGGACT 2032
QY 2045 GTTACAGGCTGCTCACTACGAGCGGGGCGCGGCCCGCGCTCTGGGGGCTCTGTGCT 2104
    |||||
Db 2033 GTTACAGGCTGCTCACTACGAGCGGGGCGCGGCCCGCGCTCTGTGGGCTCTGTGCT 2092
QY 2105 GGGCTCGAGAGATATCCACAGAGGCGCTGCGCCACCTTGTGCTGCTGCTGCGGGCCAGGA 2164
    |||||
Db 2093 GGGCTCGAGAGATATCCACAGAGGCGCTGCGCCACCTTGTGCTGCTGCTGCGGGCCAGGA 2152
QY 2165 CCGCGCGCTGAGCTGTA-----CATCCC 2188
    |||||
Db 2153 CCGCGCGCTGAGCTGTA-----CATCCC 2112
QY 2189 CCAGGACAGGCTACGAGGAGTCTATGCCAGCATCAAAACCCAGAGACGCTACTGCGT 2248
    |||||
Db 2213 CCAGGACAGGCTACGAGGAGTCTATGCCAGCATCAAAACCCAGAGACGCTACTGCGT 2272
QY 2249 GCGTCGCTATGCGCTGCTGCTCAGAGAGGCGCCCATGCGGCGAGCTCCGAGGCTTAAAG 2308
    |||||
Db 2273 GCGTCGCTATGCGCTGCTGCTCAGAGAGGCGCCCATGCGGCGAGCTCCGAGGCTTAAAG 2332
QY 2309 CCAGCTCTACTCTGACAGACCTCCAGCGCTACATGCGACAGTTCGTGGCTCACTGCA 2368
    |||||
Db 2333 CCAGCTCTACTCTGACAGACCTCCAGCGCTACATGCGACAGTTCGTGGCTCACTGCA 2392
QY 2369 GAGAGACAGCCCGCTGAGGAGTGCCTGCTCATGAGCAGAGCTCTCCCTGATGAGGC 2428
    |||||
Db 2393 GAGAGACAGCCCGCTGAGGAGTGCCTGCTCATGAGCAGAGCTCTCCCTGATGAGGC 2452
QY 2429 CAGCAGTGGGCTCTGACAGCTTCTTACGCTTCACTGTGCCACAGCGCTGCCATCAG 2488
    |||||
Db 2453 CAGCAGTGGGCTCTGACAGCTTCTTACGCTTCACTGTGCCACAGCGCTGCCATCAG 2512
QY 2489 GGGCAAGTCTACAGTCCAGTCCAGAGGATCCCGAGGCGCTCAATCCCTTCCAGCTGCT 2548
    |||||
Db 2513 GGGCAAGTCTACAGTCCAGTCCAGAGGATCCCGAGGCGCTCAATCCCTTCCAGCTGCT 2572
QY 2549 CTGCAAGCTGCTGACAGGCGCATGAGAGAACAGCTGTTGCGGGGATGCGCGGAGCG 2608
    |||||
Db 2573 CTGCAAGCTGCTGACAGGCGCATGAGAGAACAGCTGTTGCGGGGATGCGCGGAGCG 2632
QY 2609 GCTGCTCTGCTGCTGCTGATGATTTCTTGTGGTACACCTTCACTCCACCGGAA 2668
    |||||
Db 2633 GCTGCTCTGCTGCTGCTGATGATTTCTTGTGGTACACCTTCACTCCACCGGAA 2692
QY 2669 AACCTTCTCAGAGACCTGCTGCGAGGTGCTCCCTGAGTATGCTGCTGCTGCTGCTGCT 2728
    |||||
Db 2693 AACCTTCTCAGAGACCTGCTGCGAGGTGCTCCCTGAGTATGCTGCTGCTGCTGCTGCT 2752
QY 2729 GAAGACAGTGTGATGATGCTGCTGTAAGAGCAGAGCGCTGCTGCTGCTGCTGCTGCTGCT 2788
    |||||
Db 2753 GAAGACAGTGTGATGATGCTGCTGTAAGAGCAGAGCGCTGCTGCTGCTGCTGCTGCTGCT 2812
QY 2789 GATGCGGCGCCACAGGCTATTCCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 2848
    |||||
Db 2813 GATGCGGCGCCACAGGCTATTCCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 2872
QY 2849 GGTGAGAGAGGACTACTCCAGCTATGCTCCGAGCTCCATCAGAGCAGTCTCACTTCAA 2908
    |||||
Db 2873 GGTGAGAGAGGACTACTCCAGCTATGCTCCGAGCTCCATCAGAGCAGTCTCACTTCAA 2932
QY 2909 CCGCGGCTTCAAGGCTGGAGAGAACATGCTGCAAACTCTTTGGGCTTTGGCGGTAA 2968
    |||||
Db 2933 CCGCGGCTTCAAGGCTGGAGAGAACATGCTGCAAACTCTTTGGGCTTTGGCGGTAA 2992
QY 2969 GTGTCAACAGCTGTTTCTGATTTTCTGAGGTGAACAGCCCTCCAGAGAGTGTGCACCAAT 3028
    |||||
Db 2993 GTGTCAACAGCTGTTTCTGATTTTCTGAGGTGAACAGCCCTCCAGAGAGTGTGCACCAAT 3052
QY 3029 CTACAGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3088
    |||||
Db 3053 CTACAGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3112
QY 3089 TCATCAGCAAGTTTGAAGAACCCACATTTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 3148
    |||||
Db 3113 TCATCAGCAAGTTTGAAGAACCCACATTTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 3172
QY 3149 CCGTGTCTACTCTCACTCTGAAAGCCAGAGACGAGGATGCTGCTGCGGCGCAAGGCGCG 3208
    |||||
Db 3173 CCGTGTCTACTCTCACTCTGAAAGCCAGAGACGAGGATGCTGCTGCGGCGCAAGGCGCG 3232
QY 3209 CGCGGCGCTTGCCTTCCGAGGCGTGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3268
    |||||
Db 3233 CGCGGCGCTTGCCTTCCGAGGCGTGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3292
QY 3269 GCTGACTGACACCGCTGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3328
    |||||
Db 3293 GCTGACTGACACCGCTGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3352
QY 3329 GCACCTAGTGTGAGAGTCCCGGGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3388
    |||||
Db 3353 GCACCTAGTGTGAGAGTCCCGGGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3412
QY 3389 GGCACCTGCTGACACTTCAAGACATCTGAGTATGAGGCGCACCGGCGCACAGGCGAG 3448
    |||||
Db 3413 GGCACCTGCTGACACTTCAAGACATCTGAGTATGAGGCGCACCGGCGCACAGGCGAG 3472
QY 3449 CGAGAGCAGACACAGAGCGCTGCTACAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3508
    |||||
Db 3473 CGAGAGCAGACACAGAGCGCTGCTACAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3532
QY 3509 GCCCAGACCCAGGCGCGCACCGCTGAGGCTGAGGCGCTGAGTGTGTTGGCGGAGGC 3568
    |||||
Db 3533 GCCCAGACCCAGGCGCGCACCGCTGAGGCTGAGGCGCTGAGTGTGTTGGCGGAGGC 3592
QY 3569 CTGATGCTGCGGCTGAGGCTGAGTGTGCGGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGG 3628
    |||||
Db 3593 CTGATGCTGCGGCTGAGGCTGAGTGTGCGGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGG 3652
QY 3629 GCTGAGTGTCCAGACACCTGCTGCTTCACTTCCACAGAGGCTGCGCTGCGCTCCAGC 3688
    |||||
Db 3653 GCTGAGTGTCCAGACACCTGCTGCTTCACTTCCACAGAGGCTGCGCTGCGCTCCAGC 3712
QY 3689 CCAGGCGCGCTTCTTCTCCAGAGAGGCGCGGCTTCCACTCCCACTAGCAATAGTCCA 3748
    |||||
Db 3713 CCAGGCGCGCTTCTTCTCCAGAGAGGCGCGGCTTCCACTCCCACTAGCAATAGTCCA 3772
QY 3749 TCCCAAGATTGCGCATGTTGTAACCCCTGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCT 3808
    |||||
Db 3773 TCCCAAGATTGCGCATGTTGTAACCCCTGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCT 3832
QY 3809 TCCAGTGTGAGAACCTTGAAGAGACCTGAGGAGCTCTGAGAAATTTGAGTGAACCAAGT 3868
    |||||
Db 3833 TCCAGTGTGAGAACCTTGAAGAGACCTGAGGAGCTCTGAGAAATTTGAGTGAACCAAGT 3892
QY 3869 GTGCTTGTACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3928
    |||||
Db 3893 GTGCTTGTACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3952
QY 3929 GGGAGAGTGTGCTGGAGTAAATATGATATGATTTTCACTTTTGAAGAAAAA 3988
    |||||
Db 3953 GGGAGAGTGTGCTGGAGTAAATATGATATGATTTTCACTTTTGAAGAAAAA 4012
QY 3989 AAAAAAAAAAAAAAAAAA 4005
```

Thu Apr 17 08:21:55 2003

us-09-424-686b-1del.rni

Page 27

Db 4013 AAAAAAAAAAAAAAAAAA 4029

RESULT 12
 US-08-854-050-173
 Sequence 173, Application US/08854050
 Patent No. 6261836
 GENERAL INFORMATION:
 APPLICANT: Cecchi, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: No. 6261836el Telomerase
 TITLE OF SEQUENCES: 225
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/854,050
 FILING DATE: 09-MAY-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-0029300S
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 173:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4029 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY:
 LOCATION: 1..4029 /note="preliminary sequence for
 OTHER INFORMATION: human TRT cDNA insert of
 OTHER INFORMATION: plasmid pCR121"
 US-08-854-050-173

```
Query Match      95.7%; Score 3832.6; DB 4; Length 4029
```

[illegible]

Dh 1017 CCGGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCAGGCGCAAGNA - CACTCGC 1074
Oy 1088 GCCCTCTCTCTACTC - AGCTCTCTGAGGCCAGGCTACTGGGCGTC - GGAGGCTCGTG 1145
Dh 1075 NCCCTCTCTCTACTCAATATATCTGAGGCCCAAGCTACTGGGCTTGGAGGCTCTG 1134
Oy 1146 GAGACCACTCTTCTGGGTTCCAGGCCCTGATGCCAGGAGTCCCGGAGTTGGCCGC 1205
Dh 1135 GAGACANTCTTCT - GATTCCAGGCTTGATGCCA - GATTTCGCCGAGTTGGCCGC 1192
Oy 1206 CCGCCCGAGGCTTCTGCAATGCGGCCCTGTTCTGAGGCTCTTGGAAACACCGC 1265
Dh 1193 CTGCCCGAGGCTTCTGCAATGCGGCCCTGTTCTGAGCTCTTGGAAACACCGC 1252
Oy 1266 CAGTCCCTCTACGGGCTCTCTCTCAAGACGACTCCCGCTGCGAGCTGGGTCACCCA 1325
Dh 1253 CAGTCCCTCTACGGGCTCTCTCTCAAGACGACTCCCGCTGCGAGCTGGGTCACCCA 1312
Oy 1326 GCAGCGGCTGTCTGTGCCCCGAGAAAGCCCGAGGCTGTGTGGCGGCCCGAGAGAG 1385
Dh 1313 GCAGCGGCTGTCTGTGCCCCGAGAAAGCCCGAGGCTGTGTGGCGGCCCGAGAGAG 1372
Oy 1386 G - ACACAGACCCCGTCCGCTGAGTCACTCTCCGAGAGACAGACCCCTGGCAGT 1444
Dh 1373 GAACACAGACCCCGTCCGCTGAGTCACTCTCCGAGAGACAGACCCCTGGCAGT 1432
Oy 1445 GTAGGCTCTGTGGGCGCTCTCTGCGCGGCTGGTCCCGAGGCTCTGGGCTCTGAG 1504
Dh 1433 GTAGGCTCTGTGGGCGCTCTCTGCGCGGCTGGTCCCGAGGCTCTGGGCTCTGAG 1492
Oy 1505 GCACACAGACGCGCTCTCTCTGAGACACCAAGATTCTCTCTGGGAGACATGC 1564
Dh 1493 GCACACAGACGCGCTCTCTCTGAGACACCAAGATTCTCTCTGGGAGACATGC 1552
Oy 1565 CAAGCTCTGCTGGAGGAGCTGAGTGGAGATGAGCTGGGAGCTGGCTGGCTGG 1624
Dh 1553 CAAGCTCTGCTGGAGGAGCTGAGTGGAGATGAGCTGGGAGCTGGCTGGCTGG 1612
Oy 1625 CAGAGCCCAAGGCTGTGCTCTGCGCGGAGAGACCGCTGCTGGAGAGATCT 1684
Dh 1613 CAGAGCCCAAGGCTGTGCTCTGCGCGGAGAGACCGCTGCTGGAGAGATCT 1672
Oy 1685 GCGCAAGTCTGCACTGGCTGATGATGTGTAGCTGCTGCAAGCTCTTCTT 1744
Dh 1673 GCGCAAGTCTGCACTGGCTGATGATGTGTAGCTGCTGCAAGCTCTTCTT 1732
Oy 1745 TTATGTCCGAGAGCACTTCAAAAGACAGGCTCTTTTCTACGCGAGAGAGTGTG 1804
Dh 1733 TTATGTCCGAGAGCACTTCAAAAGACAGGCTCTTTTCTACGCGAGAGAGTGTG 1792
Oy 1805 GAGCAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGACGTGGGAGCT 1864
Dh 1793 GAGCAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGACGTGGGAGCT 1852
Oy 1865 GTGGAGACAGAGTCAAGGACATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGCT 1924
Dh 1853 GTGGAGACAGAGTCAAGGACATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGCT 1912
Oy 1925 CCGGTATATCCCAAGGCTGAGGCGCTGGGCGCAATTGGAACATGAGCTACGTCTGGG 1984
Dh 1913 CCGGTATATCCCAAGGCTGAGGCGCTGGGCGCAATTGGAACATGAGCTACGTCTGGG 1972
Oy 1985 AGCCAGAACTTCCGAGAGAAAGAGGCGGAGGCTGCTCACTCGAGGTTGAAGGACT 2044
Dh 1973 AGCCAGAACTTCCGAGAGAAAGAGGCGGAGGCTGCTCACTCGAGGTTGAAGGACT 2032
Oy 2045 GTTACAGGCTGCTCACTCAAGAGCGGCGGCGCCCGCTCTGAGGCGCTCTGTCT 2104
Dh 2033 GTTACAGGCTGCTCACTCAAGAGCGGCGGCGCCCGCTCTGAGGCGCTCTGTCT 2092
Oy 2105 GGGCTTGAGCATATCCACAGAGGCTGGCGCACTTGTGCTGGTGGCGGCCACAGA 2164
Dh 2093 GGGCTTGAGCATATCCACAGAGGCTGGCGCACTTGTGCTGGTGGCGGCCACAGA 2152

Oy 2165 CCGCGCGCTGAGCTGTA-----CATCC 2188
Dh 2153 CCGCGCGCTGAGCTGTA-----CATCC 2212
Oy 2189 CCAGACAGGCTCAAGGAGTGCATGCGAGCATCAACCCCAAGAACAGTACTGCT 2248
Dh 2213 CCAGACAGGCTCAAGGAGTGCATGCGAGCATCAACCCCAAGAACAGTACTGCT 2272
Oy 2249 GCGTGGATGCGGCTGCAAGGAGGCGCATGAGGAGCTCCGCAAGGCTCAAGAG 2308
Dh 2273 GCGTGGATGCGGCTGCAAGGAGGCGCATGAGGAGCTCCGCAAGGCTCAAGAG 2332
Oy 2309 CCAGTCTCTACTTGAAGAGCTCCAGGCTTACATGCGAGAGTCTGCTCACTGCA 2368
Dh 2333 CCAGTCTCTACTTGAAGAGCTCCAGGCTTACATGCGAGAGTCTGCTCACTGCA 2392
Oy 2369 GGAGACAGGCGCTGAGGAGTGCCTGCTGATGAGACAGCTCTCTGATGAGG 2428
Dh 2393 GGAGACAGGCGCTGAGGAGTGCCTGCTGATGAGACAGCTCTCTGATGAGG 2452
Oy 2429 CAGAGTGGCTCTTCAAGGCTTCTCAAGGCTTCAAGGCTTCAAGGCTTCAAGG 2488
Dh 2453 CAGAGTGGCTCTTCAAGGCTTCTCAAGGCTTCAAGGCTTCAAGGCTTCAAGG 2512
Oy 2489 GGGCAAGTCTACAGTCCAGTCCAGGAGATCCCGAGGCTCCATCTCTCAGCTGCT 2548
Dh 2513 GGGCAAGTCTACAGTCCAGTCCAGGAGATCCCGAGGCTCCATCTCTCAGCTGCT 2572
Oy 2549 CTGCAAGCTGTGCTACAGGCTGATGAGACACAGCTCTTTCGGGAGATTCGGGAGG 2608
Dh 2573 CTGCAAGCTGTGCTACAGGCTGATGAGACACAGCTCTTTCGGGAGATTCGGGAGG 2632
Oy 2609 GCTGCTCTGCTGCTTGGAGTGAATTTCTGTGGTGAACCTCACTCACTCACTCA 2668
Dh 2633 GCTGCTCTGCTGCTTGGAGTGAATTTCTGTGGTGAACCTCACTCACTCACTCA 2692
Oy 2669 AACCTTCTCAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2728
Dh 2693 AACCTTCTCAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2752
Oy 2729 GAAGACAGTGTGAATCTTCTGTAAGAGAGAGGCTCTGGTGGAGCTTGTGCA 2788
Dh 2753 GAAGACAGTGTGAATCTTCTGTAAGAGAGAGGCTCTGGTGGAGCTTGTGCA 2812
Oy 2789 GATGCGGCGCCAGGCTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2848
Dh 2813 GATGCGGCGCCAGGCTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2872
Oy 2849 GGTGAGAGCACTTCACTCAGCTATGCGGAGCTCTCAAGAGCCAGCTCACTTCAA 2908
Dh 2873 GGTGAGAGCACTTCACTCAGCTATGCGGAGCTCTCAAGAGCCAGCTCACTTCAA 2932
Oy 2909 CCGGCGCTTCAAGGCTGGGAGAGATGCTGCGCAACTCTTGGGCTCTGGGCTGAA 2968
Dh 2933 CCGGCGCTTCAAGGCTGGGAGAGATGCTGCGCAACTCTTGGGCTCTGGGCTGAA 2992
Oy 2969 GTGTACAGGCTGTTTGGATTGAGTGGAGTGAAGAGCTTCAAGAGGCTGACCAACAT 3028
Dh 2993 GTGTACAGGCTGTTTGGATTGAGTGGAGTGAAGAGCTTCAAGAGGCTGACCAACAT 3052
Oy 3029 CTACAGATCTCTGCTGCAAGGCTTACAGGCTTCAAGAGTGTGCTGACCTCCATT 3088
Dh 3053 CTACAGATCTCTGCTGCAAGGCTTACAGGCTTCAAGAGTGTGCTGACCTCCATT 3112
Oy 3089 TCATCAGCAAGTTGGAAGAACCCCAATTTTCTGCGGCTCATCTGTGACAGGCTCT 3148
Dh 3113 TCATCAGCAAGTTGGAAGAACCCCAATTTTCTGCGGCTCATCTGTGACAGGCTCT 3172
Oy 3149 CCTGTGCTACATCTTGAAGAACCAAGAGGAGTGTGCTGGGCGGCAAGGCGC 3208
Dh 3173 CCTGTGCTACATCTTGAAGAACCAAGAGGAGTGTGCTGGGCGGCAAGGCGC 3232

QY 2489 GGGCAAGTCTACGTCACGTCAGGAGGATCCGACAGGGGCTCCATCCCTCTCCACGCTCT 2548
 DB 2513 GGGCAAGTCTACGTCACGTCAGGAGGATCCGACAGGGGCTCCATCCCTCTCCACGCTCT 2572
 QY 2549 GTGAGAGTCTACGTCACGTCAGGAGGATCCGACAGGGGCTCCATCCCTCTCCACGCTCT 2608
 DB 2573 GTGAGAGTCTACGTCACGTCAGGAGGATCCGACAGGGGCTCCATCCCTCTCCACGCTCT 2632
 QY 2609 GTGAGAGTCTACGTCACGTCAGGAGGATCCGACAGGGGCTCCATCCCTCTCCACGCTCT 2668
 DB 2633 GTGAGAGTCTACGTCACGTCAGGAGGATCCGACAGGGGCTCCATCCCTCTCCACGCTCT 2692
 QY 2669 AACCTTCTCAGAGACCTGTCAGAGGATCCGACAGGGGCTCCATCCCTCTCCACGCTCT 2728
 DB 2693 AACCTTCTCAGAGACCTGTCAGAGGATCCGACAGGGGCTCCATCCCTCTCCACGCTCT 2752
 QY 2729 GAGAGAGTGTGAACCTTCTGAGAGGATCCGACAGGGGCTCCATCCCTCTCCACGCTCT 2788
 DB 2753 GAGAGAGTGTGAACCTTCTGAGAGGATCCGACAGGGGCTCCATCCCTCTCCACGCTCT 2812
 QY 2789 GATGCGGCGCCAGGCTCTATCCCTGCTGCGGCTCTGAGAGGATCCGACAGGGGCTCC 2848
 DB 2813 GATGCGGCGCCAGGCTCTATCCCTGCTGCGGCTCTGAGAGGATCCGACAGGGGCTCC 2872
 QY 2849 GGTCCAGAGGAGTACTCTCAGAGGATCCGACAGGGGCTCCATCCCTCTCCACGCTCT 2908
 DB 2873 GGTCCAGAGGAGTACTCTCAGAGGATCCGACAGGGGCTCCATCCCTCTCCACGCTCT 2932
 QY 2909 CCGGCGGCTTCAAGGCTGGGAGAGACATGCGTCCGACAACTTTGGGGTCTTGGGGCTGAA 2968
 DB 2933 CCGGCGGCTTCAAGGCTGGGAGAGACATGCGTCCGACAACTTTGGGGTCTTGGGGCTGAA 2992
 QY 2969 GTGTACAGGCTTTTCTGAGATTTGAGTGTGAGTGTGAGAGGCTCCAGAGGCTGTGACACAAAT 3028
 DB 2993 GTGTACAGGCTTTTCTGAGATTTGAGTGTGAGTGTGAGAGGCTCCAGAGGCTGTGACACAAAT 3052
 QY 3029 CTGAGAGATCTCTCTGTCAGAGGCTGTGAGTGTGAGAGGCTCCAGAGGCTGTGACACAAAT 3088
 DB 3053 CTGAGAGATCTCTCTGTCAGAGGCTGTGAGTGTGAGAGGCTCCAGAGGCTGTGACACAAAT 3112
 QY 3089 TGTAGAGATTTTGGAG 3148
 DB 3113 TGTAGAGATTTTGGAG 3172
 QY 3149 CCTGTGCTACTCTCTCTGAG 3208
 DB 3173 CCTGTGCTACTCTCTCTGAG 3232
 QY 3209 CCGCGGCTCTGCTCTCTGAG 3268
 DB 3233 CCGCGGCTCTGCTCTCTGAG 3292
 QY 3269 GCTGAGTGTGAG 3328
 DB 3293 GCTGAGTGTGAG 3352
 QY 3329 GAGAGTGTGAG 3388
 DB 3353 GAGAGTGTGAG 3412
 QY 3389 GAGAGTGTGAG 3448
 DB 3413 GAGAGTGTGAG 3472
 QY 3449 GAGAGTGTGAG 3508
 DB 3473 GAGAGTGTGAG 3532
 QY 3509 GCGGAG 3568
 DB 3533 GCGGAG 3592

QY 3569 GTGAGTGTGAG 3628
 DB 3593 GTGAGTGTGAG 3652
 QY 3629 GTGAGTGTGAG 3688
 DB 3653 GTGAGTGTGAG 3712
 QY 3689 CCAG 3748
 DB 3713 CCAG 3772
 QY 3749 TCCGAGATGTGAG 3808
 DB 3773 TCCGAGATGTGAG 3832
 QY 3809 TCCAGAGTGTGAG 3868
 DB 3833 TCCAGAGTGTGAG 3892
 QY 3869 GTGAGTGTGAG 3928
 DB 3893 GTGAGTGTGAG 3952
 QY 3929 GGGAGAGTGTGAG 3988
 DB 3953 GGGAGAGTGTGAG 4012
 QY 3989 AAAAAAAAAAAAAAAAAA 4005
 DB 4013 AAAAAAAAAAAAAAAAAA 4029

RESULT 14
 US-08-974-549A-4
 Sequence 4 Application US/08974549A
 Patent No. 616178
 GENERAL INFORMATION:
 APPLICANT: Czech, Thomas R.
 APPLICANT: Lininger, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morlin, Gregg B.
 APPLICANT: Hartley, Calvin B.
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-NOV-1997
 CLASSIFICATION: 536
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00261005
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3855 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3855 /note= "nucleic acid sequence with an
OTHER INFORMATION: open reading frame encoding a delta-182
OTHER INFORMATION: variant polypeptide"
FEATURE:
NAME/KEY: CDS
LOCATION: 56..2479
OTHER INFORMATION: /product= "delta-182 variant
OTHER INFORMATION: polypeptide"
US-08-974-549A-4
Query Match 94.8%; Score 3797; DB 4; Length 3855;
Best Local Similarity 94.6%; Pred. No. 2.3e-224;
Matches 3817; Conservative 0; Mismatches 0; Indels 218; Gaps 2;

301 CCGAGTGTGAGAGAGCTGTGCGAGCGCGGCGGAAGACGTGTGGCTTCGGCTTCGC 360
QY 368 GCTGTGAGACGGGGCGCCGGGGGGCCCCCGAGGCTTACACACAGCTGGCGACGTA 427
DB 361 GCTGTGAGACGGGGCGCCGGGGGGCCCCCGAGGCTTACACACAGCTGGCGACGTA 420
QY 428 CCGTCCCAACACAGGTGACCGACGACTGGGGGGAGGGGGCGTGGGGGGCTGTGCTGGC 487
DB 421 CCTGCCCAACACAGGTGACCGACGACTGGGGGGAGGGGGCGTGGGGGGCTGTGCTGGC 480
QY 488 CCGGCTGGGGGACGACGCTGTGCTGCTACCTGTGTCACGCTGTGGCGCTTTTGTGTGT 547
DB 481 CCGGCTGGGGGACGACGCTGTGCTGCTACCTGTGTCACGCTGTGGCGCTTTTGTGTGT 540
QY 548 GGCCTCCAGCTGGCGCTACACAGGTGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 607
DB 541 GGCCTCCAGCTGGCGCTACACAGGTGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 600
QY 608 TCAGGCGCGGCGCGCGCGCACAGCTAGTGAACCCCGAAGGCGCTGGATGCGAACGGGC 667
DB 601 TCAGGCGCGGCGCGCGCGCACAGCTAGTGAACCCCGAAGGCGCTGGATGCGAACGGGC 660
QY 668 CTGAACCATATAGGTGAGGGAGGCGCGGGTCCCTGTGGGCTGTGACGCGCGGTGGAG 727
DB 661 CTGAACCATATAGGTGAGGGAGGCGCGGGTCCCTGTGGGCTGTGACGCGCGGTGGAG 720
QY 728 GAGGCGCGGGGCGAGTGCACGCGCAAGTCTGCGTTCGCAAGAGGCGCGAGCGCGGC 787
DB 721 GAGGCGCGGGGCGAGTGCACGCGCAAGTCTGCGTTCGCAAGAGGCGCGAGCGCGGC 780
QY 788 TGGCCCTGAGCGCGGAGCGGACCGCGGCTGTGGAGGGTCTGTGGCGCACCGCGGAC 847
DB 781 TGGCCCTGAGCGCGGAGCGGACCGCGGCTGTGGAGGGTCTGTGGCGCACCGCGGAC 840
QY 848 GCGTGAACGAGTGAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
DB 841 GCGTGAACGAGTGAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 908 CACGCTTTTGGAGGGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 967
DB 901 CACGCTTTTGGAGGGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
QY 968 GCACACGCGGGCG 1027
DB 961 GCACACGCGGGCG 1020
QY 1028 CCGGCTGAGCGCGGAGACCAAGACATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1087
DB 1021 CCGGCTGAGCGCGGAGACCAAGACATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1080
QY 1088 GCGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1147
DB 1081 GCGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1140
QY 1148 GACCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1207
DB 1141 GACCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
QY 1208 GCCCAGCGGTACGAGGAATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1267
DB 1201 GCCCAGCGGTACGAGGAATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1260
QY 1268 GTGCGCCCTACGGGGGTGCTCTTCAAGACGACGCTCCGCTGCGAGCTGGCGGTAC 1327
DB 1261 GTGCGCCCTACGGGGGTGCTCTTCAAGACGACGCTCCGCTGCGAGCTGGCGGTAC 1320
QY 1328 AGCGGCTGTGTGTGCGCGGAGAAAGCCAGGCTCTGTGGCGCGCGCGAGAGAGGA 1387
DB 1321 AGCGGCTGTGTGTGCGCGGAGAAAGCCAGGCTCTGTGGCGCGCGCGAGAGAGGA 1380
QY 1388 CACAGACCCCGCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1447
DB 1381 CACAGACCCCGCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440

QY 1448 CGGCTTCGTCGGGCTTCGCTGGCCGGGCTGGTGGCCCGAAGGCTCTGTGGGGCTCCAGCA 1507
 Db 1441 CGGCTTCGTCGGGCTTCGCTGGCCGGGCTGGTGGCCCGAAGGCTCTGTGGGGCTCCAGCA 1500
 QY 1508 CAACGAGCGCGCTTCCTCCAGCAACACCAAGATTCATCTCCCTGGGAGACATGCCAA 1567
 Db 1501 CAACGAGCGCGCTTCCTCCAGCAACACCAAGATTCATCTCCCTGGGAGACATGCCAA 1560
 QY 1568 GCTCTCGCTCCAGAGACTGACGTGGAAGTAGAGCTGGGAGTCTGCGCTTGGCTGGCAG 1627
 Db 1561 GCTCTCGCTCCAGAGACTGACGTGGAAGTAGAGCTGGGAGTCTGCGCTTGGCTGGCAG 1620
 QY 1628 GAGCCCAAGGGGTTGGCTGTGTTCGCGCCGAGAGACACCGTCTCGTGAAGAGATCTGGC 1687
 Db 1621 GAGCCCAAGGGGTTGGCTGTGTTCGCGCCGAGAGACACCGTCTCGTGAAGAGATCTGGC 1680
 QY 1688 CAAGTTCCTGACCTGGCTGATGAGTGTGACGTGTCGAGCTCGTCAAGTCTTCTTTTA 1747
 Db 1681 CAAGTTCCTGACCTGGCTGATGAGTGTGACGTGTCGAGCTCGTCAAGTCTTCTTTTA 1740
 QY 1748 TGTCAAGGAGACACGTTTCAAAAGACAGGCTTTTCTACCGGAGAGATGTGAG 1807
 Db 1741 TGTCAAGGAGACACGTTTCAAAAGACAGGCTTTTCTACCGGAGAGATGTGAG 1800
 QY 1808 CAAGTTCGAAAGCATTTGGAATCAGACAGCATTTGAAGAGGAGTGTGAGTGTGGAGCTGTG 1867
 Db 1801 CAAGTTCGAAAGCATTTGGAATCAGACAGCATTTGAAGAGGAGTGTGAGTGTGGAGCTGTG 1860
 QY 1868 GGAAGCAGAGGTGACGACATCGGGAAGCCAGGCGCCGCTGTGACGTCCAGACTCCG 1927
 Db 1861 GGAAGCAGAGGTGACGACATCGGGAAGCCAGGCGCCGCTGTGACGTCCAGACTCCG 1920
 QY 1928 CTTTCATCCCAAGGCTTGACGGGCTGCGGCGGATTTGTAACATGACATCTGCGGAGC 1987
 Db 1921 CTTTCATCCCAAGGCTTGACGGGCTGCGGCGGATTTGTAACATGACATCTGCGGAGC 1980
 QY 1988 CAGAGCTTCCGCGAGAGAAAAAGAGGGCCGAGCGCTCTCACTCGAGGAGTGAAGCACTGTT 2047
 Db 1981 CAGAGCTTCCGCGAGAGAAAAAGAGGGCCGAGCGCTCTCACTCGAGGAGTGAAGCACTGTT 2040
 QY 2048 CAGCGTGTCAACTAGAGGCGGGCGGCGCCCGGCTCTCTGGGCGCTCTGTGCTGGG 2107
 Db 2041 CAGCGTGTCAACTAGAGGCGGGCGGCGCCCGGCTCTCTGGGCGCTCTGTGCTGGG 2100
 QY 2108 CTTGAGAGATTCAGAGAGGCGGCGGACCTTCTGCTGCTGCTGGGCGGCGGAGACCC 2167
 Db 2101 CTTGAGAGATTCAGAGAGGCGGCGGACCTTCTGCTGCTGCTGGGCGGCGGAGACCC 2160
 QY 2168 GCGGCTGAGCGTGA-----CATGCCCA 2191
 Db 2161 GCGGCTGAGCGTGA-----CATGCCCA 2220
 QY 2192 GAGACGCTCAGAGAGTCAATGCGCCAGCATATCAAAAGCCGAGAACAGTACGTGGTGG 2251
 Db 2221 GAGACGCTCAGAGAGTCAATGCGCCAGCATATCAAAAGCCGAGAACAGTACGTGGTGG 2280
 QY 2252 TCGGTATGCGGTGTCCAGAGAGCGCCCATGAGGAGCTGCGCAAGGCTTTCAGAGCCA 2311
 Db 2281 TCGGTATGCGGTGTCCAGAGAGCGCCCATGAGGAGCTGCGCAAGGCTTTCAGAGCCA 2340
 QY 2312 CGTCTCTACCTTGAGAGACCTCCAGCGCTTACATGCGAGAGTTGCTGCTCAGAGA 2371
 Db 2341 C----- 2341
 QY 2372 GAGCAGCGCGGTGAGAGATGCGTGTGATCAGACAGAGCTCTCCCTGAATGAGGCGAG 2431
 Db 2342 ----- 2341
 QY 2432 CAGTGGCTCTTTCAGAGCTTCTTACAGCTTCATGTCACACAGCGCTGTGGCATAGGGG 2491
 Db 2342 ----- 2341

QY 2492 CAATGCTACGTCAAGTGTCCAGAGGAGATCCGCAAGGCTTCATCTCTTCAAGCTGCTGTG 2551
 Db 2342 ----CTCTCAAGTGTCCAGAGGAGATCCGCAAGGCTTCATCTCTTCAAGCTGCTGTG 2398
 QY 2552 CAGCGTGTCTAGGCGGACATGAGAGAACAACTGTTTGGGGGATTTGGCGGAGGAGGCT 2611
 Db 2399 CAGCGTGTCTAGGCGGACATGAGAGAACAACTGTTTGGGGGATTTGGCGGAGGAGGCT 2458
 QY 2612 GCTGCGGCTTTGGGAGTATTTCTTGTGTGACACCTCACCTCACCCAGCGCAAAAC 2671
 Db 2459 GCTGCGGCTTTGGGAGTATTTCTTGTGTGACACCTCACCTCACCCAGCGCAAAAC 2518
 QY 2672 CTTGCTGAGAGGCTGCTGTCAGAGTGTGCTGCTGATGAGTGTGAGTGTGAGAA 2731
 Db 2519 CTTGCTGAGAGGCTGCTGTCAGAGTGTGCTGCTGATGAGTGTGAGTGTGAGAA 2578
 QY 2732 GACAGGTGTAACTTCCCTGTGAAGAGAGGCGGCTGGGAGAGGCTTTGTGAGAT 2791
 Db 2579 GACAGGTGTAACTTCCCTGTGAAGAGAGGCGGCTGGGAGAGGCTTTGTGAGAT 2658
 QY 2792 GCGGCGCCACGCGCTATTCCCTGTGTGGGCTGCTGTGATACCGGACCTGAGAT 2851
 Db 2639 GCGGCGCCACGCGCTATTCCCTGTGTGGGCTGCTGTGATACCGGACCTGAGAT 2698
 QY 2852 GCAAGAGACTACTACACTATGCGCGACCTCCATCAAGAGCCAGTCACTTCAACCG 2911
 Db 2699 GCAAGAGACTACTACACTATGCGCGACCTCCATCAAGAGCCAGTCACTTCAACCG 2758
 QY 2912 CCGCTTCAAGGCTGGGAGAGAACATGCTGCAAACTCTTGGGGCTTGGCGCTGAAGT 2971
 Db 2759 CCGCTTCAAGGCTGGGAGAGAACATGCTGCAAACTCTTGGGGCTTGGCGCTGAAGT 2818
 QY 2972 TCACAGGCTTTCTGAGATTTGAGGTGAAGAGCCCTCCAGAGGCTGTGACCAACATCTA 3031
 Db 2819 TCACAGGCTTTCTGAGATTTGAGGTGAAGAGCCCTCCAGAGGCTGTGACCAACATCTA 2878
 QY 3032 CAAGATCTCTCTGTCAGAGGAGGCTGACAGGTTTCAAGCATGTGCTGACAGCTCCCATTTCA 3091
 Db 2879 CAAGATCTCTCTGTCAGAGGAGGCTGACAGGTTTCAAGCATGTGCTGACAGCTCCCATTTCA 2938
 QY 3092 TCAGCAAGTTTGAAGAACCCACATTTTCTGCGGCTCATCTGACAGAGGCTCCCT 3151
 Db 2939 TCAGCAAGTTTGAAGAACCCACATTTTCTGCGGCTCATCTGACAGAGGCTCCCT 2998
 QY 3152 CTGCTACTCATCTCTGAAGGCCAAGAACGAGGATGCTGTGGGGGCAAGGGGCGCGC 3211
 Db 2999 CTGCTACTCATCTCTGAAGGCCAAGAACGAGGATGCTGTGGGGGCAAGGGGCGCGC 3058
 QY 3212 CGGCGCTGTGCGCTTCCAGAGCGGTGCAAGTGGCTGTGCCAAGCAATTCCTGCTCAAGCT 3271
 Db 3059 CGGCGCTGTGCGCTTCCAGAGCGGTGCAAGTGGCTGTGCCAAGCAATTCCTGCTCAAGCT 3118
 QY 3272 GACTGAGACCGGTGACCTTACCTTACCTTCTGCGGCTCACTGAGAGAGCCAGAGCA 3331
 Db 3119 GACTGAGACCGGTGACCTTACCTTACCTTCTGCGGCTCACTGAGAGAGCCAGAGCA 3178
 QY 3332 GCTGAGTGGAGAGTCCCGGGGAGAGAGCTGACTGCTCTGAGAGCGCAGCCAGCCGAG 3391
 Db 3179 GCTGAGTGGAGAGTCCCGGGGAGAGAGCTGACTGCTCTGAGAGCGCAGCCAGCCGAG 3238
 QY 3392 ACTGCGCTCAAGCTTCAAGACCATCTGAGACTGATGAGCCACCGCCACAGCGCAGCGCA 3451
 Db 3239 ACTGCGCTCAAGCTTCAAGACCATCTGAGACTGATGAGCCACCGCCACAGCGCAGCGCA 3298
 QY 3452 GAGCAGACACAGAGCGCTGTCAGAGCGGCGGCTGACGTCCAGAGGAGGAGGAGGCGGCG 3511
 Db 3299 GAGCAGACACAGAGCGCTGTCAGAGCGGCGGCTGACGTCCAGAGGAGGAGGAGGCGGCG 3358
 QY 3512 CACACCGAGCGCGCAGCGCTGGAGCTGAGAGGCTGAGAGTGTGAGGCGGAGGCGGCTG 3571
 Db 3359 CACACCGAGCGCGCAGCGCTGGAGCTGAGAGGCTGAGAGTGTGAGGCGGAGGCGGCTG 3418
 QY 3572 CATGTCCGAGTGAAGGCTGAGTGTGCGGCTGAGGCTGAGCGAGTGTCCAGCAAGGCT 3631

Db	3419	CATGTCGGCGTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAGGGCT	3478
QY	3632	GAGTGTCCAGCACACCTGCGCTTTCACATTCCACAGGCTGAGCTGCGCTCCAGCCCA	3691
Db	3479	GAGTGTCCAGCACACCTGCGCTTTCACATTCCACAGGCTGAGCTGCGCTCCAGCCCA	3538
QY	3692	GGGCGAGTTTTTCTCACCAGAGAGCCGGCTTCACTCCCAACATAGAAATGTCATTC	3751
Db	3539	GGGCGAGTTTTTCTCACCAGAGAGCCGGCTTCACTCCCAACATAGAAATGTCATTC	3598
QY	3752	CCAGATTGCGCATTTGTCACCCCGCGCCCTTCCTTGGCTTCCACCCGACATTC	3811
Db	3599	CCAGATTGCGCATTTGTCACCCCGCGCCCTTCCTTGGCTTCCACCCGACATTC	3658
QY	3812	AGGTGAGAGCCCTGAGAAAGAGACCTGGAGACTGTGGAAATTTGGAGTACCCAAAGGTG	3871
Db	3659	AGGTGAGAGCCCTGAGAAAGAGACCTGGAGACTGTGGAAATTTGGAGTACCCAAAGGTG	3718
QY	3872	CCCTGTACACAGCGAGAGCCCTGACACTGGATGGGGGTCCCTGTGGGTCAAAATGGGGG	3931
Db	3719	CCCTGTACACAGCGAGAGCCCTGACACTGGATGGGGGTCCCTGTGGGTCAAAATGGGGG	3778
QY	3932	GAGGTGCTGGGGAGATTAATAATTAATGATTTTCAGTTTGAIAAAAAAAAAA	3991
Db	3779	GAGGTGCTGGGGAGATTAATAATTAATGATTTTCAGTTTGAIAAAAAAAAAA	3838
QY	3992	AAAAAAAAAAAAAAAAA 4006	
Db	3839	AAAAAAAAAAAAAAAAA 3853	

RESULT 15
US-08-974-549A-721
; Sequence 721, Application US/08974549A
; Patent No. 6166178

GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morlin, Gregg B.
 APPLICANT: Hartley, Calvin B.
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend and Crew LLP
STREET: 200 Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843

```

1 FILING DATE: 06-MAY-1997
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: US 08/854,050
4 FILING DATE: 09-MAY-1997
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: US 08/911,312
7 FILING DATE: 14-AUG-1997
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: US 08/912,951
10 FILING DATE: 14-AUG-1997
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 08/915,503
13 FILING DATE: 14-AUG-1997
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: WO PCT/US97/17618
16 FILING DATE: 01-OCT-1997
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: WO PCT/US97/17885
19 FILING DATE: 01-OCT-1997
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Apple, Randolph Ted
22 REGISTRATION NUMBER: 36,429
23 REFERENCE/DOCKET NUMBER: 015389-002610US
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (415) 576-0200
26 TELEFAX: (415) 576-0300
27 INFORMATION FOR SEQ. ID NO: 721:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 3451 base pairs
30 TYPE: nucleic acid
31 STRANDEDNESS: single
32 TOPOLOGY: linear
33 MOLECULE TYPE: DNA
34 FEATURE:
35 NAME/KEY: -
36 LOCATION: 1..3451
37 OTHER INFORMATION: /note="HTRT sequence employing codon
38 OTHER INFORMATION: distribution preferentially used by
39 OTHER INFORMATION: highly expressed genes in E. coli
40 OTHER INFORMATION: containing SacI and XhoI sites"
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947

```

[illegible]

QY 483 CTGCGCCGCTGGGCGACGACGTGCTGTTCACTGCTGGACGCTGCGCTTTGTG 542
Db 448 CTGCGCTGT 507
QY 543 CTGCGCTGT 602
Db 508 CTGCGCTGT 567
QY 603 GCGCACTGAGGCG 662
Db 568 GCTTACCAAGGCTGT 627
QY 663 CGGCGCTGGAACCATAGCTGACGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 722
Db 628 GCTGCTGTGAACTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 687
QY 723 GCGAAGGCG 782
Db 688 GCTGCTGT 747
QY 783 GCGCGTGTGCTGT 842
Db 748 GGT 807
QY 843 AGGACGCTGT 902
Db 808 GCTGCTGT 867
QY 903 GAAAGCACTCTTTGT 962
Db 868 GAAAGCACTCTTTGT 927
QY 963 GCGGCACTGAGGCG 1022
Db 928 GCTTACCAAGGCTGT 987
QY 1023 TGT 1082
Db 988 TGT 1047
QY 1083 CTGCGCGCTGT 1142
Db 1048 CTGCGCGCTGT 1107
QY 1143 GTGGAACATCTTTGT 1202
Db 1108 GTTGAACATCTTTGT 1167
QY 1203 CGCGT 1262
Db 1168 CGT 1227
QY 1263 GCGGCACTGAGGCG 1322
Db 1228 GCTTACCAAGGCTGT 1287
QY 1323 CCAGGACGCGGT 1382
Db 1288 CGGCGT 1347
QY 1383 GAGGACATGAGGCG 1442
Db 1348 GAGGACATGAGGCG 1407
QY 1443 GT 1502
Db 1408 GTTGT 1467
QY 1503 AGGCAACATGAGGCG 1562
Db 1468 CCGT 1527

QY 1563 GCCAAGCTCTGCTGT 1622
Db 1528 GCTTAACTGT 1587
QY 1623 CGGAGAGGCG 1682
Db 1588 GCTGT 1647
QY 1683 CTGCGCTGT 1742
Db 1648 CTGCGCTGT 1707
QY 1743 TTTGT 1802
Db 1708 TTTGT 1767
QY 1803 TGT 1862
Db 1768 TGT 1827
QY 1863 CTGT 1922
Db 1828 CTGT 1887
QY 1923 CTGCGCTGT 1982
Db 1888 CTGCGCTGT 1947
QY 1983 GGAAGCACTCTTTGT 2042
Db 1948 GGT 2007
QY 2043 CTGT 2102
Db 2008 CTGT 2067
QY 2103 CTGT 2162
Db 2068 CTGT 2127
QY 2163 GACCGCGCTGT 2186
Db 2128 GACCGCGCTGT 2187
QY 2187 CCCAGGACGAGCTGT 2246
Db 2188 CCGGAGGACGCTGT 2247
QY 2247 GTTGT 2306
Db 2248 GTTGT 2307
QY 2307 AGGCACTGT 2366
Db 2308 TCCAGGCTGT 2367
QY 2367 CAGGAGGACGCGGT 2426
Db 2368 CAGGAGGACGCGGT 2427
QY 2427 GCGAGGACGCGGT 2486
Db 2428 GCGAGGACGCGGT 2487
QY 2487 AGGAGGAGCTGT 2546
Db 2488 GGT 2547
QY 2547 CTGT 2606
Db 2548 CTGT 2607
QY 2607 GCGGT 2666

us-09-424-686b-1del.rge

Page 1

SUMMARIES

```
Run on: .      April 16, 2003, 14:48:19 ; Search time 10138 Seconds
              (without alignments)
```

(Without alignments)
11499.886 Million cell updates/sec

```
Perfect score: 4006
Sequence: 1 gtttcagcagcgtgcgtc.....aaaaaaaaaaaaaaaaaaaa 4006
```

Searched: 2054640 seqs, 14551402878 residues

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Maximum match 100%
Listing first 45 summaries

```
GenEmbl:*
1: gb_ba:*
2: gb_htq:*
```

Pred. No. is the number of results predicted by chance to have a

ALIGNMENTS

JOURNAL Patent: WO 9859040-A 1 30-DEC-1998;

us-09-424-686b-1del.rge

Page 2

Query Match	99.8%;
Best Local Similarity	99.1%;
Matches 4006; Conservative	0. Mismatched

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

Qy	901	AAGAACCACTCTTTGGAGGGTGGCGTCTCTGTGGCAGCGCACTCCACCAATCCGTGG	9
Db	901	AAGAAACCACCTCTTTGGAGGGTGGCGTCTGTGGCAGCGCACTCCACCAATCCGTGG	9
Qy	961	GGCGCAGACACGCGGGGGCCCCCATTCACATTCGGGGCCACCAAGTCCCTGGAGACGC	5
Db	961	GGCGCAGACACGCGGGGGCCCCCATTCACATTCGGGGCCACCAAGTCCCTGGAGACGC	5
Qy	1021	CTTTGCCCGGGTGTACGCCGAGACCAAGACATTCCCTACTCTGTAGGCCACAGCTGGCGCTGGAGAGC	1
Db	1021	CTTTGCCCGGGTGTACGCCGAGACCAAGACATTCTCTACTCTGTAGGCCAAGAGAGC	1
Qy	1081	AGCTGGGGCCCTCTCTTCTACTAGCTCTCTGTAGGCCACAGCTGGACTGGCGCTGGAGAGC	1
Db	1081	AGCTGGGGCCCTCTCTTCTACTAGCTCTCTGTAGGCCACAGCTGGACTGGCGCTGGAGAGC	1
Qy	1141	TCGTGAGAGACCATCTTCTGGGTTTCCAGAGCCCTGGATGTGCAGAGACTCCCGCAGGTTGC	1
Db	1141	TCGTGAGAGACCATCTTCTGGGTTTCCAGAGCCCTGGATGTGCAGAGACTCCCGCAGGTTGC	1
Qy	1201	CCGCGCTGCCCCACGCGCTACTGGCAAAATCGGCGCCCTGTCTTGTGAGACTGTTGGAAAC	1
Db	1201	CCGCGCTGCCCCACGCGCTACTGGCAAAATCGGCGCCCTGTCTTGTGAGACTGTTGGAAAC	1
Qy	1261	ACGCGCAGTGGCCCTACGGGGGTGCTCTCAAGACGCACTGCGCCGTGAGCTGGCTCA	1
Db	1261	ACGCGCAGTGGCCCTTACGGGGGTGCTCTCAAGACGCACTGCGCCGTGAGCTGGCTCA	1
Qy	1321	CCCCACACCGGCTGTCTGTGTGCGGGGAAAGCCCAAGGGCTGTGTGGCGCCCGGAGG	13
Db	1321	CCCCACACCGGCTGTGTGTGCGGGGAAAGCCCAAGGGCTGTGTGGCGCCCGGAGG	13
Qy	1381	AGAGAGACACACACCCCGCTGGCCGTGGTGCAGCTGTCTCCGCACACAGCAGCCCTTGC	14
Db	1381	AGAGAGACACACACCCCGCTGGCCGTGGTGCAGCTGTCTCCGCACACAGCAGCCCTTGC	14
Qy	1441	AGGTGTACGGCTTGTGTGCGGGCGTGCCTGGCGCGGGTGTGTGCCCTCTGTGGGCT	15
Db	1441	AGGTGTACGGCTTGTGTGCGGGCGTGCCTGGCGCGGGTGTGTGCCCTCTGTGGGCT	15
Qy	1501	CCAGGCACAAAGAACGCGCGTCTCTCAAGAAACCAAGAAATTCTTCCCTGGGGAGC	15
Db	1501	CCAGGCACAAAGAACGCGCGTCTCTCAAGAAACCAAGAAATTCTTCCCTGGGGAGC	15
Qy	1561	ATGCGACAGCTGTGCTGCAGAGACTGACGCGAAGATGTAGCGTGGGGGACGTGCCGTTGGC	16
Db	1561	ATGCGCAAGCTGTGCTGCAGAGACTGACGCGAAGATGTAGCGTGGGGGACGTGCCGTTGGC	16
Qy	1621	TGCGCAGAGACCCCAAGGGGTTGGTGTGTTCGCGCGACAGACCCGTTGCTGGTAGAGA	16
Db	1621	TGCGCAGAGACCCCAAGGGGTTGGTGTGTTCGCGCGACAGACCCGTTGCTGGTAGAGA	16
Qy	1681	TCTCGGCGCAAGTTCGTGCACTGAGTATGATGTGTACTGTGTGAGAGTGTCTCAAGGCTT	174
Db	1681	TCTCGGCGCAAGTTCGTGCACTGAGTATGATGTGTACTGTGTGAGAGTGTCTCAAGGCTT	174
Qy	1741	TCTTTTATGTCAAGGGAGACAGTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAGAGT	180
Db	1741	TCTTTTATGTCAAGGGAGACAGTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAGAGT	180
Qy	1801	TCTGGAGCAAGTTGGAAATCAGACAGCACTTGAAGAGGGTGCACCTCGGG	186
Db	1801	TCTGGAGCAAGTTGGAAAGCAATTGGAATCAGACAGCACTTGAAGAGGGTGCACCTCGGG	186
Qy	1861	AGCTGTCGAACCAAGGTGAGGAGCATGTGGGAAAGCCAGGCCCGCTGTGACTGTCA	192
Db	1861	AGCTGTCGAACCAAGGTGAGGAGCATGTGGGAAAGCCAGGCCCGCTGTGACTGTCA	192
Qy	1921	GACTCCGCTTATCCTCCAAAGCCTTACGGGCTGGCGCGATTTGTAACATGAGACTACGTGC	198
Db	1921	GACTCCGCTTATCCTCCAAAGCCTTACGGGCTGGCGCGATTTGTAACATGAGACTACGTGC	198
Qy	1981	TGGGAGCCAGAACTTCCGACAGAAAGAGGGCGAGCGTCTCACTGTGAGAGGTGAAGG	2040

Db	1981	TGGAGACCGAAGACTTTCGCCAGAAABAAABAGGGCCGAGAGCTTCACCTCGAAGGGTGAAG	2040
Qy	2041	CAGCTTTCAGAGCTGCTCAGCTTCAGAGGGGGGGGGGGCCGGGGCTCTGGGGGCGCTCTG	2100
Db	2041	CACGTTCAGAGCTGCTCAGCTTCAGAGGGGGGGGGGGCCGGGGCTCTGGGGGCGCTCTG	2100
Qy	2101	TGCTGGGCGCTGAGAGATATCCAGACAGGGGCTGGGGGAGCTTGGTGTGCGTGGTGGGGGCC	2160
Db	2101	TGCTGGGCGCTGAGAGATATCCAGAGGGGCTGGGGGAGCTTGGTGTGCGTGGTGGGGGCC	2160
Qy	2161	AGGACCCCGCGCGCTGAGCTGTGA-----CA	2184
Db	2161	AGGACCCCGCGCGCTGAGCTGTGACTTGTTCAGGTGATGTGAGGGGGCGCTTCAGACACA	2220
Qy	2185	TCCCCCGAGAGCAGGGTCAAGGAGTCAATGCCAGCATATCAACCCAGAACAGTACT	2244
Db	2221	TCCCCCGAGAGCAGGGTCAAGGAGTCAATGCCAGCATATCAACCCAGAACAGTACT	2280
Qy	2245	GGTGTGCGCGATTCGCGTGGTTCAGAAAGGCCGCCCATGAGCAGCTCCGCAAGGCTTCA	2304
Db	2281	GGTGTGCGCGATTCGCGTGGTTCAGAAAGGCCGCCCATGAGCAGCTCCGCAAGGCTTCA	2340
Qy	2305	AAGAGCAAGCTCTCTACCTTCAGACAGCACTCCAGCCGATAGTCAGCAGTTGTGGCTCAC	2364
Db	2341	AAGAGCAAGCTCTCTACCTTCAGACAGCACTCCAGCCGATAGTCAGCAGTTGTGGCTCAC	2400
Qy	2365	TGCAGAGAACACACCCGGGTGAGGAGTGCCTGCTCATTCAGACAGAGACTCTCCCTGAATG	2424
Db	2401	TGCAGAGAACACACCCGGGTGAGGAGTGCCTGCTCATTCAGACAGAGACTCTCCCTGAATG	2460
Qy	2425	AGGCCAGAGTGGCTCTTCAGAGCTTCTTCAGCGCTTCATGTGCACACAGCCGCTGGACA	2484
Db	2461	AGGCCAGAGTGGCTCTTCAGAGCTTCTTCAGCGCTTCATGTGCACACAGCCGCTGGACA	2520
Qy	2485	TCAAGGGGCAAGTCTCTACGTCAAGTGCACAGGGGATCCCGAGGGGCTCCATCTCTCCACGC	2544
Db	2521	TCAAGGGGCAAGTCTCTACGTCAAGTGCACAGGGGATCCCGAGGGGCTCCATCTCTCCACGC	2580
Qy	2545	TGCTCTGAGGCTGTGCTACGGGCACTGAGAAACAAGCTGTGTGGGGGATTCGGCGGG	2604
Db	2581	TGCTCTGAGGCTGTGCTACGGGCACTGAGAAACAAGCTGTGTGGGGGATTCGGCGGG	2640
Qy	2605	ACGGGCTGCTCTCGCTGTTGGTGATATTTCTGTGTGACACATCTCACTCAACCCAGC	2664
Db	2641	ACGGGCTGCTCTCGCTGTTGGTGATATTTCTGTGTGACACATCTCACTCAACCCAGC	2700
Qy	2665	CGAAAACTTCTCTAGAGACCTCGTTCGAGAGTGTCCCTGAGTATGGCTCGGTGTGAAT	2724
Db	2701	CGAAAACTTCTCTAGAGACCTCGTTCGAGAGTGTCCCTGAGTATGGCTCGGTGTGAAT	2760
Qy	2725	TGCGGAAGACAGTGGTGAATCTCCCTCTAGAAAGAGAGGCGCTGGGTGGACGCGTTTG	2784
Db	2761	TGCGGAAGACAGTGGTGAATCTCCCTCTAGAAAGAGAGGCGCTGGGTGGACGCGTTTG	2820
Qy	2785	TTTCAGATAGCGGCGCCAGGCGCTATTCGCCGTGGTGGGCGCTGCTGTGATACCCGGAGCC	2844
Db	2821	TTTCAGATAGCGGCGCCAGGCGCTATTCGCCGTGGTGGGCGCTGCTGTGATACCCGGAGCC	2880
Qy	2845	TGGAGGTGACAGAGCAGTACAGTCCAGCTATGCGCGAGCTCCATCAGAGCCAGTCCACT	2904
Db	2881	TGGAGGTGACAGAGCAGTACAGTCCAGCTATGCGCGAGCTCCATCAGAGCCAGTCCACT	2940
Qy	2905	TCAACCGGCTTCAGAGGCTGGAGAGACATGCGTGCAGAACTCTTTGGGGCTTTGGCGC	2964
Db	2941	TCAACCGGCGCTTCAGAGGCTGGAGAGAACATGCGTGCAGAACTCTTTGGGGCTTTGGCGC	3000
Qy	2965	TGAAGTGCACAGCTCTTTCGTGGATTTGGAGGTGAACAGCCTCCAGAGAGGTGGACCA	3024
Db	3001	TGAAGTGCACAGCTCTTTCGTGGATTTGGAGGTGAACAGCCTCCAGAGAGGTGGACCA	3060
Qy	3025	ACATCTACAGATCTCTGCTGAGGCGTACAGTTTACGCACTGTGCTGAGAGCTCC	3084

[illegible]

KEYWORDS human.
SOURCE human.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 4042)
AUTHORS Wick, M. and Hagen, G.
TITLE Regulatory dna sequences of the human catalytic telomerase sub-unit
gene, diagnostic and therapeutic use thereof
JOURNAL Patent: WO 9933998-A 2 08-JUL-1999;
WICK MARESA (DE); BAYER AG (DE)
FEATURES
Source 1..4042
Location/Qualifiers
BASE COUNT 684 a 1364 c 1277 g 717 t
ORIGIN
Query Match 99.8%; Score 3996; DB 6; Length 4042;
Best Local Similarity 99.1%; Pred. No. 2e-93;
Matches 4006; Conservative 0; Mismatches 0; Indels 36; Gaps 1;
QY 1 GTTTCAGGACGCGCTGCTCTGCTGCGACGCTGGAGACCTGGCCCGCCACCCCG 60
DB 1 GTTTCAGGACGCGCTGCTCTGCTGCGACGCTGGAGACCTGGCCCGCCACCCCG 60
QY 61 CGATGCGGCGGCTCCCGCTGCGGCGCTGCGCTCCGCTGCGGACCACTACCGCG 120
DB 61 CGATGCGGCGGCTCCCGCTGCGGCGCTGCGCTCCGCTGCGGACCACTACCGCG 120
QY 121 AGGTGCTGCGCTGCGACGCTGCTGCGGCGCTGCGGCGGCGGCGGCGGCTGCTG 180
DB 121 AGGTGCTGCGCTGCGACGCTGCTGCGGCGCTGCGGCGGCGGCGGCGGCTGCTG 180
QY 181 AGCGGCGGACCGCGCGCTTTCCGCGCTGCTGCGGCGGCGGCGGCGGCGGCTGCT 240
DB 181 AGCGGCGGACCGCGCGCTTTCCGCGCTGCTGCGGCGGCGGCGGCGGCGGCTGCT 240
QY 241 GGGAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
DB 241 GGGAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
QY 301 TGGTGGCGCGAGTGTGTCAGAGAGCTGTGCGAGCGCGCGCGGCGGAGAGAGCTGCT 360
DB 301 TGGTGGCGCGAGTGTGTCAGAGAGCTGTGCGAGCGCGCGCGGCGGAGAGAGCTGCT 360
QY 361 GCTTGGCGCTGTGTCAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 420
DB 361 GCTTGGCGCTGTGTCAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGCT 420
QY 421 GCAGCTACCTGCGCAACAGAGTGTGTCAGAGAGCTGTGCGAGCGGCGGCGGCGGCTG 480
DB 421 GCAGCTACCTGCGCAACAGAGTGTGTCAGAGAGCTGTGCGAGCGGCGGCGGCGGCTG 480
QY 481 TGGTGGCGCGCTGTGTCAGAGAGCTGTGTCAGAGAGCTGTGCGAGCGGCGGCTT 540
DB 481 TGGTGGCGCGCTGTGTCAGAGAGCTGTGTCAGAGAGCTGTGCGAGCGGCGGCTT 540
QY 541 TGGTGGCGCGCTGTGTCAGAGAGCTGTGTCAGAGAGCTGTGCGAGCGGCGGCTT 600
DB 541 TGGTGGCGCGCTGTGTCAGAGAGCTGTGTCAGAGAGCTGTGCGAGCGGCGGCTT 600
QY 601 CTGCGCACTAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 660
DB 601 CTGCGCACTAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 660
QY 661 AACGGCGCTGGAACATAGCTGTCAGAGAGCGGCGGCGGCGGCGGCGGCGGCTG 720
DB 661 AACGGCGCTGGAACATAGCTGTCAGAGAGCGGCGGCGGCGGCGGCGGCGGCTG 720
QY 721 GTGGGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 780
DB 721 GTGGGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 780

QY 781 GTGGGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
DB 781 GTGGGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
QY 841 GCAGAGCGGTGGACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 GCAGAGCGGTGGACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 AAGAACCACTTTTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 AAGAACCACTTTTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 GCGCGGAGCAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1020
DB 961 GCGCGGAGCAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1020
QY 1021 CTGTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 CTGTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 AGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 AGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 TGTGGAGACATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1141 TGTGGAGACATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1201 CCGCGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1201 CCGCGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1261 AGCGGAGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 AGCGGAGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 CCGCGAGCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 CCGCGAGCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 AGGAGGACAGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1381 AGGAGGACAGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1441 AGGTGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1441 AGGTGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1501 CCAGGACAGACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1501 CCAGGACAGACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1561 ATGCGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB 1561 ATGCGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1621 TGGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGCT 1680
DB 1621 TGGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGCT 1680
QY 1681 TCGTGGCAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
DB 1681 TCGTGGCAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
QY 1741 TCTTTTATGTCAAGAGACAGCTTCAAAAGACAGCTTCTTTTCTTCAAGAGAGCTG 1800
DB 1741 TCTTTTATGTCAAGAGACAGCTTCAAAAGACAGCTTCTTTTCTTCAAGAGAGCTG 1800
QY 1801 TCTGAGCAAGTTCGCAACATTTGATGATGAGAGAGCTTGAAGAGGCTGAGCTGCGG 1860
DB 1801 TCTGAGCAAGTTCGCAACATTTGATGATGAGAGAGCTTGAAGAGGCTGAGCTGCGG 1860

1861 ACCTGTGGAAGAGAGGTACAGAGCATGCGGAAGCCAGGCGCCGCTGTGTACGTCGA 1920
1861 ACCTGTGGAAGAGAGGTACAGAGCATGCGGAAGCCAGGCGCCGCTGTGTACGTCGA 1920
1921 GACTCGGCTTCATCCCAAGCTCAGCGGCTGCGCGGATTTGTGAACATGAGACAGTGG 1980
1921 GACTCGGCTTCATCCCAAGCTCAGCGGCTGCGCGGATTTGTGAACATGAGACAGTGG 1980
1921 GACTCGGCTTCATCCCAAGCTCAGCGGCTGCGCGGATTTGTGAACATGAGACAGTGG 1980
1981 TGGGAGCCAGAAAGTTCCGAGAGAAAAGAGCCGAGAGCTCTACCTCGAGGTGGAAG 2040
1981 TGGGAGCCAGAAAGTTCCGAGAGAAAAGAGCCGAGAGCTCTACCTCGAGGTGGAAG 2040
2041 CACTGTGAGGTGCTCACTACAGAGCGGCGCGGCGCCGCGCTCTGCGGCTCTG 2100
2041 CACTGTGAGGTGCTCACTACAGAGCGGCGCGGCGCCGCGCTCTGCGGCTCTG 2100
2101 TGTGCGGCTGAGAGATTCACAGAGCGGCGCGGCGCCGCGCTCTGCGGCTCTG 2160
2101 TGTGCGGCTGAGAGATTCACAGAGCGGCGCGGCGCCGCGCTCTGCGGCTCTG 2160
2161 AGGACCGCGCGCTGAGCTGA-----CA 2184
2161 AGGACCGCGCGCTGAGCTGA-----CA 2184
2185 TCCCGGAGAGAGCTCAGAGAGTCAACGACATCAATCAAAACCCAGAGAGCTACT 2244
2221 TCCCGGAGAGAGCTCAGAGAGTCAACGACATCAATCAAAACCCAGAGAGCTACT 2280
2245 GCGTGCCTGCGATGCGCTGCTCCAGAGAGCGCCGCGAGAGCTGCGAGAGCTTCA 2304
2281 GCGTGCCTGCGATGCGCTGCTCCAGAGAGCGCCGCGAGAGCTGCGAGAGCTTCA 2340
2305 AGAGGACAGCTCTCTACCTTGAAGAGCTCCAGCGGATGAGAGAGCTCTGCTGCTACG 2364
2341 AGAGGACAGCTCTCTACCTTGAAGAGCTCCAGCGGATGAGAGAGCTCTGCTGCTACG 2400
2365 TGCAG 2424
2401 TGCAG 2460
2425 AGGACAG 2484
2461 AGGACAG 2520
2485 TCAAGGAG 2544
2521 TCAAGGAG 2580
2545 TGCCTGAG 2604
2581 TGCCTGAG 2640
2605 AGGACAG 2664
2641 AGGACAG 2700
2665 CGAAAG 2724
2701 CGAAAG 2760
2725 TGCAG 2784
2761 TGCAG 2820
2785 TGCAG 2844
2821 TGCAG 2880
2845 TGCAG 2904
2881 TGCAG 2940
2905 TCAACCGCGCGCTCAAGGCTGGAGAGAAATGCGCAAACTCTTGGGCTCTGCGGC 2964

2941 TCAACCGCGCGCTCAAGGCTGGAGAGAAATGCGCAAACTCTTGGGCTCTGCGGC 3000
2965 TGAAGTGTACAG 3024
3001 TGAAGTGTACAG 3060
3025 ACATCTCAAG 3084
3061 ACATCTCAAG 3120
3085 CATTTCAACAG 3144
3121 CATTTCAACAG 3180
3145 CCTCCCTGCTACTCTCACTCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3204
3181 CCTCCCTGCTACTCTCACTCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3240
3205 GCGCGCGCGCGCTGCGCTGCGAG 3264
3241 GCGCGCGCGCGCTGCGCTGCGAG 3300
3265 TCAAGTGTACAG 3324
3301 TCAAGTGTACAG 3360
3325 AGAGGAG 3384
3361 AGAGGAG 3420
3385 AGCGGAG 3444
3421 AGCGGAG 3480
3445 AGCGGAG 3504
3481 AGCGGAG 3540
3505 GCGCGCGCGCGCTGCGCTGCGAG 3564
3541 GCGCGCGCGCGCTGCGCTGCGAG 3600
3565 AGCGGAG 3624
3601 AGCGGAG 3660
3625 AGCGGAG 3684
3661 AGCGGAG 3720
3685 CACCGAG 3744
3721 CACCGAG 3780
3745 TCCATCCCAAGATTCGCAATGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3804
3781 TCCATCCCAAGATTCGCAATGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3840
3805 ACATCCAG 3864
3841 ACATCCAG 3900
3865 AGGTTGAG 3924
3901 AGGTTGAG 3960
3925 TGGGAG 3984
3961 TGGGAG 4020
3985 AAAAAAAAAAAAAAAAAAAAAA 4006

	35	Indels	36	Gaps
OY	8	GCAGCCTGTGCCTCTCTCTGTGGCACGTGGGAAGCCCTTGGGCCGCCGCCGCCGAGTTGCC		
Db	1	GCAGCGCTGTGTTCTCTGTGTGGCACGTGGGAAGCCCTTGGGCCGCCGCCGCCGAGTTGCC		
OY	68	GGCGGCTCCCCGCTGGCCGAGCCGTGGCTCCCTTGGCGGCCACGACACTACCGGAGCTCT		
Db	61	GGCGCTCTCCCTGCGCTGGAGCCGTGGGCTCCTCTGCTGCGACCCACTACCGGAGAGTCT		
OY	128	GCCGCTGGCAGCTTCTGTGGCGGCGGCTGGGGCCCGAGAGGTGGCGGCTGTGTACAGCGGG		
Db	121	GCCGCTGGGCAAGTTCTGTGGCGGCGGCTGGGGCCCGAGGAGGTGGCGGCTGTGTACAGCGGG		
OY	188	GGACCCGGCGGCTTTCGCGCGCTGTGTGGCCACAGTCCGTGTGTGGCGGCTGTGTGGGAGCG		
Db	181	GGACCCGGCGGCTTTCGCGCGCTGTGTGGCCACAGTCCGTGTGTGGCGGCTGTGTGGGAGCG		
OY	248	ACGGCCGCGCCCGCGCGGCGGCGGCTCTTCCGTCAGGTGCTGTGCTGAAGAGAGCTGTGGC		
Db	241	ACGGCCGCGCCCGCGCGGCGGCGGCTCTTCCGTCAGGTGCTGTGCTGAAGAGAGCTGTGGC		
OY	308	CCGAGTGTGACGAGGCTGTGTGACGAGCGGCGGACGAAGAGTGTGGCTTTCGGCTTCGC		

[illegible]

OY	3572	CATGTCGGCGTGAAGACGTGAGTGCTCCGGCTGAGGCCTGAGCGAAGTGTCACCAAGGCGT	3631
Db	3601	CATGTCGGCGTGAAGACGTGAGTGCTCCGGCTGAGGCCTGAGCGAAGTGTCACCAAGGCGT	3660
OY	3632	GAGTGTCCAGCAGCACACTCCCGTCTTCACTTCCGCCACAGAGCTGGCCCTCGGCCTCACACC	3691
Db	3661	GAGTGTCCAGCAGCACACTCCCGTCTTCACTTCCGCCACAGAGCTGGCCCTCGGCCTCACACC	3720
OY	3692	GGGCCAGCTTTTTCCTCACCAGAGAGCCCGGCTTCCACTCCCCACATAGAAATAGTCCATCC	3751
Db	3721	GGGCCAGCTTTTTCCTCACCAGAGAGCCCGGCTTCCACTCCCCACATAGAAATAGTCCATCC	3780
OY	3752	CCAGATTGGCATGTGTACCCCTGGCCCTGGCCCTGCTTGGCTTCCACCCCACCATCC	3811
Db	3781	CCAGATTGGCATGTGTGTACCCCTGGCCCTGGCCCTGCTTGGCTTCCACCCCACCATCC	3840
OY	3812	AGGTGAGACACCCCTGAGAAGAACCTTGGAGAGCTCTGGAAATTTGGAGTGAACCAAAGGTGTG	3871
Db	3841	AGGTGAGACACCCCTGAGAAGAACCTTGGAGAGCTCTGGAAATTTGGAGTGAACCAAAGGTGTG	3900
OY	3872	CCCTGTACACAGCGCAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAAATTTGGGGG	3931
Db	3901	CCCTGTACACAGCGCAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAAATTTGGGGG	3960
OY	3932	GAGGTGCTGTGGGAGATAAAATTAATTAATATGAGTTTTCAGTTTTCAGTTTTGAAAAAAA	3991.
Db	3961	GAGGTGCTGTGGGAGATAAAATTAATTAATATGAGTTTTCAGTTTTCAGTTTTGAAAAAAA	4020
OY	3992	AAAAAAAAAAAAAA 4006	
Db	4021	AAAAAAAAAAAAAA 4035	
RESULT 4	E36819	LOCUS	4037 bp DNA linear PAT 18-JUN-2001
DEFINITION	E36819	Human telomerase catalytic subunit promoter.	
VERSION	E36819.1	GI:13022782	
KEYWORDS	JP 1999253177-A/27.		
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 4037)		
AUTHORS	Thomas,R.S., Joachim,U.R., Toru,N., Karen,B.C., Greg,B.M., Calvin,B.H. and William,H.A.		
TITLE	Human telomerase catalytic subunit promoter		
JOURNAL	Patent: JP 1999253177-A-27 21-SEP-1999;		
COMMENT	JERON CORP, UNIVERSITY TECHNOLOGY CORP OS Unidentified PN JP 1999253177-A/27 PD 21-SEP-1999 PF 15-OCT-1998 JP 1998320169 PR 01-OCT-1996 US 08/724,643,18-APR-1997 US 08/844,419, PR 25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR 09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR 14-AUG-1997 US 08/912,951,14-AUG-1997 US 08/915,503 PI THOMAS, R SECHUI,J JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B MORIN. PI CALVIN B HAREI,WILLIAM H ANDREWS PC C12N15/09,A6IK31/70,A6IK38/55,A6IK39/395,A6IK39/395,A6IK48/00, PC C12O1/02, PC C12O1/48,C12O1/68,G01N33/15,G01N33/48,G01N33/50//CO7K14/47, PC CO7K16/40, PC C12M1/19,C12N1/21,C12N5/10,C12M9/12,C12P21/08,(C12N1/19, PC C12R1/84), PC (C12N1/21,C12R1/19),(C12N9/12,C12R1/19),(C12M9/12,C12R1/84), PC (C12N9/12,C12R1/91),C12N15/00,A6IK37/64,C12N5/00 CC Strandedness: Single; CC Topology: Linear; FH Key Location/Qualifiers FT CDS 56..343d. Location/Qualifiers		
FEATURES	FT	CDS	Location/Qualifiers

[illegible]


```

REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.
TITLE          Jones, C. J., Kipling, D. G., Wilkinson, G., Moshary, B. D. and
                Skinner, J. W.
JOURNAL         Cell lines, their preparation and use
                Patent: WO 021655-A 1 28-FEB-2002;
                University of Wales College of Medicine (GB)
FEATURES       Location/Qualifiers
                1..4070
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
BASE COUNT     670 a 1383 c 1296 g 721 t
ORIGIN
Query Match    99.1%; Score 3969.4; DB 6; Length 4070;
Best Local Similarity 99.1%; Pred. No. 9.2e-93;
Matches 3980; Conservative 0; Mismatches 1; Indels 36; Gaps 1
QY      6 AGGACAGCGCGCGCCCTCGCGCGGACAGCTGGGAAGCCCTGAGCCCGGACACCCCGGAGT
Db      19 ACGGAGCGCTGCTCTCTGCTGGACAGTGGGAAGCCCTGAGCCCGGACACCCCGGAGT
QY      66 CCGGCGGCTCCCGGCTGCGGAGCCGTGGGCTCCCGGCGGCGAGCCACTACCCGAGGTG
Db      79 CCGCGGCTCCCGGCTGCGGAGCCGTGGGCTCCCGGCGGCGAGCCACTACCCGAGGTG
QY      126 CTGCGCGCTGACAGCTGCTGGCGGCGCCCGGAGGCGCCAGGCGTGGGAGCGCC
Db      139 CTGCGCGCTGACAGCTGCTGGCGGCGCCCGGAGGCGCCAGGCGTGGGAGCGCC
QY      186 GGGGAGCCCGGCGGCTTCCGCGCCTGCTGGTGGCCAGTGCCTGGTGGCTGCGCCGAGC
Db      199 GGGGAGCCCGGCGGCTTCCGCGCCTGCTGGTGGCCAGTGCCTGGTGGCTGCGCCGAGC
QY      246 GCACGCGCGCCCGCGCGCCCTCTCTTCCGCGCAGTGTCTGCTTAAGAGAGCTGATG
Db      259 GCACGCGCGCCCGCGCGCCCTCTCTTCCGCGCAGTGTCTGCTTAAGAGAGCTGATG
QY      306 GCCGAGTGTGTGAGAGGTGTGTGAGGCGCGCGCGAGAGAACGTGCTGGCTTGGGCTTC
Db      319 GCCGAGTGTGTGAGAGGTGTGTGAGGCGCGCGCGAGAGAACGTGCTGGCTTGGGCTTC
QY      366 GCGGTGTGTGAGCGGGGCGCGGGGGCCCGGAGGCGCTTACACACAGCGCGCAGC
Db      379 GCGGTGTGTGAGCGGGGCGCGGGGGCCCGGAGGCGCTTACACACAGCGCGCAGC
QY      426 TACCTGCCCAACACGCTGTGACCGAGCCACTGTGGGGGAGACGGGGGCGTGGGGCTGTGCTG
Db      439 TACCTGCCCAACACGCTGTGACCGAGCCACTGTGGGGGAGACGGGGGCGTGGGGCTGTGCTG
QY      486 CCGCGGTGTGGGGAGAGAGTGTGTTACCTGCTGTGACAGCTGTGCGCGGCTTTGTGGCTG
Db      499 CCGCGGTGTGGGGAGAGAGTGTGTTACCTGCTGTGACAGCTGTGCGCGGCTTTGTGGCTG
QY      546 GTGAGTCCAGCTGTGCGCTTACAGAGTGGGGGCGCGCTGTACCAAGTGTGCGCTGCC
Db      559 GTGAGTCCAGCTGTGCGCTTACAGAGTGGGGGCGCGCTGTACCAAGTGTGCGCTGCC
QY      606 ACTCAGGCGCGGGCCCGGCGCACACGCTAGTGAACCCCGAAGAGCTGTGGAGTGGGAACGG
Db      619 ACTCAGGCGCGGGCCCGGCGCACACGCTAGTGAACCCCGAAGAGCTGTGGAGTGGGAACGG
QY      666 GCGTGGAAACATATAGCGTCAAGGAGGCGGGGATCCCTGTTGGGCTGTGCCAGCCCGGGTGGC
Db      679 GCGTGGAAACATATAGCGTCAAGGAGGCGGGGATCCCTGTTGGGCTGTGCCAGCCCGGGTGGC
QY      726 AGGAGGCGCGGGGAGAGTGTGCACAGCGGAAGTGTCCGCTTGCCCAAGAGAGCCAGGCGGGC
Db      739 AGGAGGCGCGGGGAGAGTGTGCACAGCGGAAGTGTCCGCTTGCCCAAGAGAGCCAGGCGGGC
QY      786 GCTGCCCTGTAGCGGAGCGGACGCGCTGTGGGCGAGGGGCTGTGGGCCCAAGCCCGGAGG

```



```

QY 2970 TGTACAGCCTGTTTCTGATTTTCAGAGTGAACAGCCTCCAGACGGTGTGCACCAATC 3029
Db 3019 TGTACAGCCTGTTTCTGATTTTCAGAGTGAACAGCCTCCAGACGGTGTGCACCAATC 3078
QY 3030 TACAAGATCTCTGCTGTCAGAGCGCTACAGGTTTCAGCAATGTGTCTGACAGCTCCATTT 3089
Db 3079 TACAAGATCTCTGCTGTCAGAGCGGTACAGGTTTCAGCAATGTGTCTGACAGCTCCATTT 3138
QY 3090 CACAGCAAGTTTGAAGAAGCCCAATTTTCTGCGGTCATCTGACAGCGCCCTCC 3149
Db 3139 CACAGCAAGTTTGAAGAAGCCCAATTTTCTGCGGTCATCTGACAGCGCCCTCC 3198
QY 3150 CTGCTGACCTCACTCTGTAAGCAAGACGAGAGATGTGCTGGGGCCCAAGGGCC 3209
Db 3199 CTGCTGACCTCACTCTGTAAGCAAGACGAGAGATGTGCTGGGGCCCAAGGGCC 3258
QY 3210 GCCGGCCCTCTGCTCCAGAGCCGTGCAAGTGTGTGTCACCAAGATTTCTGTCAG 3269
Db 3259 GCCGGCCCTCTGCTCCAGAGCCGTGCAAGTGTGTGTCACCAAGATTTCTGTCAG 3318
QY 3270 CTGACCTGACAGCTGTGTACCTACCTAGCTGCACTCTGCGGTCACACAGCAAGCC 3329
Db 3319 CTGACCTGACAGCTGTGTACCTACCTAGCTGCACTCTGCGGTCACACAGCAAGCC 3378
QY 3330 CAGCTGAGTCTGGAAGCTCCCGGGGACAGCGTGCCTGGAAGCCGACCAACCG 3389
Db 3379 CAGCTGAGTCTGGAAGCTCCCGGGGACAGCGTGCCTGGAAGCCGACCAACCG 3438
QY 3390 GCACCTGCTGAGACTTCAAGACCATCTGTGACTGATGAGCAAGCCGACCAAGCC 3449
Db 3439 GCACCTGCTGAGACTTCAAGACCATCTGTGACTGATGAGCAAGCCGACCAAGCC 3498
QY 3450 GAGAGCAGACAGCAGACAGCCCTGTCAAGCGCGGCTCTAGCTCCAGAGGAGGGGCG 3509
Db 3499 GAGAGCAGACAGCAGACAGCCCTGTCAAGCGCGGCTCTAGCTCCAGAGGAGGGGCG 3558
QY 3510 CCCACACCCAGGCGCCGACCGGAGAGTCTGAGGCTGTGAGTGTGTTGGCGAGGCG 3569
Db 3559 CCCACACCCAGGCGCCGACCGGAGAGTCTGAGGCTGTGAGTGTGTTGGCGAGGCG 3618
QY 3570 TGCATTCGCGGCTGAAGGCTGAGTGTGCGGCTGAGGCTGAGGAGTGTGTTGGCGAGGCG 3629
Db 3619 TGCATTCGCGGCTGAAGGCTGAGTGTGCGGCTGAGGCTGAGGAGTGTGTTGGCGAGGCG 3678
QY 3630 CTGAGTGTCCACACAGCTGCGGCTGACCTCCACAGAGCTGCGCTGCGCTCCACCC 3689
Db 3679 CTGAGTGTCCACACAGCTGCGGCTGACCTCCACAGAGCTGCGCTGCGCTCCACCC 3738
QY 3690 CAGGCGCAGCTTTCTTCTACAGGAGCCGCGCTTCCACTCCCAATAGGAATAGTCAT 3749
Db 3739 CAGGCGCAGCTTTCTTCTACAGGAGCCGCGCTTCCACTCCCAATAGGAATAGTCAT 3798
QY 3750 CCCCAGATTCGCAATGTTCACCCCTGCGCCCTCTCTTTCCTTCCACCCCAACAT 3809
Db 3799 CCCCAGATTCGCAATGTTCACCCCTGCGCCCTCTCTTTCCTTCCACCCCAACAT 3858
QY 3810 CCAGTGTGAACCTTGAGAGACCTTGGAGCTTGGGAATTTGGAGTGAACCAAGTG 3869
Db 3859 CCAGTGTGAACCTTGAGAGACCTTGGAGCTTGGGAATTTGGAGTGAACCAAGTG 3918
QY 3870 TGGCTGTACACAGGAGGAGACCTGACCTGATGAGGCTGCTGAGTGAATTTGG 3929
Db 3919 TGGCTGTACACAGGAGGAGACCTGACCTGATGAGGCTGCTGAGTGAATTTGG 3978
QY 3930 GGGAGTGTGAGGAGTAAATTAATATATAGTGTGTTTGAATTTGAATTTGA 3986
Db 3979 GGGAGTGTGAGGAGTAAATTAATATATAGTGTGTTTGAATTTGAATTTGA 4035

```

RESULT 6
 ARI04587
 LOCUS ARI04587
 DEFINITION Sequence 224 from patent US 6093809. 4015 bp DNA linear PAT 14-FEB-2001

```

ACCESSION ARI04587
VERSION ARI04587.1 GI:12817295
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Cech, T. R. and Lingner, J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 224 25-JUL-2000;
FEATURES
    Location/Qualifiers
        source 1..4015
        BASE COUNT 663 a 1363 c 1275 g 714 t
        ORIGIN
Query Match
Best Local Similarity 99.18; Score 3969; DB 6; Length 4015.
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;
QY 8 GCACGCTGCGTCTGCTGCGCAGTGGAGAGCCCTGCGCCCGCCCGCAGCCGATGCC 67
Db 1 GCACGCTGCGTCTGCTGCGCAGTGGAGAGCCCTGCGCCCGCCCGCAGCCGATGCC 60
QY 68 GCGGCTGCCGCTGCGCAGAGCTGCGCTCCTGCTGCGCAGCCACTACGCGAGGTGCT 127
Db 61 GCGGCTGCCGCTGCGCAGAGCTGCGCTCCTGCTGCGCAGCCACTACGCGAGGTGCT 120
QY 128 GCGGCTGCCAGCTGTGTCGCGCGCCCTGCGCGCCCGCAGGCGTGGGCTGTGAGCG 187
Db 121 GCGGCTGCCAGCTGTGTCGCGCGCCCTGCGCGCCCGCAGGCGTGGGCTGTGAGCG 180
QY 188 GGAACCGGCGGCTTTCGCGGCGCTGTCGCGCCAGTGCCTGTGCTGCTGGAGCG 247
Db 181 GGAACCGGCGGCTTTCGCGGCGCTGTCGCGCCAGTGCCTGTGCTGCTGGAGCG 240
QY 248 ACGGCGCGCCCGCCGCGCCCTTTCGCGCAGTGTCTGCTGCGCAGGTCTGCTGCG 307
Db 241 ACGGCGCGCCCGCCGCGCCCTTTCGCGCAGTGTCTGCTGCGCAGGTCTGCTGCG 300
QY 308 CCGAGTGTGAGAGAGCTGTGCGAGCGGCGGCGGAAGACGTCTGCGCTTGGCTGCG 367
Db 301 CCGAGTGTGAGAGAGCTGTGCGAGCGGCGGCGGAAGACGTCTGCGCTTGGCTGCG 360
QY 368 GCTGTGAGAGCGGCGCGCGCGCGCCCGCGAGGCTTTCACACAGAGTGGAGCTGA 427
Db 361 GCTGTGAGAGCGGCGCGCGCGCGCCCGCGAGGCTTTCACACAGAGTGGAGCTGA 420
QY 428 CTTGCCCAACAGAGTACGACGACTGCGGGGAGCGGGCGTGGGGCTGTGCTGCG 487
Db 421 CTTGCCCAACAGAGTACGACGACTGCGGGGAGCGGGCGTGGGGCTGTGCTGCG 480
QY 488 CCGCGTGGGAGAGAGTGTCTGTACCTGTGACGCTGCGCGCTTGTGCTGTGCT 547
Db 481 CCGCGTGGGAGAGAGTGTCTGTACCTGTGACGCTGCGCGCTTGTGCTGTGCT 540
QY 548 GGTCTCCACCTGCGCTACAGAGTGTGCGGGCGCGCGCTGTACAGCTGCGCGCTGC 607
Db 541 GGTCTCCACCTGCGCTACAGAGTGTGCGGGCGCGCGCTGTACAGCTGCGCGCTGC 600
QY 608 TCAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 667
Db 601 TCAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY 668 CTGGAACCATAGCTCAGAGGAGCGCGGGGCTCCCTGCGGCTGCGCAGCGCGGTCGAG 727
Db 661 CTGGAACCATAGCTCAGAGGAGCGCGGGGCTCCCTGCGGCTGCGCAGCGCGGTCGAG 720
QY 728 GAGGCGCGGGGCGAGTGGCGCAAGCTGTGCGCTTGGCCAGAGAGCCGAGGCGTGGCG 787
Db 721 GAGGCGCGGGGCGAGTGGCGCAAGCTGTGCGCTTGGCCAGAGAGCCGAGGCGTGGCG 780
QY 788 TGGCCTTGAGCCGAGCGAGCGCGCTTGGGAGGGGTCTGCGGCCACCGCGGCGAGGAC 847

```


[illegible]

RESULT 7			
ARI75848			
LOCUS	4015 bp	DNA	linear
ARI75848			PAT 17-DEC-2001

```

DEFINITION      Sequence 224 from patent US 6309867.
ACCESSION       AR175848
VERSION         AR175848.1  GI:17917147
KEYWORDS
SOURCE
ORGANISM
REFERENCE       1 (bases 1 to 4015)
AUTHORS        Cech,T.R. and Nakamura,T.
TITLE          Telomerase
JOURNAL        Patent: US 6309867-A 224 30-OCT-2001;
FEATURES
    source      1..4015
                Location/Qualifiers
BASE COUNT      663 a 1363 c 1275 g 714 t
ORIGIN
Query Match     99.1%;   Score 3969;  DB 6;   Length 4015;
Best Local Similarity 99.1%;   Pred. No. 9,4e-93;
Matches 3379;  Conservative 0;  Mismatches 0;  Indels 36;  Gaps 1

```

	Query Match	99.1%;	Score 3969;	DB 6;	Length 4015;
	Best Local Similarity	99.1%;	Pred. No. 9.4e-93;		
	Matches 3979;	Conservative	0;	Mismatches	0; Indels 36; Gaps
OY	8	GCAAGCTGTCCTGTCTGGCCACGTGGGAAGCCCTGGCCCCCGGCACACCCTCCGATGCC	67		
Dd	1	GCAGGCTGCGTCCCTGTCTGGCCACGTGGGAAGCCCTGGCCCCCGGCACACCCTCCGATGCC	60		
OY	68	GCGGCTCCCGCTGGGAGCGTGCGCTCCCTGCTGGAGCACAACGCGAGAGTGCT	127		
Dd	61	GCGGCTCCCGCTGGGAGCGTGCGCTCCCTGCTGGAGCACAACGCGAGAGTGCT	120		
OY	128	GCCGCTGGCCAACTGTCGTGGCCGCGCTGGGGCCCAGAGGCTGGGAGGCTGTGTGACCCGG	187		
Dd	121	GCCGCTGGCCAAAGTTGATGGGGCGCTGTGGGCCCCAGAGGCTGTGGGAGGCGGG	180		
OY	188	GGACCCGGCGGCTTTCGCGCGCTGTGTGGCCAACTGCTGTGCTGCTCCCTGGACGC	247		
Dd	181	GGACCCGGCGGCTTTCGCGCGCTGTGTGGCCAACTGCTGTGCTGCTCCCTGGACGC	240		
OY	248	ACGGCGCGCGCGCGCGCGCGCGCTCCCTTCGCGCAGGTGTCGCGCTGAAGAAGCTGTGGGC	307		
Dd	241	ACGGCGCGCGCGCGCGCGCGCGCTCCCTTCGCGCAGGTGTCCTGCTGAAGAAGCTGTGGGC	300		
OY	308	CCGAGTGTCTGAGAGAGGCTGTGTGCGAGCGCGGCGGCGAAGAACCTGTGCGCTTTCGGCTTCGC	367		
Dd	301	CCGAGTGTCTGAGAGAGGCTGTGTGCGAGCGCGGCGGCGAAGAACCTGTGCGCTTTCGGCTTCGC	360		
OY	368	GCTGCTGCAAGCGGGCGCGCGGGGGCCCCCGGAGGCTTCAACCAACAGCTGGCCACTA	427		
Dd	361	GCTGCTGCAAGCGGGCGCGCGGGGGCCCCCGGAGGCTTCAACCAACAGCTGGCCACTA	420		
OY	428	CCTGCGCCAACACAGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGCGTGTGTGGC	487		
Dd	421	CCTGCGCCAACACAGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGCGTGTGTGGC	480		
OY	488	CCGCGTGGGCGACGACGTGTGTTCACCTCTGTGGCACGTCGCGCGCTTATTGTGTGT	547		
Dd	481	CCGCGTGGGCGACGACGTGTGTTCACCTCTGTGGCACGTCGCGCGCTTATTGTGTGT	540		
OY	548	GCGTCCCAAGCTGCGCTTAACAGGTGTGGGGGCGCGCGCTGTACCAGCTCGGGCGTGGCAC	607		
Dd	541	GCGTCCCAAGCTGCGCTTAACAGGTGTGGGGGCGCGCGCTGTACCAGCTCGGGCGTGGCAC	600		
OY	608	TCAAGCCCGCGCGCGCCACACAGGTAGTGTGACCCCGAAGGCGTGTGGGATCCGAACGGGC	667		
Dd	601	TCAAGCCCGCGCGCGCCACACAGGTAGTGTGACCCCGAAGGCGTGTGGGATCCGAACGGGC	660		
OY	668	CTGGAACCATAGCGTCAAGGAGGCGCGGGTCCCTGTGGGCTGTGCACGCCCGGGTGTGCAG	727		
Dd	661	CTGGAACCATAGCGTCAAGGAGGCGCGGGTCCCTGTGGGCTGTGCACGCCCGGGTGTGCAG	720		
OY	728	GAGGCGCGGGGCGAGTGCACCGCAAGTCTTCCTGTGCGCAAAGGCCCGCAGCGCTGGCGC	787		
Dd	721	GAGGCGCGGGGCGAGTGCACCGCAAGTCTTCCTGTGCGCAAAGGCCCGCAGCGCTGGCGC	780		

Qy	788	TCGCCCTGAGCCGAGAGGACACCCGTTGGGCGAGGGGGTCCTGGCCCAACCCGGGCAAGAC	847
Db	781	TCGCCCTGAGCCGAGAGGAGGAGGCGCCGTTGGGCGAGGGGGTCCTGGGCGACACCCGGGCAAGAC	840
Qy	848	GGCTGAGACCGAGTGAACCGTGGTTTTCTGTGTGTGTCTACTGTCCGACAGCCCGCGAAGAAAC	907
Db	841	GGCTGAGACCGAGTGAACCGTGGTTTTCTGTGTGTGTGTACTGTCCGACAGCCCGCGAAGAAAC	900
Qy	908	CACCTCTTTTGGAGGGGTGGCGCTCTGTGGCAGCGCCACTCCACCATCCGTGGGGCCGCA	967
Db	901	CACCTCTTTTGGAGGGGTGGCGCTCTGTGGCAGCGCCACTCCACCATCCGTGGGGCCGCA	960
Qy	968	GCACACGAGGGGACCCCCATCCACATCCGAGGCCACACAGTCCCTGGGACAGCTTGTCC	1027
Db	961	GCACACGAGGGGACCCCCATCCACATCCGAGGCCACACAGTCCCTGGGACAGCTTGTCC	1020
Qy	1028	CCGGGTGACGCGCGAGACCAAGACACTTCTCTCTACTCTTAGGGCAACAGAGACAGTGGG	1087
Db	1021	CCGGGTGACGCGCGAGACCAAGACACTTCTCTCTACTCTTAGGGCAACAGAGACAGTGGG	1080
Qy	1088	GGCCCTCTTCTACTACACTCTCTGTGAGGCCAGCCAGCTGAGTGGGCGCTGTGGAGGCTGTGA	1147
Db	1081	GGCCCTCTTCTACTACACTCTCTGTGAGGCCAGCCAGCTGAGTGGGCGCTGTGGAGGCTGTGA	1140
Qy	1148	GACATCTTTTCTGGGTTCACAGCCCTCGATCCAGAGACTCCCGCAGSTTCCCGCCCT	1207
Db	1141	GACATCTTTTCTGGGTTCACAGCCCTCGATCCAGAGACTCCCGCAGSTTCCCGCCCT	1200
Qy	1208	GGCCAGAGGCTACTGGCAATATGGGGCCCTCGTTTCTTGAGCTGTGTGGAAACAGCGCA	1267
Db	1201	GGCCAGAGGCTACTGGCAATATGGGGCCCTCGTTTCTTGAGCTGTGTGGAAACAGCGCA	1260
Qy	1268	GTCGCCCTAGGGGGTCTCTCAAGAGCGACGCGCGCTGACGTCGGGTCAACCCAGC	1327
Db	1261	GTCGCCCTAGGGGGTCTCTCTCAAGAGCGACGCGCGCTGACGTCGGGTCAACCCAGC	1320
Qy	1328	AGCCGGTGTCTGTGTCCCGGGAGAAAGCCCAAGGGGCTGTGTGGGGGCCCCCGAGAGAGAGA	1387
Db	1321	AGCCGGTGTCTGTGTCCCGGGAGAAAGCCCAAGGGGCTGTGTGGGGGCCCCCGAGAGAGAGA	1380
Qy	1388	CACAGACCCCCGCTGGCTGTGTGTGACAGTGGTCCGGCGACACACAGACCCCTGGAGGTGA	1447
Db	1381	CACAGACCCCCGCTGGCTGTGTGTGACAGTGGTCCGGCGACACACAGACCCCTGGAGGTGA	1440
Qy	1448	CGGCTTGTGGGGGCTGCCCTGCGCGGCTGGTGGCCCGACAGCGCTGTGGGGCTCCAGGCA	1507
Db	1441	CGGCTTGTGGGGGCTGCCCTGCGCGGCTGGTGGCCCGACAGCGCTGTGGGGCTCCAGGCA	1500
Qy	1508	CAAGCAACCCGCTTCTCTAGGAAACACCAAGATTCCTCCCTGGGGAAAGATGCCAA	1567
Db	1501	CAAGCAACCCGCTTCTCTAGGAAACACCAAGATTCCTCCCTGGGGAAAGATGCCAA	1560
Qy	1568	GCTCTGCTGACAGAGTGAACGTGAGAGATGAGCGTGGGAGACTGGCTTGTGGCTGGCAG	1627
Db	1561	GCTCTGCTGACAGAGTGAACGTGAGAGATGAGCGTGGGAGACTGGCTTGTGGCTGGCAG	1620
Qy	1628	GAGGCCAGGGGGTGGCTGTGTTCGCGCGCGAGAGACACCGTCTGGTGAAGAGATCCTGGC	1687
Db	1621	GAGGCCAGGGGGTGGCTGTGTTCGCGCGCGAGAGACACCGTCTGGTGAAGAGATCCTGGC	1680
Qy	1688	CAGGCTCTGACACTGGCTGATGATGTGTACGTCGTCAGGCTGCTAGGCTTCTTTTAA	1747
Db	1681	CAGGCTCTGACACTGGCTGATGATGTGTACGTCGTCAGGCTGCTAGGCTTCTTTTAA	1740
Qy	1748	TTCTACGAGAGACCAAGTTCAAAAGAACAGGCTCTTTTCTACCGGAAAGAGTGTCTGAG	1807
Db	1741	TTCTACGAGAGACCAAGTTCAAAAGAACAGGCTCTTTTCTACCGGAAAGAGTGTCTGAG	1800
Qy	1808	CAGGTTGCAAGCAATGGATATGACACACACTTGAAGAGGGGTGACACTCGGGAGAGCTGTC	1867
Db	1801	CAGGTTGCAAGCAATGGATATGACACACACTTGAAGAGGGGTGACACTCGGGAGAGCTGTC	1860
Qy	1868	GGAGCAGAGAGTGAAGCAGATCGGGAAGCCAGGGCCGCTGTGACGTCCAGACTCCG	1927

Db	1861	GGAGGCGAGAGGTCAAGGACACATCCGGGAAGCGAGGCCCGCTGTGATGCTCAGACTCCG	1920
Qy	1928	CTTCACTCCCAAGCCTGACGGGCTTCGGCGGATTTGTGAATATGAGCTACGCTGTGGAGGC	1987
Db	1921	CTTATCTCCCAAGCCTCAGGGGCTGTCCGGCGATTTGTATACATGACTACGCTGTGGAGGC	1980
Qy	1988	GAGAACCTTTCGCGAGAGAAAAGGGCGCGAGCGTCTCACTCGAGGGTGAAGGCACTGTT	2047
Db	1981	CAGAACCTTTCGCGAGAGAAAAGGGCGCGAGCGTCTCACTCGAGGGTGAAGGCACTGTT	2040
Qy	2048	CAGAGTCTCACTACAGAGCGGGCGCGCGCCCGCCGACTCTCTGGCGCTTGTGCTGGG	2107
Db	2041	CAGGCTCTCACTACAGAGCGGGCGCGCGCCCGCCGACTCTCTGGCGCTTGTGCTGGG	2100
Qy	2108	CCTGGAGATATCCACAGAGCGCGCGCGACTCTTCGTGTGCGTGTGCGGGCCAGAACCC	2167
Db	2101	CCTGGAGATATCCACAGAGCGCGCGCGACTCTTCGTGTGCGTGTGCGGGCCAGAACCC	2160
Qy	2168	GGCGGCTGAGCTGTG-----CATGCCCA	2191
Db	2161	GGCGGCTGAGCTGTGACTTGTGAAAGTGGATGTGAGCGGCGCGAGACACATCCCA	2220
Qy	2192	GGACAGCTCAGAGAGGTACATGCCGAGATATCAACCCAGAACACTACTCGTGC	2251
Db	2221	GGACAGGTATCAGAGAGTCACTCCGACGATATCAACCCAGAACACTACTCGTGC	2280
Qy	2252	TGGATATCCGTGTCTCAAGAGGCGCGCCATAGGGGCACTGCGCAAGGCTTCAAGACCA	2311
Db	2281	TGGATATCCGTGTCTCAAGAGGCGCGCCATAGGGGCACTGCGCAAGGCTTCAAGACCA	2340
Qy	2312	CGTCTTACCTTACAGACCTCCAGCGCTTAATAGCCAGTGTGTGGCTCACTGTGAGGA	2371
Db	2341	CGTCTTACCTTACAGACCTCCAGCGCTTAATAGCCAGTGTGTGGCTCACTGTGAGGA	2400
Qy	2372	GACCAAGCCCGCTAGGGAGTGCCTGTCTATGAGACAGACTCTTCCTGAATGAGGCGAG	2431
Db	2401	GACCAAGCCCGCTAGGGAGTGCCTGTCTATGAGACAGACTCTTCCTGAATGAGGCGAG	2460
Qy	2432	CAGTAGCCTCTGAGAGTCTTCTACGCTTCACTGTGACACAGCGCTCGCATCAGAGG	2491
Db	2461	CAGTAGCCTCTGAGAGTCTTCTACGCTTCACTGTGACACAGCGCTCGCATCAGAGG	2520
Qy	2492	CAGTAGCTACCTCAGTGTGCGAGGGAGTCCCGAGGGCTCCATCTCTCCACGCTGCTCG	2551
Db	2521	CAGTAGCTACCTCAGTGTGCGAGGGAGTCCCGAGGGCTCCATCTCTCCACGCTGCTCG	2580
Qy	2552	CAGCTGTGTACAGGGGAGATGAGAGAACAGCTGTTTGGCGGGATTGGCGGGAGCGAGT	2611
Db	2581	CAGCTGTGTGTACAGGGGAGATGAGAGAACAGCTGTTTGGCGGGATTGGCGGGAGCGAGT	2640
Qy	2612	GCCTCTGCGTTTGGTGGATGATTTCTTGTGGTGAACCTCACTCACCCAGCGCAAAAC	2671
Db	2641	GCCTCTGCGTTTGGTGGATGATTTCTTGTGGTGAACCTCACTCACCCAGCGCAAAAC	2700
Qy	2672	CTTCTCAGAGACCTGTGTCGAGAGTTCCTGAGATATGGTGGTGGTGAAGTCTGGGAA	2731
Db	2701	CTTCTCAGAGACCTGTGTCGAGAGTTCCTGAGATATGGTGGTGGTGAAGTCTGGGAA	2760
Qy	2732	GACAGTGTGAATCTTCCTGTGAGAAAGACAGAGCCTGGGGTGGAGAGGCTTTTGTCAAGT	2791
Db	2761	GACAGTGTGAATCTTCCTGTGAGAAAGACAGAGCCTGGGGTGGAGAGGCTTTTGTCAAGT	2820
Qy	2792	GGCGGCGCAAGGACTTATCCCTGGTGGGCGCTGTCTGATATCCCGAGACCTGGAAGT	2851
Db	2821	GGCGGCGCAAGGACTTATCCCTGGTGGGCGCTGTCTGATATCCCGAGACCTGGAAGT	2880
Qy	2852	GGAGAGGAGTACTCAGAGTATGCCCGAGACTTCATCAGAGCCAGTCTACCTTCAACCG	2911
Db	2881	GGAGAGGAGTACTCAGAGTATGCCCGAGACTTCATCAGAGCCAGTCTACCTTCAACCG	2940
Qy	2912	CGGCTTCAAGGCTGGGAGGAACATCGTCCGAACCTTTTGGGCTTTGCGGCTGAAGTG	2971

[illegible]


```
|||||
Db 2941 CGGCTTCAGAGGCTGGGAGAACATGCTGCGCAAACTCTTGGGGCTTGGGCTCAAGTG 3000
Qy 2972 TCACAGCGCTTCTTGATTTGAGGTGTAACAGCTCCAGAGCGTGTCCACCAACATCTA 3031
Db 3001 TCACAGCGCTTCTTGATTTGAGGTGTAACAGCTCCAGAGCGTGTCCACCAACATCTA 3060
Qy 3032 CAAGATCTCTGCTGACAGGCTGACAGGTTTACGATCTGTGCTGACGCTCCATTCTCA 3091
Db 3061 CAAGATCTCTGCTGACAGGCTGACAGGTTTACGATCTGTGCTGACGCTCCATTCTCA 3120
Qy 3092 TCAGCAAGTTTGGAGAACCCACATTTTCTCGCGCTCATCTCTGACAGCGCTCCCT 3151
Db 3121 TCAGCAAGTTTGGAGAACCCACATTTTCTCGCGCTCATCTCTGACAGCGCTCCCT 3180
Qy 3152 CTGCTACTCATCTGGAAGCAAGAACGAGGAGTGTGCTGGGGGCAAGGGCGCGC 3211
Db 3181 CTGCTACTCATCTGGAAGCAAGAACGAGGAGTGTGCTGGGGGCAAGGGCGCGC 3240
Qy 3212 CGGGCTCTGCTCCGAGGCGCTGACAGTGTGCTGCGCACCAGCATCTTCTGCTCAAGCT 3271
Db 3241 CGGGCTCTGCTCCGAGGCGCTGACAGTGTGCTGCGCACCAGCATCTTCTGCTCAAGCT 3300
Qy 3272 GACTGACACCGTGTCACTACGTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3331
Db 3301 GACTGACACCGTGTCACTACGTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
Qy 3332 GCTAGTGTGAAAGTCTCCCGGAGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3391
Db 3361 GCTAGTGTGAAAGTCTCCCGGAGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
Qy 3392 ACTGCTCAGACTTCAAGACCATCTGAGACTGAGTGGCCACCGCCGACAGCCAGCCGA 3451
Db 3421 ACTGCTCAGACTTCAAGACCATCTGAGACTGAGTGGCCACCGCCGACAGCCAGCCGA 3480
Qy 3452 GAGCAGACACACAGACCCCTGTGACGCGCGGCTCTACGTCCAGAGGAGGAGGCGGCGC 3511
Db 3481 GAGCAGACACACAGACCCCTGTGACGCGCGGCTCTACGTCCAGAGGAGGAGGCGGCGC 3540
Qy 3512 CACACCCAGGCGCGACCCCTGGAGTGTGAGGCGTGTGAGTGTGTTGGCCGAGGCGCTG 3571
Db 3541 CACACCCAGGCGCGACCCCTGGAGTGTGAGGCGTGTGAGTGTGTTGGCCGAGGCGCTG 3600
Qy 3572 CATGTCCGCTGAAAGCTGAGTGTCCGGCTGAGGCTGAGGAGTGTGCTGAGGAGGCT 3631
Db 3601 CATGTCCGCTGAAAGCTGAGTGTCCGGCTGAGGCTGAGGAGTGTGCTGAGGAGGCT 3660
Qy 3632 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGGGCTGCTGCTGCTGCTGCTGCT 3691
Db 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGGGCTGCTGCTGCTGCTGCTGCT 3720
Qy 3692 GGGCAGGCTTCTCCACACAGAGCGCGCTTCACTTCCCAAGTGTGCTGCTGCTGCTGCT 3751
Db 3721 GGGCAGGCTTCTCCACACAGAGCGCGCTTCACTTCCCAAGTGTGCTGCTGCTGCTGCT 3780
Qy 3752 CCAGATTGCGCATTTGTTACCCCTGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 3811
Db 3781 CCAGATTGCGCATTTGTTACCCCTGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
Qy 3812 AGGAGGAGCCCTGAGAGACCTGAGGAGCTGTGGAATTTGGAGTGTGAGTGTGAGTGTG 3871
Db 3841 AGGAGGAGCCCTGAGAGACCTGAGGAGCTGTGGAATTTGGAGTGTGAGTGTGAGTGTG 3900
Qy 3872 CCCGTGTACAGAGGAGGAGCCCTGACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 3931
Db 3901 CCCGTGTACAGAGGAGGAGCCCTGACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 3960
Qy 3932 GAGGTGTGTGGAGTGAATTAATGATGTTTTCAGTGTGTAATTAATGATGTTTTCAGTGT 3966
Db 3961 GAGGTGTGTGGAGTGAATTAATGATGTTTTCAGTGTGTAATTAATGATGTTTTCAGTGT 4015
```

RESULT 9

```
AX019310
LOCUS AX019310 4015 bp DNA Linear PAT 07-SEP-2000
DEFINITION Sequence 10 from Patent WO9940221.
ACCESSION AX019310
VERSION AX019310.1 GI:10043297
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 4015)
AUTHORS Dahn,M.W., Phelps,R.C. and Brockmeyer,C.
TITLE Method for quantitatively analyzing tumor cells in a body fluid and
JOURNAL test kits suited therefor
PATENT: WO 9940221-A 10-12-AUG-1999;
DAHN MICHAEL W (DE); PHELPS ROBERT C (DE); BROCKMEYER CARSTEN (DE)
FEATURES
source location/Qualifiers
1..4015
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 663 a 1363 c 1275 g 714 t
ORIGIN
Query Match 99.1%; Score 3969; DB 6; Length 4015;
Best Local Similarity 99.1%; Pred. No. 9,4e-93;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1:
Qy 8 GCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 67
Db 1 GCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Qy 68 GCGGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 127
Db 61 GCGGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Qy 128 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187
Db 121 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Qy 188 GGAACCGGCGGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
Db 181 GGAACCGGCGGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Qy 248 ACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 307
Db 241 ACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Qy 308 CCGAGTGTCTGCAAGAGCTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
Db 301 CCGAGTGTCTGCAAGAGCTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Qy 368 GCTGCTGACGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 427
Db 361 GCTGCTGACGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Qy 428 CCGTGCACCAACAGGTGTGACCAAGCACTGCGGAGAGCGGAGCGGAGCGGAGCGGAGCGGAG 487
Db 421 CCGTGCACCAACAGGTGTGACCAAGCACTGCGGAGAGCGGAGCGGAGCGGAGCGGAGCGGAG 480
Qy 488 CCGGCTGGGAGCAAGCGTGTGACCAAGCACTGCGGAGAGCGGAGCGGAGCGGAGCGGAGCGG 547
Db 481 CCGGCTGGGAGCAAGCGTGTGACCAAGCACTGCGGAGAGCGGAGCGGAGCGGAGCGGAGCGG 540
Qy 548 GCGTCTCCAGCTGCGCTTACCAAGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
Db 541 GCGTCTCCAGCTGCGCTTACCAAGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Qy 608 TCAGGCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 667
Db 601 TCAGGCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Qy 668 CTGGAACCATAGGCTAGGAGGCGCGGAGTCCCGCTGGGCTGCGAGCCCGCGGCTGCGAG 727
```

Db 611 CTGGAACCAATAGCGTCAGAGAGAGCCGGGTTCCCTGGGCTTCCAGAGCCCGGGGTGCGAG 720
QY 728 GAGGCGGGGGGAGTGGCCACCGGAAGTGTGCCCTTGCCCAAGAGGGCCAGGCGTGGCCG 787
Db 721 GAGGGGGGGGGAGTGGCCACCGGAAGTGTGCCCTTGCCCAAGAGGGCCAGGCGTGGCCG 780
QY 788 TGCCTCTAGAGCGAGAGAGAGCCCGTGGGCGAGGGGTCTGGGGCCCAAGCGGGCGAGAG 847
Db 781 TGCCTCTAGAGCGAGAGAGAGCCCGTGGGCGAGGGGTCTGGGGCCCAAGCGGGCGAGAG 840
QY 848 GCGTGGAGCGAGTACCGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
Db 841 GCGTGGAGCGAGTACCGT 900
QY 908 CAGCTCTTTGGAGGGGTGGCGCTCTCTGGACAGCGCACTCCACCCTCGTGGGCGGCA 967
Db 901 CAGCTCTTTGGAGGGGTGGCGCTCTCTGGACAGCGCACTCCACCCTCGTGGGCGGCA 960
QY 968 GCACACAGGGGGGGGGCCCATCCACATCGCGCCACACAGTCCCTGGAGACCCCTTGTTC 1027
Db 961 GCACACAGGGGGGGGGCCCATCCACATCGCGCCACACAGTCCCTGGAGACCCCTTGTTC 1020
QY 1028 GCGGTGTACGCGAGACCAAGCACTTCTCTACTCTCTAGAGCGACAAAGAGAGAGAGTGGC 1087
Db 1021 CCGGGTGTACGCGAGACCAAGCACTTCTCTACTCTCTAGAGCGACAAAGAGAGAGAGTGGC 1080
QY 1088 GCGCTCTTCTACTAGCTCTGTAGAGCCAGGCTGACTGGCGCTGGAGGCTGTGGA 1147
Db 1081 GCGCTCTTCTACTAGCTCTGTAGAGCCAGGCTGACTGGCGCTGGAGGCTGTGGA 1140
QY 1148 GACCATCTTGTGGTTCAGAGCGCCGTGATGTCAGGGAGTCCCGCAGTGTGCCGCT 1207
Db 1141 GACCATCTTGTGGTTCAGAGCGCCGTGATGTCAGGGAGTCCCGCAGTGTGCCGCT 1200
QY 1208 GCGCCAGCGCTACTGGAATGCGGCGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1267
Db 1201 GCGCCAGCGCTACTGGAATGCGGCGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
QY 1268 GTGCCCCCTACGGGGTGTCTCTCAAGACGACTGCGCGCTGTGAGCGTGGGGTCAACCGAC 1327
Db 1261 GTGCCCCCTACGGGGTGTCTCTCAAGACGACTGCGCGCTGTGAGCGTGGGGTCAACCGAC 1320
QY 1328 AGCGGGTGTGTGTGCGCGGAGAAAGCCCAAGGGCTGTGTGGCGGGCCCGAGAGAGAGGA 1387
Db 1321 AGCGGGTGTGTGTGCGCGGAGAAAGCCCAAGGGCTGTGTGGCGGGCCCGAGAGAGAGGA 1380
QY 1388 CACAGACCCCGTGTGCGCTGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1447
Db 1381 CACAGACCCCGTGTGCGCTGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
QY 1448 CCGCTTGTGGGGGCGTGCCTGCGCGGCTGTGTGCCAGGCTGTGGGCTTCAGGCA 1507
Db 1441 CCGCTTGTGGGGGCGTGCCTGCGCGGCTGTGTGCCAGGCTGTGGGCTTCAGGCA 1500
QY 1508 CAACGAAGCGCGCTTCTCTCAGGAACCAAGAAATCTCTCTCTGGGAGCATGTCCAA 1567
Db 1501 CAACGAAGCGCGCTTCTCTCAGGAACCAAGAAATCTCTCTCTGGGAGCATGTCCAA 1560
QY 1568 GCTGT 1627
Db 1561 GCTGT 1620
QY 1628 GAGCCCAAGGGGT 1687
Db 1621 GAGCCCAAGGGGT 1680
QY 1688 CAAATTCCTGACGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1747
Db 1681 CAAATTCCTGACGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
QY 1748 TGTACAGAGACCAAGCTTTCAAAAGAAAGAGCTTTTCTACCGAGAGATGTGTGAG 1807
Db 1741 TGTACAGAGACCAAGCTTTCAAAAGAAAGAGCTTTTCTACCGAGAGATGTGTGAG 1800

QY 1808 CAAATTCGAAGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1867
Db 1801 CAAATTCGAAGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
QY 1868 GGAAGCAGAGGTGACAGAGATGAGGAAAGCCAGGCGCGCTGTGACGTCAAGCTCCG 1927
Db 1861 GGAAGCAGAGGTGACAGAGATGAGGAAAGCCAGGCGCGCTGTGACGTCAAGCTCCG 1920
QY 1928 CTATATCCCAAGCGGTGAGGGGTGTGGGCGCATTTGTGAACATGAGTACGTGTGGAGG 1987
Db 1921 CTATATCCCAAGCGGTGAGGGGTGTGGGCGCATTTGTGAACATGAGTACGTGTGGAGG 1980
QY 1988 CAGAACCTTCCGAGAGAAAGAGGCGGAGCGTCTCACTCTGAGGGTGAAGCACTGTT 2047
Db 1981 CAGAACCTTCCGAGAGAAAGAGGCGGAGCGTCTCACTCTGAGGGTGAAGCACTGTT 2040
QY 2048 CAGCGTGTCAACTACAGAGCG 2107
Db 2041 CAGCGTGTCAACTACAGAGCG 2100
QY 2108 CCTGAGCATATATCACAGGGGCTGGCGACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2167
Db 2101 CCTGAGCATATATCACAGGGGCTGGCGACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
QY 2168 GCGCGCTGAGCTGTA-----CATCCGCCA 2191
Db 2161 GCGCGCTGAGCTGTA-----CATCCGCCA 2220
QY 2192 GGAACAGGCTACAGAGGATCATGCGACATCATCAAAACCCAGAACGTAAGTGTGGG 2251
Db 2221 GGAACAGGCTACAGAGGATCATGCGACATCATCAAAACCCAGAACGTAAGTGTGGG 2280
QY 2252 TCGGTATGCGGTGTCCAGAGAGCGCGCCATGAGGACGTCCGCAAGGCTTCAGAGCA 2311
Db 2281 TCGGTATGCGGTGTCCAGAGAGCGCGCCATGAGGACGTCCGCAAGGCTTCAGAGCA 2340
QY 2312 CGTCTACTACTGTGACAGACTCCAGCCGATACATGACAGAGTTCGTGTCTACTCTCAGGA 2371
Db 2341 CGTCTACTACTGTGACAGACTCCAGCCGATACATGACAGAGTTCGTGTCTACTCTCAGGA 2400
QY 2372 GACCAAGCGGCTGAGAGGATGCGGTGATGACAGAGAGTCTCTCTGTAAGTGGCCAG 2431
Db 2401 GACCAAGCGGCTGAGAGGATGCGGTGATGACAGAGAGTCTCTCTGTAAGTGGCCAG 2460
QY 2432 CAGTGGCTTCTGACGTCTTCTAGCGCTCATGTGACACAGCGCGTGGCATCAGGG 2491
Db 2461 CAGTGGCTTCTGACGTCTTCTAGCGCTCATGTGACACAGCGCGTGGCATCAGGG 2520
QY 2492 CAAATCTACGTCAAGTCCAGGGGATCCCGAGAGGCTCATCTCTCAAGCGCTGTG 2551
Db 2521 CAAATCTACGTCAAGTCCAGGGGATCCCGAGAGGCTCATCTCTCAAGCGCTGTG 2580
QY 2552 CAGCGTGTGTACGCGAGCATGAGAAAGTCTTTGGGGATTTGGGGGAGCGGGCT 2611
Db 2581 CAGCGTGTGTACGCGAGCATGAGAAAGTCTTTGGGGATTTGGGGGAGCGGGCT 2640
QY 2612 GCTGT 2671
Db 2641 GCTGT 2700
QY 2672 CTTCCTCAGAGACCTGTGCGAGGTGTCCCTGAGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2731
Db 2701 CTTCCTCAGAGACCTGTGCGAGGTGTCCCTGAGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2760
QY 2732 GAGAGTGTGAATCTCCGTGTGAAGAGAGAGGCGCTGTGGTGGACGAGCTTTTGTTCAGAT 2791
Db 2761 GAGAGTGTGAATCTCCGTGTGAAGAGAGAGGCGCTGTGGTGGACGAGCTTTTGTTCAGAT 2820
QY 2792 GCGGGGCGCAAGGCTATATCCCTGTGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2851
Db 2821 GCGGGGCGCAAGGCTATATCCCTGTGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2880

[illegible]

```
Db 601 TCAGGCCGCGCCCGCCACACGCTAGTGAACCCCGAAGGCGTCGAGGATGGAAGGCGC 660
Qy 668 CTGGAACCACTATACGTCAGAGAGGCGGGGTCCCGCTGGGCGCTGGACGCCCCGGGTGGCAG 727
Db 661 CTGGAACCACTATACGTCAGAGAGGCGGGGTCCCGCTGGGCGCTGGACGCCCCGGGTGGCAG 720
Qy 728 GAGGCGCGGGGGGAGTGCACGAGAGTCTGGCGGTGGCCAAAGAGGCGCCAGGCGTGGCGC 787
Db 721 GAGGCGCGGGGGGAGTGCACGAGAGTCTGGCGGTGGCCAAAGAGGCGCCAGGCGTGGCGC 780
Qy 788 TGGCCCTGAGCCGGAGCGGACGCCGTTGGGCAAGGGTCTTGGGCCCAACCCGGGAGAGAC 847
Db 781 TGGCCCTGAGCCGGAGCGGACGCCGTTGGGCAAGGGTCTTGGGCCCAACCCGGGAGAGAC 840
Qy 848 GCGTGAACCGAGTGAACGCTGTCTGTGTGTGTACCTGTCGACAGCCCGCCGGAAGAAC 907
Db 841 GCGTGAACCGAGTGAACGCTGTCTGTGTGTGTGTACCTGTCGACAGCCCGCCGGAAGAAC 900
Qy 908 CACCTCTTTGGAGGGTGGCTCTGTGGACGCGCACACTCCACCCATCCGTGGGCGGCA 967
Db 901 CACCTCTTTGGAGGGTGGCTCTGTGGACGCGCACACTCCACCCATCCGTGGGCGGCA 960
Qy 968 GCACCAAGCGGGGCGCCCATCCACATCGCGGCGCACAGCTCCCTGGGAGACAGGCTTGTCC 1027
Db 961 GCACCAAGCGGGGCGCCCATCCACATCGCGGCGCACAGCTCCCTGGGAGACAGGCTTGTCC 1020
Qy 1028 CCCGGTGTAGCGCGGAGACAAAGCACTTCTCTACTCTCAGGCGCACAAGAGAGAGCTGCG 1087
Db 1021 CCCGGTGTAGCGCGGAGACAAAGCACTTCTCTACTCTCAGGCGCACAAGAGAGAGCTGCG 1080
Qy 1088 GCGCTCTCTTCTACTAGCTCTCTGTAGGCGCCAGCGCTGAGCGTGGCGTGGAGAGTGTGA 1147
Db 1081 GCGCTCTCTTCTACTAGCTCTCTGTAGGCGCCAGCGCTGAGCGTGGCGTGGAGAGTGTGA 1140
Qy 1148 GACCATCTTTTGGGGTTCAGAGCGCCGAGATGCGAGGACTCCCGCGAGGTTGCCCGGCT 1207
Db 1141 GACCATCTTTTGGGGTTCAGAGCGCCGAGATGCGAGGACTCCCGCGAGGTTGCCCGGCT 1200
Qy 1208 GCCCGAGCGCTACTGTGGAATATGGCGCCCTGTCTTCTGTGAGAGTCTGTGGAGAACAGCGCA 1267
Db 1201 GCCCGAGCGCTACTGTGGAATATGGCGCCCTGTCTTCTGTGAGAGTCTGTGGAGAACAGCGCA 1260
Qy 1268 GTGCGCCCTAGGGGGGTGCTCTCAAGAGCGCACTGCGCGTGGAGTGGTGCACCGCAC 1327
Db 1261 GTGCGCCCTAGGGGGGTGCTCTCAAGAGCGCACTGCGCGTGGAGTGGTGCACCGCAC 1320
Qy 1328 AGCGGATGTGTGTGCGGGAGAGCGCCAGAGGCTGTGTGGGGCGCCCGAGAGAGAGA 1387
Db 1321 AGCGGATGTGTGTGCGGGAGAGCGCCAGAGGCTGTGTGGGGCGCCCGAGAGAGAGA 1380
Qy 1388 CACAGACCCCCGTGCTGTGAGTGTCTCCGACAGCACAGACGCCCTGGCAGGTGA 1447
Db 1381 CACAGACCCCCGTGCTGTGAGTGTCTCCGACAGCACAGACGCCCTGGCAGGTGA 1440
Qy 1448 CGGCTCTGTGGGCGCTGCTGCGCGGCTGTGGCCCGCAGGCTCTGTGGGCTCCAGCA 1507
Db 1441 CGGCTCTGTGGGCGCTGCTGCGCGGCTGTGGCCCGCAGGCTCTGTGGGCTCCAGCA 1500
Qy 1508 CAACGAAGCGCGCTTCTCTAGGAACACCAAGAACTCATCTCCCTGGGGAAGATGCCAA 1567
Db 1501 CAACGAAGCGCGCTTCTCTAGGAACACCAAGAACTCATCTCCCTGGGGAAGATGCCAA 1560
Qy 1568 GCTCTGCTGAGAGAGCTGAGTGAAGATAGGCTGCGGAGTGCCTTGGGTGGCAG 1627
Db 1561 GCTCTGCTGAGAGAGCTGAGTGAAGATAGGCTGCGGAGTGCCTTGGGTGGCAG 1620
Qy 1628 GAGCCAGAGGTTGGCTGTGTTCCGGCGCAGAGACAGCTGCTGAGTGAAGAGATCCGTGC 1687
Db 1621 GAGCCAGAGGTTGGCTGTGTTCCGGCGCAGAGACAGCTGCTGAGTGAAGAGATCCGTGC 1680
Qy 1688 CAAGTTCCTGCACTGGCTGATGAGTGTAGCTGTGAGAGCTGCTCAGAGCTTTCTTTTA 1747
Db 1681 CAAGTTCCTGCACTGGCTGATGAGTGTAGCTGTGAGAGCTGCTCAGAGCTTTCTTTTA 1740

Qy 1748 TGTACAGGAGACCAAGCTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAGAGTCTGGAG 1807
Db 1741 TGTACAGGAGACCAAGCTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAGAGTCTGGAG 1800
Qy 1808 CAAGTTCGAAGCACTTGGAACTGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTC 1867
Db 1801 CAAGTTCGAAGCACTTGGAACTGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTC 1860
Qy 1868 GGAAGCAGAGTCAAGCAGCATCGGAGACGACGCGCCCTGCTAGCTCCAACTCCG 1927
Db 1861 GGAAGCAGAGTCAAGCAGCATCGGAGACGACGCGCGCCCTGCTAGCTCCAACTCCG 1920
Qy 1928 CTTCATCCCAAGCTGACAGGCTGCGGCGCGATGTTGAACTGAGACTACGTCGAGGAGC 1987
Db 1921 CTTCATCCCAAGCTGACAGGCTGCGGCGCGATGTTGAACTGAGACTACGTCGAGGAGC 1980
Qy 1988 CAGAGGTTCCGACAGAGAAAGAGGCGCAGCGCTCTACCTGAGAGGTTGAAGGCACTGTT 2047
Db 1981 CAGAGGTTCCGACAGAGAAAGAGGCGCAGCGCTCTACCTGAGAGGTTGAAGGCACTGTT 2040
Qy 2048 CAGCGTGTCAACTAGAGAGCGGCGCGGCGCCCGGCTCCTGGGCGCCTCTGTGTGGG 2107
Db 2041 CAGCGTGTCAACTAGAGAGCGGCGCGGCGCGCGCCCGGCTCCTGGGCGCCTCTGTGTGGG 2100
Qy 2108 CTTGAGCATATCCACAGAGGCGCTGGCACCTTCTGTGCTGTGCGGAGGCGCAGAGACC 2167
Db 2101 CTTGAGCATATCCACAGAGGCGCTGGCACCTTCTGTGCTGTGCGGAGGCGCAGAGACC 2160
Qy 2168 GCGGCTGAGCTGA-----CATCCGCA 2191
Db 2161 GCGGCTGAGCTGACTTTGTCAAGTGTGATGTGACGGGCGGTGACGACACATCCGCA 2220
Qy 2192 GGAAGAGGCTCAGGAGGATGATGCGCAGCATCATCAAAACCCAGAGAGCTGCTGCGG 2251
Db 2221 GGAAGAGGCTCAGGAGGATGATGCGCAGCATCATCAAAACCCAGAGAGCTGCTGCGG 2280
Qy 2252 TCGGTATGCGGTGTCCAGAGGCGCGCCATGGGAGAGCTCCGAAAGCTTTCAGAGCA 2311
Db 2281 TCGGTATGCGGTGTCCAGAGGCGCGCCATGGGAGAGCTCCGAAAGCTTTCAGAGCA 2340
Qy 2312 GGTCTCTACTGTGACAGACTTCAGGCGGTCAATGAGAGTGTGGTCTACGACGCGA 2371
Db 2341 GGTCTCTACTGTGACAGACTTCAGGCGGTCAATGAGAGTGTGGTCTACGACGCGA 2400
Qy 2372 GACCAAGCCGCTGAGGATGCGGTCTCTCATCGACAGAGCTCTCCCTGAATGAGGCGAG 2431
Db 2401 GACCAAGCCGCTGAGGATGCGGTCTCTCATCGACAGAGCTCTCCCTGAATGAGGCGAG 2460
Qy 2432 CAGTGGCTCTTGAAGCTTCTTCTTACAGCTTCAATGTGACCAAGCGCTGCGCATCAGGG 2491
Db 2461 CAGTGGCTCTTGAAGCTTCTTCTTACAGCTTCAATGTGACCAAGCGCTGCGCATCAGGG 2520
Qy 2492 CAAGTCTAGGTCAGTGCAGAGGATCCGCAAGGCGCTCCATCTCTCACGCTGCTG 2551
Db 2521 CAAGTCTAGGTCAGTGCAGAGGATCCGCAAGGCGCTCCATCTCTCACGCTGCTG 2580
Qy 2552 CAGCCTGTGTAGCGGAGACATGAGAAACAAGCTGTTTGGGGGATTTCGGCGGAGCGGCT 2611
Db 2581 CAGCCTGTGTGTAGCGGAGACATGAGAAACAAGCTGTTTGGGGGATTTCGGCGGAGCGGCT 2640
Qy 2612 GCTCTGCGGTTGGTGGATGATTTCTTGTGTGTGACACTTCACTCACCACAGGAAAC 2671
Db 2641 GCTCTGCGGTTGGTGGATGATTTCTTGTGTGTGACACTTCACTCACCACAGGAAAC 2700
Qy 2672 CTTCCTCAGAGACCTGCTCGAGAGTGCCTGAGTATGAGTGGCTGCTGTAACCTTGCAGAA 2731
Db 2701 CTTCCTCAGAGACCTGCTCGAGAGTGCCTGAGTATGAGTGGCTGCTGTAACCTTGCAGAA 2760
Qy 2732 GACAGTGTGAACTTCCCTGTGAAGAGAGAGGCGCGGAGGCGCAAGGCTTTTGTTCAGAT 2791
Db 2761 GACAGTGTGAACTTCCCTGTGAAGAGAGAGGCGCGGAGGCGCAAGGCTTTTGTTCAGAT 2820
```


QY	2792	GC	CGCCGACGACGCTATTCCCTCGGTGGCGCGCTCGCTGGATGATCCCGACGACCTGGAAGT	2851
Db	2821	GC	CGCGCCCGACGGGCTATTCCCTCGGTGGCGCGCTCGCTGGATGATCCCGACGACCTGGAAGT	2880
QY	2852	GC	AGAGCGAGCTACTCTCCAGCTATGCCCGGACCTTCATCAGAGCGCACTGCACCTTCAACCG	2911
Db	2881	GC	AGAGCGAGCTACTCTCCAGCTATGCCCGGACCTTCATCAGAGCGCACTGCACCTTCAACCG	2940
QY	2912	CG	CTTCAAGCGCTGGGGGAAACATGGGTGGCAACCTCTTTGGGGCTTGGCGGTGAAGTG	2971
Db	2941	CG	CTTCAAGCGCTGGGGGAAACATGGGTGGCAACCTCTTTGGGGCTTGGCGGTGAAGTG	3000
QY	2972	TC	ACAGCGCTGTTCTGTGATTTGCAAGGTGAACAGCCCTCCAGACGGGTGTGCACCAACATCTA	3031
Db	3001	TC	ACAGCGCTGTTCTGTGATTTGCAAGGTGAACAGCCCTCCAGACGGGTGTGCACCAACATCTA	3060
QY	3032	CA	AAATCCTCTCTGTGTGAGGCGTACAGAGTTTCAACGATGTGTCTGACAGCTCCATTTC	3091
Db	3061	CA	AAATCCTCTCTGTGTGAGGCGTACAGAGTTTCAACGATGTGTCTGACAGCTCCATTTC	3120
QY	3092	TC	ACAAGTTTGGAAAGAACCCCAATTTTTCCGCGCGCATCTGTGAACGGGCTCCCT	3151
Db	3121	TC	ACAAGTTTGGAAAGAACCCCAATTTTTCCGCGCGCATCTGTGAACGGGCTCCCT	3180
QY	3152	CT	GTAATCTCCATCTCTGAAGCCCAAGAACGAGGATGTGCTGTGGGGCCCAAGGGCGCGC	3211
Db	3181	CT	GTAATCTCCATCTCTGAAGCCCAAGAACGAGGATGTGCTGTGGGGCCCAAGGGCGCGC	3240
QY	3212	CG	GGCCCTGTGGCCCTCCGAGGCGCGTGGAGTGGGTGTCCACAAAGATTTCTGCTCAACT	3271
Db	3241	CG	GGCCCTGTGGCCCTCCGAGGCGCGTGGAGTGGGTGTCCACAAAGATTTCTGCTCAACT	3300
QY	3272	GAC	TGACACCGCTGTGTCACTACGTTGCTACTCTGTGGGGTCACTCAGAGACAGCCACAGCGCA	3331
Db	3301	GAC	TGACACCGCTGTGTCACTACGTTGCTACTCTGTGGGGTCACTCAGAGACAGCCACAGCGCA	3360
QY	3332	GCT	AGTGTGGAAGGTTCCCGGGGGAGACAGCTGATGTCCTGTGGAGGGCCGACCCACACCGCGC	3391
Db	3361	GCT	AGTGTGGAAGGTTCCCGGGGGAGACAGCTGATGTCCTGTGGAGGGCCGACCCACACCGCGC	3420
QY	3392	ACT	GCCTTCAAGACTTCAAGACCAATCTGTGACTGATGGCACCGGCCACAGCAGCGACGCGA	3451
Db	3421	ACT	GCCTTCAAGACTTCAAGACCAATCTGTGACTGATGGCACCGGCCACAGCAGCGACGCGA	3480
QY	3452	GAG	CAGACACCAACGACGACCCCTGTACAGCCGCGGCTCTACGTTCCAGGAGGAGGGGCGGCC	3511
Db	3481	GAG	CAGACACCAACGACGACCCCTGTACAGCCGCGGCTCTACGTTCCAGGAGGAGGGGCGGCC	3540
QY	3512	CAC	AGCCAGGCGCGCCACCGCTGGGAGTGTGAGGACCTGATGTAGTGTGTTGGCCGAGGCGCTG	3571
Db	3541	CAC	AGCCAGGCGCGCCACCGCTGGGAGTGTGAGGACCTGATGTAGTGTGTTGGCCGAGGCGCTG	3600
QY	3572	CAT	GTCCGGCTGAAGGCTGTGAGTGTCCGGCTGAGGCGCTGAAGAGTGTCCAGCCAGGCGCT	3631
Db	3601	CAT	GTCCGGCTGAAGGCTGTGAGTGTCCGGCTGAGGCGCTGAAGAGTGTCCAGCCAGGCGCT	3660
QY	3632	GAG	GTGTACAGACACACCGGCGCTTACACTTCCCAAGAGCTGGCGCTGGCTCCACCCCA	3691
Db	3661	GAG	GTGTACAGACACACCGGCGCTTACACTTCCCAAGAGCTGGCGCTGGCTCCACCCCA	3720
QY	3692	GGG	CAGACTTTTCTCTACACAGAGACCCCGGCTTCCACTCCCAACATAGAAATAGTCCATCTC	3751
Db	3721	GGG	CAGACTTTTCTCTCTACACAGAGACCCCGGCTTCCACTCCCAACATAGAAATAGTCCATCTC	3780
QY	3752	CCA	ATTTCCGCAATTGTTCACCCCTCGCGCTGCGCTCTTTGGCTTCCACCCCAACATCTC	3811
Db	3781	CCA	ATTTCCGCAATTGTTCACCCCTCGCGCTGCGCTCTTTGGCTTCCACCCCAACATCTC	3840
QY	3812	AGG	TGAGACCTCTAGAAAGACCTCTGGAGACTTGGGAATTTGGAGTGACCAAAAGTGTG	3871
Db	3841	AGG	TGAGACCTCTCTAGAAAGACCTCTGGAGACTTGGGAATTTGGAGTGACCAAAAGTGTG	3900
QY	3872	CC	CTGTACACAGGCGAGGACCTTGACCTGTGATGGGGGTCCCTGTGGCTCAATTTGGGGG	3931

Dd	3901	CCTGTACACAGGCGAGGCCCTGCACCCTGGATGGGGCCCTGTGGGTCAAAATTGGGGG	3960
Oy	3932	GAGTGTCTGTGGAGTAATAATCTGAATATATGACTTTTCAGTTTGAAAAAAA	3986
Dd	3961	GAGGTGCTGTGGAGTAATAATCTGAATATATGACTTTTCAGTTTGAAAAAAA	4015
RESULT 11			
BD011044			
LOCUS	BD011044	4015 bp	DNA linear PAT 31-JAN-2002
DEFINITION	Human telomerase catalytic subunit.		
ACCESSION	BD011044		
VERSION	BD011044.1 GI:18639417		
KEYWORDS	JP 2001081042-A/1.		
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 4015)		
AUTHORS	Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morl,G.B., Harley,C.B. and Andrews,W.H.		
TITLE	Human telomerase catalytic subunit.		
JOURNAL	Patent: JP 2001081042-A 1, 27-MAR-2001;		
COMMENT	GERON CORP, UNIVERSITY TECHNOLOGY CORP OS Unidentified PN JP 2001081042-A/1 PD 27-MAR-2001 PF 27-JUL-2000 JP 2000227474 PR 01-OCT-1996 US 08/724643, 18-APR-1997 US 08/844419 PR PR 01-OCT-1997 US 08/846017, 06-MAY-1997 US 08/851843 PR 25-APR-1997 US 08/854050, 14-AUG-1997 US 08/911312 PR 09-MAY-1997 US 08/912951, 14-AUG-1997 US 08/915503 PI THOMAS R SECHI, JOACHIM LINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG B MORIN		
FEATURES			
Source	Location/Qualifiers		
BASE COUNT	663 a 1363 c 1275 g 714 t		
ORIGIN			
Query Match	99.1%; Score 3969; DB 6; Length 4015;		
Best Local Similarity	99.1%; Pred. No. 9.4e-93;		
Matches 3979; Conservative	0; Mismatches 0; Indels 36; Gaps 1;		
Oy	8	GGAGGCGTCCGTCGTCGTCGCGCAGCGGGAACCCCTGGGCCCGGCGCACCCCGCATGCC	67
Dd	1	GGAGGCGTCCGTCGTCGTCGCGCAGCTGGGAACCCCTGGGCCCGGCGCACCCCGCATGCC	60
Oy	68	GGCGCTCCCCCTCCGCGCAGCGCGTCCGCTCCCTGTGCGCAGCCACAACCGGAGGTGCT	127
Dd	61	GGCGCTCCCGCGTCCGCGCAGCGCGTCCGCTCCCTGTGCGCAGCCACAACCGGAGGTGCT	120
Oy	128	GGCGCTGGCCACGTTTCGTGTCGGCGCTGGGGGCCCAAGGGCTGGCGGCTGTGTCCACGCGG	187
Dd	121	GGCGCTGGCCACGTTTCGTGTCGGCGCTGGGGGCCCAAGGGCTGGCGGCTGTGTCCACGCGG	180
Oy	188	GGAGCCGGGGGTTTTCCGGGCGCGTGGTGGCCAGTAGCCGTGCGTGCCTGGAGACG	247
Dd	181	GGAGCCGGGGGTTTTCCGGGCGCGTGGTGGCCAGTAGCCGTGCGTGCCTGGAGACG	240

Dh 2401 GACCAAGCCGCTGAGGAGTCCGCTGTCATGAGCAGAGCTCCCTGAAATGAGGCCAG 2460
Qy 2432 CAGTGGCCCTTTCAGAGCTTTCCTACGCTCATGTGCCACAGCCGCTGCGCATCAGGGG 2491
Dh 2461 CAGTGGCCCTTTCAGAGCTTTCCTACGCTCATGTGCCACAGCCGCTGCGCATCAGGGG 2520
Qy 2492 CAGTGGCCCTTTCAGAGCTTTCCTACGCTCATGTGCCACAGCCGCTGCGCATCAGGGG 2551
Dh 2521 CAGTGGCCCTTTCAGAGCTTTCCTACGCTCATGTGCCACAGCCGCTGCGCATCAGGGG 2580
Qy 2552 CAGTGGCCCTTTCAGAGCTTTCCTACGCTCATGTGCCACAGCCGCTGCGCATCAGGGG 2611
Dh 2581 CAGTGGCCCTTTCAGAGCTTTCCTACGCTCATGTGCCACAGCCGCTGCGCATCAGGGG 2640
Qy 2612 GCTCCTGCGTTCGATGATGATTTCTTGTGTGACACCTCACCACCGCAAGAAAC 2671
Dh 2641 GCTCCTGCGTTCGATGATGATTTCTTGTGTGACACCTCACCACCGCAAGAAAC 2700
Qy 2672 CTTCTCAGAGACCCCTGTCGAGAGTGTCCCTGAGATAGGCTGCTGTAACCTTGCGGAA 2731
Dh 2701 CTTCTCAGAGACCCCTGTCGAGAGTGTCCCTGAGATAGGCTGCTGTAACCTTGCGGAA 2760
Qy 2732 GACAGTGGTGAACCTTCCCTGTATGAGAGAGAGCCCTGGGTGGCAGAGCTTTTGTCAAT 2791
Dh 2761 GACAGTGGTGAACCTTCCCTGTATGAGAGAGAGCCCTGGGTGGCAGAGCTTTTGTCAAT 2820
Qy 2792 GCCGCGCCAGAGCCCTATTCCTGCTGCGGCTGCTGCTGATACCGGACCCCTGAGAGT 2851
Dh 2821 GCCGCGCCAGAGCCCTATTCCTGCTGCGGCTGCTGCTGATACCGGACCCCTGAGAGT 2880
Qy 2852 GCAGAGGACATCTCAGAGCTTATGCCGAGACCTCCATCAGAGCCAGTCCACCTTCACCG 2911
Dh 2881 GCAGAGGACATCTCAGAGCTTATGCCGAGACCTCCATCAGAGCCAGTCCACCTTCACCG 2940
Qy 2912 CGGCTTCAAGGCTGGGAGAGACATGCTGCAAACTCTTTGGGGCTTGGGGCTGAAAGTG 2971
Dh 2941 CGGCTTCAAGGCTGGGAGAGACATGCTGCAAACTCTTTGGGGCTTGGGGCTGAAAGTG 3000
Qy 2972 TCACAGCCCTGTTTGTGATTTGACAGAGTGAAGCCCTCCAGAGGCTGTCACCAACATCTA 3031
Dh 3001 TCACAGCCCTGTTTGTGATTTGACAGAGTGAAGCCCTCCAGAGGCTGTCACCAACATCTA 3060
Qy 3032 CAAGATCTCTCTGCTGACAGGCGTACAGATTTTCAGCATGTGCTGCAAGTCCCATTTCA 3091
Dh 3061 CAAGATCTCTCTGCTGACAGGCGTACAGATTTTCAGCATGTGCTGCAAGTCCCATTTCA 3120
Qy 3092 TCAGAAATTTGAAAGAACCCCAATTTTCTGCGGCTGCAATCTGTGACAGGCGCTCCCT 3151
Dh 3121 TCAGAAATTTGAAAGAACCCCAATTTTCTGCGGCTGCAATCTGTGACAGGCGCTCCCT 3180
Qy 3152 CTGCTACTCATCTCTGAAGAGCAAGAACGACAGGATGTGCTGGGGGCCAAGGGCGCGC 3211
Dh 3181 CTGCTACTCATCTCTGAAGAGCAAGAACGACAGGATGTGCTGGGGGCCAAGGGCGCGC 3240
Qy 3212 CGGCGCTTCTGCTTCCGAGAGGCGCTGAGTGTGCTGCAACCAAGCATTTCTGCTCAAGCT 3271
Dh 3241 CGGCGCTTCTGCTTCCGAGAGGCGCTGAGTGTGCTGCAACCAAGCATTTCTGCTCAAGCT 3300
Qy 3272 GACTCGACACCGTGTACACTGAGTGCACCTCTGGGGGTCACTCAGAGCAGCCAGAGCCA 3331
Dh 3301 GACTCGACACCGTGTACACTGAGTGCACCTCTGGGGGTCACTCAGAGCAGCCAGAGCCA 3360
Qy 3332 GCTGAGTGTGAAGTCTCCGGGGAGAGAGAGCTACTGCTGAGAGCCGAGCCCAACCCGCG 3391
Dh 3361 GCTGAGTGTGAAGTCTCCGGGGAGAGAGAGCTACTGCTGAGAGCCGAGCCCAACCCGCG 3420
Qy 3392 ACTGCGCTTCAACTTCAAGACATCTGATGATGGCCACCCGCGCACAGCCAGGCGCA 3451
Dh 3421 ACTGCGCTTCAACTTCAAGACATCTGATGATGGCCACCCGCGCACAGCCAGGCGCA 3480
Qy 3452 GAGCAGACACAGAGCCCTGTCAGAGCCGCGGCTACGCTCCAGAGGAGGAGGGGCGGCC 3511
Dh 3481 GAGCAGACACAGAGCCCTGTCAGAGCCGCGGCTACGCTCCAGAGGAGGAGGGGCGGCC 3540

Qy 3512 CACACCCAGGCCCGCAGCCGCTGGAGTCTGAGGCCGTGAGTGAATTTTGGCCGAGGCGCTG 3571
Dh 3541 CACACCCAGGCCCGCAGCCGCTGGAGTCTGAGGCCGTGAGTGAATTTTGGCCGAGGCGCTG 3600
Qy 3572 CATGTCCGGCTGAAAGCTGAGTGTCCGCTGAGGCTTGAAGGATGTGTACCAAGAGGCT 3631
Dh 3601 CATGTCCGGCTGAAAGCTGAGTGTCCGCTGAGGCTTGAAGGATGTGTGTACCAAGAGGCT 3660
Qy 3632 GAGTGTCCAGACACCTCCGCTCACTTCCCAAGAGGCTGGGCTGGCTCCACCCCA 3691
Dh 3661 GAGTGTCCAGACACCTCCGCTCACTTCCCAAGAGGCTGGGCTGGCTCCACCCCA 3720
Qy 3692 GGGCCAGCTTTTCCACACAGAGAGCCGCTTCCACCTCCCAACATAGGAATAGTCCATCC 3751
Dh 3721 GGGCCAGCTTTTCCACACAGAGAGCCGCTTCCACCTCCCAACATAGGAATAGTCCATCC 3780
Qy 3752 CCAGATTCGCCATTTGTTACCCCTGCGCTGCGCTCTTTGCTTTCACACCCCAACATCC 3811
Dh 3781 CCAGATTCGCCATTTGTTACCCCTGCGCTGCGCTCTTTGCTTTCACACCCCAACATCC 3840
Qy 3812 AGGTGAGACCCCTGAGAGAACCCCTGGAGGCTGCGGAATTTGAGTGACCAAGGCTG 3871
Dh 3841 AGGTGAGACCCCTGAGAGAACCCCTGGAGGCTGCGGAATTTGAGTGACCAAGGCTG 3900
Qy 3872 CCTGTACACAGGCGAGAGACCCCTGACCTGATGGGGGTCCCTGTGCTCAAAATTTGGGG 3931
Dh 3901 CCTGTACACAGGCGAGAGACCCCTGACCTGATGGGGGTCCCTGTGCTCAAAATTTGGGG 3960
Qy 3932 GAGTGTCTGTGGGAGTAAATATCTGAATATAGTATTTTACAGTTTAAAAAAA 3986
Dh 3961 GAGTGTCTGTGGGAGTAAATATCTGAATATAGTATTTTACAGTTTAAAAAAA 4015

RESULT 12
E36793
LOCUS E36793 4015 bp DNA linear PAT 18-JUN-2001
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E36793
VERSION E36793.1 GI:13022756
KEYWORDS JP 1999253177-A/1.
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
Calvin,B.H. and William,H.A.
TITLE Human telomerase catalytic subunit promoter
JOURNAL Patent: JP 1999253177-A 1 21-SEP-1999;
JERON CORP, UNIVERSITY TECHNOLOGY CORP
OS Unidentified
PN JP 1999253177-A/1
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/724,643,18-APR-1997 US 08/844,419, PR
25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR
09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR
14-AUG-1997 US 08/912,951,14-AUG-1997 US 08/915,503, PI
R SECHI, JOCHIMU RINGER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG B
MORIN.
PI CALVIN B HAREL, WILLIAM H ANDREWS
PC C12N15/09, A61K31/70, A61K38/55, A61K39/395, A61K39/395, A61K48/00,
PC C12N1/02,
PC C1201/48, C1201/68, G01N33/15, G01N33/48, G01N33/50//C07K14/47, PC
C07K16/40,
PC C12N1/19, C12N1/21, C12N5/10, C12N9/12, C12P21/08, (C12N1/19, PC
C12R1/84),
PC (C12N1/21, C12R1/19), (C12N9/12, C12R1/19), (C12N9/12, C12R1/84),
PC (C12N9/12, C12R1/91), C12N15/00, A61K37/64, C12N5/00 CC
Strandedness: Single;
CC Topology: Linear;
FH key Location/Qualifiers
FT CDS 56..3454.

QY	2048	CACGCGCTCACTACAGAGCGGGCGGGCGCCCGGCGCTCCGAGGGCGCTCGTGGCTGGG	2107
Db	2041	CACCGCTGCTCACTACAGAGCGGGCGGGCGCCCGGCGCTCCGAGGGCGCTCGTGGCTGGG	2100
QY	2108	CCGAGCAGATTCACAGAGGGCTGGCGCACTTCGTGCTGCTGTGCGGGGCCAGAGACC	2167
Db	2101	CCGAGCAGATTCACAGAGGGCTGGCGCACTTCGTGCTGCTGTGCGGGGCCAGAGACC	2160
QY	2168	GCCGCGTGAAGCTA-----CATCCCCCA	2191
Db	2161	GCCGCGTGAAGCTACTTTGTCAAGTGGATGTACGGGGCGCGTACAGACATATCCCCCA	2220
QY	2192	GGACAGGGCTCAGGGAGGTCATCCGACATATCAAAACCCAGAACAGTACTGCGTGC	2251
Db	2221	GGACAGGGCTCAGGGAGGTCATCCGACATATCAAAACCCAGAACAGTACTGCGTGC	2280
QY	2252	TCGGTATCCCGTGTGTCGAAGAGCGCGCCATAGGGCAGCTGCGCAAGGGCTTTCAAGGCA	2311
Db	2281	TCGGTATCCCGTGTGTCGAAGAGCGCGCCATAGGGCAGCTGCGCAAGGGCTTTCAAGGCA	2340
QY	2312	CGTCTCTACCTTGACAGACCTTCCAGCCGTACATGCGACAGATTGCTGCTACCTGCAGGA	2371
Db	2341	CGTCTCTACCTTGACAGACCTTCCAGCCGTACATGCGACAGATTGCTGCTACCTGCAGGA	2400
QY	2372	GACCAAGCCCGGTAGGGAGTGCCTGCTCATTCGAGAGAGTCTCTCCCTAATGAGGCCAG	2431
Db	2401	GACCAAGCCCGGTAGGGAGTGCCTGCTCATTCGAGAGAGTCTCTCCCTAATGAGGCCAG	2460
QY	2432	CAGTGGCGCTCTGACGCTCTCTCTAGCGCTTCATGTCCACACAGCGCGTGCAGTACGGG	2491
Db	2461	CAGTGGCGCTCTGACGCTCTCTCTAGCGCTTCATGTCCACACAGCGCGTGCAGTACGGG	2520
QY	2492	CAGTCTCTACGCTCAGTGGCCAGGGAGTCCCGCAGGGCTCATCTCTCTCCACGCTGCTG	2551
Db	2521	CAGTCTCTACGCTCAGTGGCCAGGGAGTCCCGCAGGGCTCATCTCTCTCCACGCTGCTG	2580
QY	2552	CAGCTGTGCTAGGGGACATGAGAAACAAGCTGTTGGGGGATTGGCGGGAGCGGCT	2611
Db	2581	CAGCTGTGCTAGGGGACATGAGAAACAAGCTGTTGGGGGATTGGCGGGAGCGGCT	2640
QY	2612	GCTCTGCGCTTTGGTGGATGATTTCTGTTGGTGACACCTCAACCTCCACCGAGAAAC	2671
Db	2641	GCTCTGCGCTTTGGTGGATGATTTCTGTTGGTGACACCTCAACCTCCACCGAGAAAC	2700
QY	2672	CTTCTCCAGAGACCCCGTCCGAGGCTGCTCCGATGATGAGTGCCTGCTGTAATTCGGAA	2731
Db	2701	CTTCTCCAGAGACCCCGTCCGAGGCTGCTCCGATGATGAGTGCCTGCTGTAATTCGGAA	2760
QY	2732	GACAGTGTGAATTCCTCGTGAAGAGACGAGGCCCTGGGTGGACGGCTTTTGTTCAAT	2791
Db	2761	GACAGTGTGAATTCCTCGTGAAGAGACGAGGCCCTGGGTGGACGGCTTTTGTTCAAT	2820
QY	2792	GCGGGCCCAAGGCCATTTCCCTCGTGGCGCTGCTGCTGTGATACCCGAGCCGAGAGT	2851
Db	2821	GCGGGCCCAAGGCCATTTCCCTCGTGGCGCTGCTGCTGTGATACCCGAGCCGAGAGT	2880
QY	2852	GCAGAGCAGTACTTCACGATATGCCCGGACCTTCATGAGACCGAGTCTCACCTTCAACG	2911
Db	2881	GCAGAGCAGTACTTCACGATATGCCCGGACCTTCATGAGACCGAGTCTCACCTTCAACG	2940
QY	2912	GCGCTTCAAGGCTGGGAGAACATGCGTCCGAAACTTTTGGGGGCTTGGCGGTGAAGTG	2971
Db	2941	GCGCTTCAAGGCTGGGAGAACATGCGTCCGAAACTTTTGGGGGCTTGGCGGTGAAGTG	3000
QY	2972	TCACAGCCTGTTTTCGGATTTGCGAGTGAACAGCTTCAGACGGTGTGCACCAACATCTA	3031
Db	3001	TCACAGCCTGTTTTCGGATTTGCGAGTGAACAGCTTCAGACGGTGTGCACCAACATCTA	3060
QY	3032	CAGATCTCTCTGCTGACGCGTACAGAGTTTACAGCATGTGTGCTCAGCTCCCATTTTA	3091
Db	3061	CAGATCTCTCTGCTGACGCGTACAGAGTTTACAGCATGTGTGCTCAGCTCCCATTTTA	3120

QY	3092	TCAGCAAGTTGGAGAAGACCACCATTTTTCCTGCGCCGTCATCTCTGACAGCGCCCTCCCT	3151
Db	3121	TCAGCAAGTTGGAGAAGACCACCATATTTTTCGCGCCGTCATCTCTGACAGCGCCCTCCCT	3180
QY	3152	CTGCTACTCCATCCTGTAAGAGCCAAAGAACGAGGAGATGTCGTGGGGCCCAAGGGCGCCG	3211
Db	3181	CTGCTACTCCATCTCTGTAAGAGCCAAAGAACGAGGAGATGTCGTGGGGCCCAAGGGCGCCG	3240
QY	3212	CGGCGCTCTGCGCCCTCGAGGCGCTGCAAGTGGCTGTGACCACCAAGCATTTCCGTCACAGCT	3271
Db	3241	CGGCGCTCTGCGCCCTCGAGGCGCTGCAAGTGGCTGTGACCACCAAGCATTTCTGCTCAAGCT	3300
QY	3272	GACTCGACACCGTGTGATCACTACCTAGCTGCTACTCTGGGGTCTACTCAGAGACGCCAGAGCA	3331
Db	3301	GACTCGACACCGTGTGATCACTACCTAGCTGCTACTCTGGGGTCTACTCAGAGACGCCAGAGCA	3360
QY	3332	GCTGAGTCGGAGAACCTCCCGGGGAGCAGCGTGCATCCCTGGAGAGCGGCACGCAACCCGGC	3391
Db	3361	GCTGAGTCGGAGAACCTCCCGGGGAGCAGCGTGCATCCCTGGAGAGCGGCACGCAACCCGGC	3420
QY	3392	ACTGCCCTGAGATTTCAAACCATCTCTGGACTGATGSCCACCCCACAGCCAGGCGCA	3451
Db	3421	ACTGCCCTGAGATTTCAAACCATCTCTGGACTGATGSCCACCCCACAGCCAGGCGCA	3480
QY	3452	GAGCAGACACACAGACAGCCCTGTCAAGCGCGGGCTCTAGCTGCCAAGGAGGGAGGGGGCGCC	3511
Db	3481	GAGCAGACACACAGACAGCCCTGTCAAGCGCGGGCTCTAGCTGCCAAGGAGGGAGGGGGCGCC	3540
QY	3512	CACACCCAGGCCCCGACCGCTGGAGTGTAGGCTCTGAGTGAATGTTTGGCCGAGGCTG	3571
Db	3541	CACACCCAGGCCCCGACCGCTGGAGTGTAGGCTCTGAGTGAATGTTTGGCCGAGGCTG	3600
QY	3572	CATGTCGGGCTGAAGGCTGATGTCTCGGCTGAGGCTGAGCCGATGTTTGGCCGAGGCTG	3631
Db	3601	CATGTCGGGCTGAAGGCTGATGTCTCGGCTGAGGCTGAGCCGATGTTTGGCCGAGGCTG	3660
QY	3632	GAGTGTCCAGACACACTGCTCGCTTTCACCTTCCACAGGCTGGGCTCGGCTCCACCCCA	3691
Db	3661	GAGTGTCCAGACACACTGCTCGCTTTCACCTTCCACAGGCTGGGCTCGGCTCCACCCCA	3720
QY	3692	GGGCCAGCTTTTCCCTCAACAAGAGACCCGGGTTTCCACCTCCCAATGAAATGTCATCC	3751
Db	3721	GGGCCAGCTTTTCCCTCAACAAGAGACCCGGGTTTCCACCTCCCAATGAAATGTCATCC	3780
QY	3752	CCAGATTGCGCATTTGTTCACTCCCTCGCGCTCGCCCTCTTGTGCTTCCACCCCAACATCC	3811
Db	3781	CCAGATTGCGCATTTGTTCACTCCCTCGCGCTCGCCCTCTTGTGCTTCCACCCCAACATCC	3840
QY	3812	AGGTGGAGACCTCTAGAGAAGACCTCTGGAGCTGTGGAAATTTGGAGTACACCAAGGTGTG	3871
Db	3841	AGGTGGAGACCTCTAGAGAAGACCTCTGGAGCTGTGGAAATTTGGAGTACACCAAGGTGTG	3900
QY	3872	CCCTGTACACAGGCGAGGACCTCTGCACCTTGATGGGGGTCCCTGTGGTCCAAATTTGGGG	3931
Db	3901	CCCTGTACACAGGCGAGGACCTCTGCACCTTGATGGGGGTCCCTGTGGTCCAAATTTGGGG	3960
QY	3932	GAGTGTCTGTGGAGTAAATACTGAAATTAAGATTTTTCAGTTTGGAAAAA	3986
Db	3961	GAGTGTCTGTGGAGTAAATACTGAAATTAAGATTTTTCAGTTTGGAAAAA	4015

[illegible]

[illegible][illegible]

QY	1388	CACGAGACCCCGCTGCGCTTGGTGCAGCTGCTCCGCCAGCAGCACAGACCCCTGGCAGGTGTAA	1447
Db	1381	CACAGACACCCCGCTGCGCTTGGTGCAGCTGCTCCGCCAGCAGCACAGACCCCTGGCAGGTGTAA	1440
QY	1448	CGCGTTCGTGGGGCCCTGCTGGGCGCGGCTGGTGGCCCCAGGCTCTGGGGCTCCAGGCA	1507
Db	1441	CGGCTTCGTGGGGCCCTGCTGGGCGCGGCTGGTGGCCCCAGGCTCTGGGGCTCCAGGCA	1500
QY	1508	CAAGCAAGCGCGCTTCCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCGCA	1567
Db	1501	CAAGCAAGCGCGCTTCCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCGCA	1560
QY	1568	GCTCTCGCTGCAGAGACTGACGTCGTGAAGATGAGCGTCGGGGACCTCGCTTGGCTGCGCAG	1627
Db	1561	GCTCTCGCTGCAGAGACTGACGTCGTGAAGATGAGCGTCGGGGACCTCGCTTGGCTGCGCAG	1620
QY	1628	GAGCCACAGGGTGGCTGGTCTTCGCCGGCGGAGAGCACCTTCGCGTGAAGAGATCCTGAGC	1687
Db	1621	GAGCCACAGGGTGGCTGGTCTTCGCCGGCGGAGAGCACCTTCGCGTGAAGAGATCCTGAGC	1680
QY	1688	CAAGTTCCTGCATGCGCTGATGAGTGTATACGTGTCGAGCTGTCAGAGCTCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCATGCGCTGATGAGTGTATACGTGTCGAGCTGTCAGAGCTCTTCTTTTA	1740
QY	1748	TGTACGAGAGCCAGCTTAAAGAAAGAACGCGCTTTTCTACCGGAAGAGTCTGGAG	1807
Db	1741	TGTACGAGAGCCAGCTTAAAGAAAGAACGCGCTTTTCTACCGGAAGAGTCTGGAG	1800
QY	1808	CAAGTTCGAAGAAGCTTGTGATTCAGACAGCATTTGAAGAGGGTGTGACGTCGGGAGCTGTC	1867
Db	1801	CAAGTTCGAAGAAGCTTGTGATTCAGACAGCATTTGAAGAGGGTGTGACGTCGGGAGCTGTC	1860
QY	1868	GGAAGCAGAGTCAAGGACGATGCGGGAAGCCAGAGCCCGCTTGTGACTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGTCAAGGACGATGCGGGAAGCCAGAGCCCGCTTGTGACTCCAGACTCCG	1920
QY	1928	CTTCATCCCGCAAGCCTCAGCGGCTGCGGCGGATGTGAACTAGGACTAGCTGCTGGAGC	1987
Db	1921	CTTCATCCCGCAAGCCTCAGCGGCTGCGGCGGATGTGAACTAGGACTAGCTGCTGGAGC	1980
QY	1988	CAGAACGTTCCGCGAGAGAAAAGAGGCGCAGCTCTACCTCGAGGGTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCCGCGAGAGAAAAGAGGCGCAGCTCTACCTCGAGGGTGAAGGCACTGTT	2040
QY	2048	CAGGCTGCTCAACTAGAGAGGGGCGGGGCGCCCGGCGCTCGGGGCGCTCTGCTGCTGGG	2107
Db	2041	CAGGCTGCTCAACTAGAGAGGGGCGGGGCGCCCGGCGCTCGGGGCGCTCTGCTGCTGGG	2100
QY	2108	CCTGGAGCATATCCACAGAGGCGCTGCGGCGACCTTCTGTGCTGTGCGGGGCCACAGAGACC	2167
Db	2101	CCTGGAGCATATCCACAGAGGCGCTGCGGCGACCTTCTGTGCTGTGCGGGGCCACAGAGACC	2160
QY	2168	GCCGCTGAGCTGTAA-----CATGCCCA	2191
Db	2161	GCCGCTGAGCTGTAA-----CATGCCCA	2220
QY	2192	GGAACAGGCTCAGGAGGTCATTCGCACAGCATCATCAAAACCCAGAAACAGTACTGGTGGCG	2251
Db	2221	GGAACAGGCTCAGGAGGTCATTCGCACAGCATCATCAAAACCCAGAAACAGTACTGGTGGCG	2280
QY	2252	TGCGATGCTCGTGTGTCAGAGAGCGCGCCCATGGGCACTGCGCAAGAGGCTTCAAGAGCCA	2311
Db	2281	TGCGATGCTCGTGTGTCAGAGAGCGCGCCCATGGGCACTGCGCAAGAGGCTTCAAGAGCCA	2340
QY	2312	GCTCTTCACTTGAACAGACTCCAGCCGCTACATGAGACAGTTCGTGGCTCACCTCAGCA	2371
Db	2341	GCTCTTCACTTGAACAGACTCCAGCCGCTACATGAGACAGTTCGTGGCTCACCTCAGCA	2400
QY	2372	GACCAGCCCGCTGAGGAGATCGCGTCGTCATCGACGAGAGACTCTCTCCCTGAAGAGGCGAG	2431
Db	2401	GACCAGCCCGCTGAGGAGATCGCGTCGTCATCGACGAGAGACTCTCTCCCTGAAGAGGCGAG	2460

QY	2432	CAGTGGCTCTTGACAGCTCTTTCTACGGCTTCATGTGCCACACAGCCGTGCGCATCAGGGG	2491
Db	2461	CAGTGGCTCTTTCCACAGCTCTTCTCTACGGCTTCATGTGCCACACAGCGGTGCGCATCAGGGG	2520
QY	2492	CAAGTCCACGTCACAGTGCACAGGGGATCCCGCAGGGGCTCCATCTCTCTCACGCTCTCTG	2551
Db	2521	CAAGTCTACGTCACAGTGCACAGGGGATCCCGCAGGGGCTCCATCTCTCTCACGCTCTCTG	2580
QY	2552	CAGCCTGTGCTACGGACATGGAACAACAAGCTGTTTGGGGGATTTGGGGGAGGCT	2611
Db	2581	CAGCCTGTGCTACGGACATGGAAGAACAGAGCTGTTTGGGGGATTTGGGGGAGGAGCT	2640
QY	2612	GCTCTGGCTTTGGTGGATGATTTCTTTGGTGGAGACCTCCATCCACCACACCGGAAAC	2671
Db	2641	GCTCTGGCTTTGGTGGATGATTTCTTTGGTGGAGACCTCCATCCACCACACCGGAAAC	2700
QY	2672	CTTCTCCAGGACCCCTGGTCCGAGAGTGCCCTGATTTGGCTCCGAGTGAACTTGGGAA	2731
Db	2701	CTTCTCCAGGACCCCTGGTCCGAGAGTGCCCTGATTTGGCTCCGAGTGAACTTGGGAA	2760
QY	2732	GACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGACAGGCTTTGTTCAAGT	2791
Db	2761	GACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGACAGGCTTTGTTCAAGT	2820
QY	2792	GCCGGCCCAAGGGCTATTCCCTGTGTGGGGCTGTCTGTCTGTGATTAACCGGACCTTGGAGT	2851
Db	2821	GCCGGCCCAAGGGCTATTCCCTGTGTGGGGCTGTCTGTCTGTGATTAACCGGACCTTGGAGT	2880
QY	2852	GCAGAGCAGCATCTCCAGCATATGCGCGGAGCTCTCATCAAGAGCAGTCTACCTTCAACG	2911
Db	2881	GCAGAGCAGCATCTCTCCAGCATATGCGCGGAGCTCTCATCAAGAGCAGTCTACCTTCAACG	2940
QY	2912	CGGCTTCAAGGCTGGGAGAACATATGCTCGCAAACTCTTTGGGGTCTTGGGGTGAAGT	2971
Db	2941	CGGCTTCAAGGCTGGGAGAACATATGCTCGCAAACTCTTTGGGGTCTTGGGGTGAAGT	3000
QY	2972	TCACAGCCTGTTTCTGTGATTTGCAAGTGGAAACACCTCCAGAGGCTGTGCACACATCTA	3031
Db	3001	TCACAGCCTGTTTCTGTGATTTGCAAGTGGAAACACCTCCAGAGGCTGTGCACACATCTA	3060
QY	3032	CAGATCTCTCTGTGTGAGAGCGTACAGAGTTTCACGATGTGTGTGACAGTCCCATTTCA	3091
Db	3061	CAGATCTCTCTGTGTGAGAGCGTACAGAGTTTCACGATGTGTGTGACAGTCCCATTTCA	3120
QY	3092	TCAGCAAGTTTGAAGAAGACCCACATTTTCTGTGGCGTATCTGTGACAGGGCTCCCT	3151
Db	3121	TCAGCAAGTTTGAAGAAGACCCACATTTTCTGTGGCGTATCTGTGACAGGGCTCCCT	3180
QY	3152	CTGCTACTTCATCTCTGAAAGCCAAAGAACGAGGAGATGTGGTGGGGGGCCAAAGGGCGCGC	3211
Db	3181	CTGCTACTTCATCTCTGAAAGCCAAAGAACGAGGAGATGTGGTGGGGGGCCAAAGGGCGCGC	3240
QY	3212	CGGCGCTTGTGCTTCCAGAGGCGGTGCAGTGGTGTGTCCACCAAGGATTTCTGTCTAAGCT	3271
Db	3241	CGGCGCTTGTGCTTCCAGAGGCGGTGCAGTGGTGTGTGTCCACCAAGGATTTCTGTCTAAGCT	3300
QY	3272	GACTCGACACCGTGTACACTAGTGGCACTCTGTGGGTCACCTCAGAGACGCCACAGAGCA	3331
Db	3301	GACTCGACACCGTGTGTACACTAGTGGCACTCTGTGGGTCACCTCAGAGACGCCACAGAGCA	3360
QY	3332	GCTGATGTGAAGTCCCCGGGGGAGACGCTGACTGCTCCGTGAGAGCGCCAGCCACCGGC	3391
Db	3361	GCTGATGTGTGAAGTCCCCGGGGGAGACGCTGACTGCTCCGTGAGAGCGCCAGCCACCGGC	3420
QY	3392	ACTGCGCTCAACATTTCAAGAACATCTCGAGCTGATGGCACCGCGCCACAGCGAGGGCGA	3451
Db	3421	ACTGCGCTCAACATTTCAAGAACATCTCGAGCTGATGGCACCGCGCCACAGCGAGGGCGA	3480
QY	3452	GAGCGATACACGAGCGCTGTACAGCGGGGGCTCTACGTCCAGAGGAGAGGAGGGCGCC	3511
Db	3481	GAGCGATACACGAGCGCTGTACAGCGGGGGCTCTACGTCCAGAGGAGAGGAGGGCGCC	3540
QY	3512	CACACCCAGGCCCGCACCGCTGGAGTCTGAGGCTGAGTGTAGTGTGTTGGCCAGAGCTT	3571

Db 607 CCGGCCCCCGCCACAGCTAGTGGACCCCGAAGCGCTCTGGATGCGAAGCGGCGTGGGA 666
QY 673 ACCATAGCGTCAAGGAGCGCGGGGTCCCTGGGCTGCGCAGCCCGGGTGTGAGAGAGC 732
Db 667 ACCATAGCGTCAAGGAGCGCGGGGTCCCTGGGCTGCGCAGCCCGGGTGTGAGAGAGC 726
QY 733 GCGGGGCGATGCGCAGCGGAAGTGTGCGGTTGCCAAGAGGCGCCAGCGCTGGCCCTGCC 792
Db 727 GCGGGGCGATGCGCAGCGGAAGTGTGCGGTTGCCAAGAGGCGCCAGCGCTGGCCCTGCC 786
QY 793 CTGAGCGGAGCGAGCGCGGTTGGGAGGAGGCTCTGGGCGCCAGCCGGGAGGAGCGGCTG 852
Db 787 CTGAGCGGAGCGAGCGCGGTTGGGAGGAGGCTCTGGGCGCCAGCCGGGAGGAGCGGCTG 846
QY 853 GACCGAGTGAACCGT 912
Db 847 GACCGAGTGAACCGT 906
QY 913 CTTTGGAGGGTGGGCTCTCTGGGACGCGGCCACTTCCACCCATCCGTGGGCGCCAGCACC 972
Db 907 CTTTGGAGGGTGGGCTCTCTGGGACGCGGCCACTTCCACCCATCCGTGGGCGCCAGCACC 966
QY 973 ACGGGGCCCCCATCCACATCCGGGCGACACAGTCCCTGGGAGAGCGCTTGTGCCCCGG 1032
Db 967 ACGGGGCCCCCATCCACATCCGGGCGACACAGTCCCTGGGAGAGCGCTTGTGCCCCGG 1026
QY 1033 TGTACGCGGAGACCAAGCACTTCTCTACTCTCAGCGAGCAAGAGAGAGAGTGGCGCT 1092
Db 1027 TGTACGCGGAGACCAAGCACTTCTCTACTCTCAGCGAGCAAGAGAGAGAGTGGCGCT 1086
QY 1093 CTTTCTACTAGTCTCTGAGGCCAGCCTGACTGGCGCTCGAGGCTCGTGGAGACA 1152
Db 1087 CTTTCTACTAGTCTCTGAGGCCAGCCTGACTGGCGCTCGAGGCTCGTGGAGACA 1146
QY 1153 TCTTTTGGGTTCCAGGCGCTGATGCGAGGAGTCCCGGAGGTTCCCGGCTGGCGCC 1212
Db 1147 TCTTTTGGGTTCCAGGCGCTGATGCGAGGAGTCCCGGAGGTTCCCGGCTGGCGCC 1206
QY 1213 AGCGCTACTGGCAATGCGGCGCTGTTTCTGAGAGTCTTGGGAAACACGCGGAGTGGC 1272
Db 1207 AGCGCTACTGGCAATGCGGCGCTGTTTCTGAGAGTCTTGGGAAACACGCGGAGTGGC 1266
QY 1273 CTTACGCGGAGTCTCTCAAGAGCACTGCGGCTGGAGTGGCGTACCCAGCAGCCG 1332
Db 1267 CTTACGCGGAGTCTCTCAAGAGCACTGCGGCTGGAGTGGCGTACCCAGCAGCCG 1326
QY 1333 GTTCTGTGCGCGGAGAAACCCAGGAGCTGTGAGGCGCGCCCGAGAGAGAGACAG 1392
Db 1327 GTTCTGTGCGCGGAGAAACCCAGGAGCTGTGAGGCGCGCCCGAGAGAGAGAGACAG 1386
QY 1393 ACCCGCGTGCCTGTGTGACGCTCTCGCGAGCAGACAGCCCTGGCAGGTGTACGGCT 1452
Db 1387 ACCCGCGTGCCTGTGTGACGCTCTCGCGAGCAGACAGCCCTGGCAGGTGTACGGCT 1446
QY 1453 TGTGTGGGCGCTGCTGTGCGCGGCTGTGCGCCAGGCTGTGGGCTCCAGGCAAGC 1512
Db 1447 TGTGTGGGCGCTGCTGTGCGCGGCTGTGCGCCAGGCTGTGGGCTCCAGGCAAGC 1506
QY 1513 AACGCGCTTCTCAGAGAACACCAAGAAATTCACTCCCGGGGGAAGCATGCGCAAGCTCT 1572
Db 1507 AACGCGCTTCTCAGAGAACACCAAGAAATTCACTCCCGGGGGAAGCATGCGCAAGCTCT 1566
QY 1573 CCGTGCAGAGAGTGAAGTGAAGATGAGTGTGCGGAGTGTGCTGTGCTGCGAGAGCC 1632
Db 1567 CCGTGCAGAGAGTGAAGTGAAGATGAGTGTGCGGAGTGTGCTGTGCTGCGAGAGCC 1626
QY 1633 CAGGAGTGTGCTGTGTTCCGCGCGCAGAGACCGTCTGCTGTGAGAGATCTGGCCAAGT 1692
Db 1627 CAGGAGTGTGCTGTGTTCCGCGCGCAGAGACCGTCTGCTGTGAGAGATCTGGCCAAGT 1686
QY 1693 TCTGTACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1752
Db 1687 TCTGTACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1746

QY 1753 CGGAGACCACGTTTCAAAAGAACAGGCTTTTCTACCGGAAAGTGTGTGAGCAAGT 1812
Db 1747 CGGAGACCACGTTTCAAAAGAACAGGCTTTTCTACCGGAAAGTGTGTGAGCAAGT 1806
QY 1813 TGCAGAGCATTTGAAATCAGACAGCACTTGAAGAGGTTGACAGTCCGGAGCTGTGGAG 1872
Db 1807 TGCAGAGCATTTGAAATCAGACAGCACTTGAAGAGGTTGACAGTCCGGAGCTGTGGAG 1866
QY 1873 CAGAGTGTGAGCAGCATGTGGAAGTCCAGGCGCGCGCTGTGTGTGTGTGTGTGTGTGT 1932
Db 1867 CAGAGTGTGAGCAGCATGTGGAAGTCCAGGCGCGCGCTGTGTGTGTGTGTGTGTGTGT 1926
QY 1933 TCCCAAGCGCTGACGGGCTGGCGCGGATTTGTGAACATGAGTACGTGTGGAGCCAGAA 1992
Db 1927 TCCCAAGCGCTGACGGGCTGGCGCGGATTTGTGAACATGAGTACGTGTGGAGCCAGAA 1986
QY 1993 CGTTCCGAGAGAAAGAGGCGCAGAGTCTACCTGTGAGGTTGAGGCACTGTTCAAGC 2052
Db 1987 CGTTCCGAGAGAAAGAGGCGCAGAGTCTACCTGTGAGGTTGAGGCACTGTTCAAGC 2046
QY 2053 TGTCTCACTACGAGCGGCG 2112
Db 2047 TGTCTCACTACGAGCGGCG 2106
QY 2113 ACGATATCCACAGGCGCTGGCGCACCTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2172
Db 2107 ACGATATCCACAGGCGCTGGCGCACCTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2166
QY 2173 CTGAGCTGTGA-----CATCCCCAGAGACA 2196
Db 2167 CTGAGCTGTGA-----CATCCCCAGAGACA 2226
QY 2197 GGCTCAGAGAGTCAATGCGCAGTCAATCAACCCCGAGACAGTGTGTGTGTGTGTGTGTGT 2256
Db 2227 GGCTCAGAGAGTCAATGCGCAGTCAATCAACCCCGAGACAGTGTGTGTGTGTGTGTGTGT 2286
QY 2257 ATGCGT 2316
Db 2287 ATGCGT 2346
QY 2317 CTACCTTGCAGAGCTTCCAGCGCTACATGTGAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 2376
Db 2347 CTACCTTGCAGAGCTTCCAGCGCTACATGTGAGAGTGTGTGTGTGTGTGTGTGTGTGT 2406
QY 2377 GCCCGTGAAGGATGCGGTGTATGAGCAGAGCTTCCCTGAATGAGGCGCAGAGTGTG 2436
Db 2407 GCCCGTGAAGGATGCGGTGTATGAGCAGAGCTTCCCTGAATGAGGCGCAGAGTGTG 2466
QY 2437 GCGTCTTGCAGAGTCTTCTACGCTTATGTGCGCACACGCGCGTGTGAGGAGGCAAGT 2496
Db 2467 GCGTCTTGCAGAGTCTTCTACGCTTATGTGCGCACACGCGCGTGTGAGGAGGCAAGT 2526
QY 2497 CTTACGTTCAGTGTGCGAGGAGATCCGAGGCTTCATCTCTCAGCGCTCTGTGAGCC 2556
Db 2527 CTTACGTTCAGTGTGCGAGGAGATCCGAGGCTTCATCTCTCAGCGCTCTGTGAGCC 2586
QY 2557 TGTGTACGCGGAGATGGAACAAAGCTTTTGGGGGATTTGGCGGGAAGGGCTGTGTC 2616
Db 2587 TGTGTACGCGGAGATGGAACAAAGCTTTTGGGGGATTTGGCGGGAAGGGCTGTGTC 2646
QY 2617 TGGCTTTGGTGAATGATTTTGTGTGTGACACCTCACTCACACCAAGCAAAACCTTCC 2676
Db 2647 TGGCTTTGGTGAATGATTTTGTGTGTGACACCTCACTCACACCAAGCAAAACCTTCC 2706
QY 2677 TCAAGACCTGTGTGCGAGTGTGCTGTGAGTATGAGTGTGTGTGTGTGTGTGTGTGTGTGT 2736
Db 2707 TCAAGACCTGTGTGCGAGTGTGCTGTGAGTATGAGTGTGTGTGTGTGTGTGTGTGTGTGT 2766
QY 2737 TGGTGAACCTTCCCTGTGAAGAGAGGCGCTGGGTGGCAGGGCTTTTGTTCAGATGGCGG 2796
Db 2767 TGGTGAACCTTCCCTGTGAAGAGAGGCGCTGGGTGGCAGGGCTTTTGTTCAGATGGCGG 2826

Qy	2797	CCACAGGCGATATTC	CCCGTGGGCGGCGCTGCTGCTGATACCCGAGACCCCTGGAGGCTGACA	2856
Db	2827	CCACAGGCGATATTC	CCCGTGGGCGGCGCTGCTGCTGATACCCGAGACCCCTGGAGGCTGACA	2886
Qy	2857	GGGACTACTGCACATATG	CGCGGACCCATCAGAGCGCATCTACACCTTCAACCGGGGT	2916
Db	2887	GGGACTACTGCACATATG	CGCGGACCCATCAGAGCGCATCTACACCTTCAACCGGGGT	2946
Qy	2917	TCAGAGCTGGGAGAGAACAT	GTGCTGCAAACTCTTTGGGGCTTGGGGCTGAGAGTGCACA	2976
Db	2947	TCAGAGCTGGGAGAGAACAT	GTGCTGCAAACTCTTTGGGGCTTGGGGCTGAGAGTGCACA	3006
Qy	2977	GCCCTGTTTCGTGATTTG	CAAGGTGCAACGCCCTCAGAGCGGTGTCACCAACTCTACAGA	3036
Db	3007	GCCCTGTTTCGTGATTTG	CAAGGTGCAACGCCCTCAGAGCGGTGTCACCAACTCTACAGA	3066
Qy	3037	TCCTCTCTGCTGACAGGCG	GTACAGATGTGTCTGACAGTCCCATTTTATCAGC	3096
Db	3067	TCCTCTCTGCTGACAGGCG	GTACAGATGTGTCTGACAGTCCCATTTTATCAGC	3126
Qy	3097	AAGTTTGGAAAGAACCCCA	ATTTTCTCTGCGGTATCTCTGACAGCGGCTCCCTCTGCT	3156
Db	3127	AAGTTTGGAAAGAACCCCA	ATTTTCTCTGCGGTATCTCTGACAGCGGCTCCCTCTGCT	3186
Qy	3157	ACTCCATCTCGAAAGAGCA	AGCAAGCATCGCTGCGGGGCGCAAGGCGCCCGCGGCGC	3216
Db	3187	ACTCCATCTCGAAAGAGCA	AGCAAGCATCGCTGCGGGGCGCAAGGCGCCCGCGGCGC	3246
Qy	3217	CTCTGCCCTCGAGGCGCG	TGAGTGGCTGTGCACACAGCATTTCTGCTCAAGTGTGACTC	3276
Db	3247	CTCTGCCCTCGAGGCGCG	TGAGTGGCTGTGCACACAGCATTTCTGCTCAAGTGTGACTC	3306
Qy	3277	GACACCGGTGACATCTAG	CGTCTGCGGGGTACATCAGACAGCGACAGCGAGCTGA	3336
Db	3307	GACACCGGTGACATCTAG	CGTCTGCGGGGTACATCAGACAGCGACAGCGAGCTGA	3366
Qy	3337	GTGCGAAGCTCCGCGGAG	CGACGCTGACGTGCGTGGAGGCGCGACGCAACCGCGGCACTGC	3396
Db	3367	GTGCGAAGCTCCGCGGAG	CGACGCTGACGTGCGTGGAGGCGCGACGCAACCGCGGCACTGC	3426
Qy	3397	CCTGAGACTTCAAGACAT	CCTGGATGATGGCCACCGCCGACAGCGCGGAGACA	3456
Db	3427	CCTGAGACTTCAAGACAT	CCTGGATGATGGCCACCGCCGACAGCGCGGAGACA	3486
Qy	3457	GACACCAAGACCTCTGCA	CGCGGCTGTACGTCCCAAGGAGGAGGCGGCGCCCAAC	3516
Db	3487	GACACCAAGACCTCTGCA	CGCGGCTGTACGTCCCAAGGAGGAGGCGGCGCCCAAC	3546
Qy	3517	CCAGGCGCGGACCGCTG	AGAGTCTGAGGCTGAGTGTATTGGCCGACGCTGCATGT	3576
Db	3547	CCAGGCGCGGACCGCTG	AGAGTCTGAGGCTGAGTGTATTGGCCGACGCTGCATGT	3606
Qy	3577	CCGAGCTGAAGGCTGATG	TCCGGCTGAGGCTGACGACGAGTGTCAAGCCAAAGGCTGAGTG	3636
Db	3607	CCGAGCTGAAGGCTGATG	TCCGGCTGAGGCTGACGACGAGTGTCAAGCCAAAGGCTGAGTG	3666
Qy	3637	TCACACACACCTGCTCT	CTTCACTTCCCAACAGGCTGACGCTGGCTCCACCCAGGCGC	3696
Db	3667	TCACACACACCTGCTCT	CTTCACTTCCCAACAGGCTGACGCTGGCTCCACCCAGGCGC	3726
Qy	3697	ACCTTTTCTCACAGAGG	CGGGCTTCCACATCTCCCAACATAGAAATAGTCATCCCCAGA	3756
Db	3727	ACCTTTTCTCACAGAGG	CGGGCTTCCACATCTCCCAACATAGAAATAGTCATCCCCAGA	3786
Qy	3757	TTTCGCAATGTGTACCC	TGCGCTGCGCTCTTGTTCCTTCACCCCAACATCAGAGTG	3816
Db	3787	TTTCGCAATGTGTACCC	TGCGCTGCGCTCTTGTTCCTTCACCCCAACATCAGAGTG	3846
Qy	3817	GAGACCTCGAAGAGACCC	TGGAGACTCTGGAGATTTGGAGTGAACCAAAGGTGTGCCCTG	3876
Db	3847	GAGACCTCGAAGAGACCC	TGGAGACTCTGGAGATTTGGAGTGAACCAAAGGTGTGCCCTG	3906
Qy	3877	TACACAGCGGAGGACCT	CTGACCTGATGGAGGTCCCTGTGTGAGTCAAAATTTGGGGAGGT	3936
Db	3907	TACACAGCGGAGGACCT	CTGACCTGATGGAGGTCCCTGTGTGAGTCAAAATTTGGGGAGGT	3966
Qy	3937	GCTGTGGAGTAAATAC	TATATACATTTTTCAGTTTGAAGAAAAA	3996
Db	3967	GCTGTGGAGTAAATAC	TATATACATTTTTCAGTTTGAAGAAAAA	4026
Qy	3997	A	3997	
Db	4027	A	4027	
RESULT 15				
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
PUBMED				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				
AUTHORS				
TITLE				
JOURNAL				

```
/rpt_family="Alu"
/rpt_type-dispersed
repeat_region
14271..14556
/rpt_family="Alu"
/rpt_type-dispersed
repeat_region
14539..17711
/rpt_family="L1"
/rpt_type-dispersed
repeat_region
18109..18398
/rpt_family="Alu"
/rpt_type-dispersed
repeat_region
complement(20818)..21123
/rpt_family="LTR1"
/rpt_type-dispersed
repeat_region
21650..21912
/rpt_family="MLT1"
/rpt_type-dispersed
repeat_region
complement(22236)..22484
/rpt_family="Alu"
/rpt_type-dispersed
repeat_region
complement(22986)..23283
/rpt_family="Alu"
/rpt_type-dispersed
repeat_region
complement(24442)..24466
/rpt_type-dispersed
gene
<24442..64466
/feature="TERT"
/join(<24442..24660,24765..26118,35473..35668,37759..37939,
38627..38806,39301..39456,45360..45455,46436..46521,
49007..49120,51105..51176,53048..53236,57040..57166,
58981..59042,62229..62353,63135..63272,63809..>63912)
/feature="TERT"
/product="telomerase catalytic subunit"
/join(24442..24660,24765..26118,35473..35668,37759..37939,
38627..38806,39301..39456,45360..45455,46436..46521,
49007..49120,51105..51176,53048..53236,57040..57166,
58981..59042,62229..62353,63135..63272,63809..63912)
/feature="TERT"
/codon_start=1
/product="telomerase catalytic subunit"
/protein_id="AAG23289.1"
/db_xref="GI:12642957"
/translation="MPRAPRCRAVRSILRSHYREVLPLATFVRRLPGOGRIQORGP
AAPALVAOCLVCPMDARPPAPSPRSROYSCLEKELVARLQRCERKANVLAFCGA
LIDGARGPREPPTTSVRSYLPNTVDLALSGAWGLLRRVGDVAVHLLARCALEV
LVAPSCAYQVGPPLVQLGATQARPPHAGSGPARRUGCCRANMHSVREAGVGLPA
PGARRRGSSRSRLPLKPRPRGAPPEPRTPYQOGSMAPGRTGSPDGFVGLSPA
RPAEATSLGALSGLTSHSPSVROHAGPSTSRPPMDTCCPVYAEYKHETLS
SGKEOGRPEFLISLRLSLTGAARLVETIFLSRPMGPPTPRRLPQRYQMRL
FLELGNHACQPCPYGILKTCPLRAATVPAQCARCPGGSVAAPPEETDRRLYO
LLROHSPNOYGFVRACLRILVPPGIMSGRHNDRFLRNTKFTSLGKRAKSLDEL
TKMSYVDCAMLRKSPGVGCPAAEHLREELTAKFLHMLMSVYVVELLSFEYVET
TQGNRLFEYKRSVSKLQSIGIROLKRVQLRELSEAVROHREARPLLSTRLPT
PKPDGLRPIVNMVYVGAATFERREKRAELTSLRKALSVLNERARPLLGSVVG
LDDIHRAMPTFELVRAODPPPELYFVKVDTGKVDYDIPDDRLEVEASTIKQONTC
VRRYAVYOKAAGHVRKAFKSHVSTLTDLOPYMROFAHLOEHSPLRDVITQSSSL
NEASSGLDFELRPMCHAVIRINKAKTSVQCGIIPQGSITLTLCSLCTGMEKNLEFG
IRRDGLRLVLDPLVPLHPLHAKTFLRLVGVPEYGGVNLKRTVAVPEVDELG
GGTAFOVMPAHGJLEPMWGLLDRTLEVOYDSSYATSRASITFNRKAKRNMR
KLEGVRLKCHSLFLDLQVNSLQTCVNIYKILLQARFHAACVLQDFPQOWKNNT
FELRVISDRTASLCSYLKAKNAGSLGACGAPLPEASEAVOWMCHOAFLKLRHRYT
YVPLGSLRTAQLSRKLPCTTLTALLEANANALBPDPFTIID"
27341..27628
/rpt_family="Alu"
/rpt_type-dispersed
repeat_region
27650..29650
/feature="VNTR"
/rpt_type-tandem
/rpt_unit-gagtagggcgctcccccgggtgtccctgtcacgtgcaggct
complement(31926..32203)
/rpt_family="Alu"
/rpt_type-dispersed
repeat_region
complement(32555..32835)
/rpt_family="Alu"
/rpt_type-dispersed
```

```
repeat_region
33569..33861
/rpt_family="Alu"
/rpt_type-dispersed
repeat_region
complement(33873..33967)
/rpt_family="MER33"
/rpt_type-dispersed
repeat_region
34111..35453
/feature="VNTR"
/rpt_type-tandem
repeat_region
complement(35993..36281)
/rpt_family="Alu"
/rpt_type-dispersed
repeat_region
41485..42324
/feature="VNTR"
/rpt_type-tandem
/rpt_unit-gtggatgtgttcattcatgtgtggtgtagtgagggagctc
complement(42856..42954)
/rpt_family="Alu"
/rpt_type-dispersed
repeat_region
43312..43618
/rpt_family="MER1"
/rpt_type-dispersed
repeat_region
44225..45115
/feature="VNTR"
/rpt_type-tandem
/rpt_unit-gggatctgattctcatgtgtggtgtagtgagggagctc
complement(48015..48300)
/rpt_family="Alu"
/rpt_type-dispersed
repeat_region
complement(49647..50276)
/rpt_family="L1"
/rpt_type-dispersed
repeat_region
53945..54234
/rpt_family="Alu"
/rpt_type-dispersed
repeat_region
57630..58735
/feature="VNTR"
/rpt_type-tandem
/rpt_unit-tgggcatctgtgcacatccctctctc
61332..61597
/rpt_family="Alu"
/rpt_type-dispersed
repeat_region
complement(66201..66323)
/rpt_family="Alu"
/rpt_type-dispersed
repeat_region
66389..66661
/rpt_family="Alu"
/rpt_type-dispersed
repeat_region
66661..66736
/feature="microsatellite"
/rpt_type-tandem
/rpt_unit-aag
67140..67583
/rpt_family="MLT1"
/rpt_type-dispersed
repeat_region
complement(73264..73377,73925..74084,76991..77080,
78049..78146,79551..79661,81950..82131,84724..84861,
85253..85393,91909..92068)
/product="joining channel-like protein"
complement(733264..73377,73925..74084,76991..77080,
78049..78146,79551..79661,81950..82131,84724..84861,
85253..85393,91909..92068)
/codon_start=1
/evidence-not-experimental
/product="sodium channel-like protein"
/protein_id="AAG23290.1"
/db_xref="GI:12642958"
/translation="MAHAPDPDPAASDLDERPKMDNKAQYLTLCTGFAVGLGNIWRF
```

Query Match 95.7% Score 3834.4; DB 9; Length 92564;
Best Local Similarity 9.5%; Pired. No. 1.3e-89; 2; Indels 38278; Gaps 16;
Matches 4004; Conservative 0; Mismatches

Oy 1 GTTTCAGGACGCGCTGCTGCTCTGTCGACGTGGGAAGCCCTTGCCGCCGACCCCGC 60
|||||
Db 24380 GTTTCAGGACGCGCTGCTGCTCTGTCGACGTGGGAAGCCCTTGCCGCCGACCCCGC 24439
Oy 61 CGATGCGCGCGCGCTCCGCTGCGAGCCGTGGCGCTCCCTGCTGCGACGCACTACCGCG 120
|||||
Db 24440 CGATGCGCGCGCTCCGCTGCGAGCCGTGGCGCTCCCTGCTGCGACGCACTACCGCG 24439
Oy 121 AGGTGCTCGCTGCGACGCTTCGTGGGCGCCCTGGGGCCCGCAAGGGCTGGCGGGTGGTC 180
|||||
Db 24500 AGGTGCTCGCTGCGACGCTTCGTGGGCGCCCTGGGGCCCGCAAGGGCTGGCGGGTGGTC 24559
Oy 181 AGCGGGGGGACCGCGGGGCTTTCGCGCGCTGGTGGCCCAATGCTGGTGGTGGCGCT 240
|||||
Db 24560 AGCGGGGGGACCGCGGGGCTTTCGCGCGCTGGTGGCCCAATGCTGGTGGTGGCGCT 24619
Oy 241 GGGAGGCAAGCG 278
|||||
Db 24620 GGGAGGCAAGCG 24679
Oy 279 ----- 278
Db 24680 GCGTCGCGCTGGGGTTGAGGGCGCGCGGGGGGAACGACGATGGGAGAGACGCGCAG 24739
Oy 279 -----CAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 316
Db 24740 GCGACTCAGGGCGCTTCCCGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 24739
Oy 317 GCAGAGGCTGTGCGAGCG 376
Db 24800 GCAGAGGCTGTGCGAGCG 24859
Oy 377 CGGGGCGCGCGGGGGCG 436
Db 24860 CGGGGCGCGGGGGCG 24919
Oy 437 CAGGTGACCGACGCACTGCGGGGGAGCGGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 496
Db 24920 CAGGTGACCGACGCACTGCGGGGGAGCGGGGGGCTGCTGCTGCTGCTGCTGCTGCTG 24979
Oy 497 CGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 556
Db 24980 CGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 25039
Oy 557 CTGCGCTTACCAAGGTGTGCGGGCGCGCGCTGTACACAGCTGCGCGCTGCTGCTGCTGCTG 616
Db 25040 CTGCGCTTACCAAGGTGTGCGGGCGCGCGCTGTACACAGCTGCGCGCTGCTGCTGCTGCTG 25099
Oy 617 GCCCGCGCACACGCTAGTGAACCCCGAAGGCGCTGCGGATGCGAAGCGGCGCTGGAACA 676
Db 25100 GCCCGCGCACACGCTAGTGAACCCCGAAGGCGCTGCGGATGCGAAGCGGCGCTGGAACA 25159
Oy 677 TAGCGTCAGGAGGCGGGGCTCCCGCTGGGCTGCGACGCGCGGGGTGCGAAGGAGCGCGG 736
Db 25160 TAGCGTCAGGAGGCGGGGCTCCCGCTGGGCTGCGACGCGCGGGGTGCGAAGGAGCGCGG 25219
Oy 737 GGGGAGTGCAGGCGGAAGTCTGCGGTGGCCAAAGGGCGCGAGGTGGCGGCTGCGCGCTGA 796
Db 25220 GGGGAGTGCAGGCGGAAGTCTGCGGTGGCCAAAGGGCGCGAGGTGGCGGCTGCGCGCTGA 25279
Oy 797 GCCGAGGCGGACCGCGCTGGGAGGGGCTGCTGGGCGCAACCGGAGCAGGACGCTGAC 856
Db 25280 GCCGAGGCGGACCGCGCTGGGAGGGGCTGCTGGGCGCAACCGGAGCAGGACGCTGAC 25339
Oy 857 GAGTGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 916
Db 25340 GAGTGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 25399
Oy 917 GAGGAGTGCAGTCTGCGACGCGCACTGCCACCATGCTGGGGCGCGCAGACGACGCG 976
Db 25400 GAGGAGTGCAGTCTGCGACGCGCACTGCCACCATGCTGGGGCGCGCAGACGACGCG 25459
Oy 977 GGGCCCCCATCATCATCGCGGCGCACACGCTCCCTGGAGCACGCGCTTGTGCCCGGCTGA 1036

|||||
Db 25460 GGGCCCCCATCATCATCGCGGCGCACACGCTCCCTGGGAGACGCGCTTGTCCCCGGGTGA 25519
Oy 1037 CCGCGAGACCAACGACTTCTCTACTCTCTCAGGCGACAAAGAGAGAGCTGGGCGCTCTT 1096
Db 25520 CCGCGAGACCAACGACTTCTCTACTCTCTCAGGCGACAAAGAGAGAGCTGGGCGCTCTT 25579
Oy 1097 CCTACTAGCTCTGAGGCGCCAGCGCTGACTGGGCGCTGGGAGGCTGCGGAGACATCTT 1156
Db 25580 CCTACTAGCTCTGAGGCGCCAGCGCTGACTGGGCGCTGGGAGGCTGCGGAGACATCTT 25639
Oy 1157 TCTGGGTTCCAGGCGCGTGAATGCGAGGACGCTCCCGAGGTTGCCGCGCTGCGCGAGG 1216
Db 25640 TCTGGGTTCCAGGCGCGTGAATGCGAGGACGCTCCCGAGGTTGCCGCGCTGCGCGAGG 25699
Oy 1217 CTACTGCGCAATGCGGCGCGCTGTTCTGAGCTGCTTGGGACACGCGCGACGCTGCTTA 1276
Db 25700 CTACTGCGCAATGCGGCGCGCTGTTCTGAGCTGCTTGGGACACGCGCGACGCTGCTTA 25759
Oy 1277 CGGGGTGCTCTTCAAGACGCACTGCCGCTGCGAGCTGCGGTACCCGACGACCGGTGT 1336
Db 25760 CGGGGTGCTCTTCAAGACGCACTGCCGCTGCGAGCTGCGGTACCCGACGACCGGTGT 25819
Oy 1337 CTGTGCGCGGAGAACCCCGAGGCTCTGTGGCGGCCCGCGAGGAGAGACACAGACCC 1396
Db 25820 CTGTGCGCGGAGAACCCCGAGGCTCTGTGGCGGCCCGCGAGGAGAGACACAGACCC 25879
Oy 1397 CCGTGGCTGTGTGACGCTGCTCGCCAGACAGCAGCCCGCTGGCAGGTGTACGGCTTGT 1456
Db 25880 CCGTGGCTGTGTGACGCTGCTCGCCAGACAGCAGCCCGCTGGCAGGTGTACGGCTTGT 25939
Oy 1457 GCGGGCGCTGCTGCGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1516
Db 25940 GCGGGCGCTGCTGCGCGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 25999
Oy 1517 CCGCTCTCTGAGAACACCAAGATTCCTCCCTGGGGAACGATGCGCAAGCTTCTGCT 1576
Db 26000 CCGCTCTCTGAGAACACCAAGATTCCTCCCTGGGGAACGATGCGCAAGCTTCTGCT 26059
Oy 1577 GCAGGACCTGACGTGAAGATGAGCTGCGGAGCTGCGCTTGGCTGCGCAGAGGCC 1633
Db 26060 GCAGGACCTGACGTGAAGATGAGCTGCGGAGCTGCGCTTGGCTGCGCAGAGGCC 26119
Oy 1634 ----- 1633
Db 26120 TGAGAGGTGTGGCGCTGCGAGGCCAGGCCCGCACGAGCTGAATGAGGGGCTCAGA 26179
Oy 1634 ----- 1633
Db 26180 AAAGGGGCGAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 26239
Oy 1634 ----- 1633
Db 26240 TTTCGCTCAGGACGTGCGATGGAACGATGATCTGCTGCTGCTGCTGCTGCTGCTG 26299
Oy 1634 ----- 1633
Db 26300 TTTCGATTAACCTTACGAGCTTCACTTCACTTTTGAATGACACCGGTTTCCAGGCGCG 26359
Oy 1634 ----- 1633
Db 26360 GAGGCGAGACGATGAACAGAGAGGCTGGCGCGCGGACGTGAGCGCGGTTGCCGCAAT 26419
Oy 1634 ----- 1633
Db 26420 GGGGAGAGTGTCTGAGACACAGAGCTGCGGAGGGTGGCTGACGTTACTATAT 26479
Oy 1634 ----- 1633
Db 26480 CCTCTTGCATTTCAAGGTGGGATGAGAGTGGGAGAGAACCCCTTCTCTGGG 26539
Oy 1634 ----- 1633

Db 26540 GGTGGAGGTAAGGGTTTTCAGTTGCACGTGTCACGCAATATGACAGGTTTGTTAA 26599
QY 1634 ----- 1633
Db 26600 GATTTAATTTGTGTGTGACGGCCAGGTGGCTGCACGCCGGTAATCCAGACATTTG 26659
QY 1634 ----- 1633
Db 26660 GGAAGCTGAGGCGAGTGGATCACCTGAGGTTCAGAGGTTTGAGACCAGCCTGACCAACATG 26719
QY 1634 ----- 1633
Db 26720 GTGAACCCATCTCTGTACTAAATAACAAAATTAGCTGGCATGTGTGTGCTGT 26779
QY 1634 ----- 1633
Db 26780 AATCCAGCTACTTGGAGGCTGAGGAGAGAAATCACTGAACCCAGAGGCGGAGGCT 26839
QY 1634 ----- 1633
Db 26840 GCAGTAGCTGAGATTGGCATTTGTACTCCAGCCTGGGCGACAAGAGTGAACCTGTCTC 26899
QY 1634 ----- 1633
Db 26900 TTTTAAAAAAAAGTGTTCGTTGATTGTGCCAGAGAGGGTAGAGGAGAGATAG 26959
QY 1634 ----- 1633
Db 26960 ACGTGTCGAGCAGCAATCTCGTCCCATCTTTAGTATGAAGGGCCACATGGAGC 27019
QY 1634 ----- 1633
Db 27020 AGAGACAGAGATGCTCCACCTGCTGAGGAAGGACAGTGTGTGGGTTCAGGGG 27079
QY 1634 ----- 1633
Db 27080 ATGTGCTGCTGGGCCCTGCCGTGTCCCAACCTGTTTCTGTGATTGATGTAGGAA 27139
QY 1634 ----- 1633
Db 27140 CTTCCGCTCCAGCCCCCTTTTGGTCCAGTGTCCAGGCCCTACCGTGGCAGCTAGAA 27199
QY 1634 ----- 1633
Db 27200 GAAGTCCGATTCACCCCTCCCAACAACTCCAAGACATGTAAGACTTCCGGCATG 27259
QY 1634 ----- 1633
Db 27260 CACACAAAGAGGGTGAACCTTTGGGGCTTTTTTTTCTTTTTTTTATGTGGC 27319
QY 1634 ----- 1633
Db 27320 AAAAGTCATATACATGATGATGTGGCACTCCTAACACCGTTTCTGTGTACAGTGCAGAA 27379
QY 1634 ----- 1633
Db 27380 TGTAACTCGCGCGTGTTTACAGCAGGTTCCTGAATGCTGCGTTCGTGACTGGAA 27439
QY 1634 ----- 1633
Db 27440 GTCCCTAACCATGAACGGAGCTGCCTCACACCTGCTGGGCTCAGGTGGACACGCGG 27499
QY 1634 ----- 1633
Db 27500 AGTCAGATAGAGCTCATGCAACCCAGTTTGTCTTGTCTCCAGTTCCTTCGTTGAG 27559
QY 1634 ----- 1633
Db 27560 GAGAGTTTGAATTCTGTATCAGAGACTGTGCTGATTCGTCTCTGACTTCAGATG 27619
QY 1634 ----- 1633
Db 27620 AGGTGACATCTGCCCCCTGGCTTATGCAGGAGTGAAGGCGTGTCCCGGGTGTCCCTGT 27679

QY 1634 ----- 1633
Db 27680 CACGTGAGGGTAGTAGAGCGTTTCCCCAGGTGTCCCTGTACAGTGTAGGGTAGTGA 27739
QY 1634 ----- 1633
Db 27740 GCGCGGCCCCGGGTGTCCCTGTCCCGTGCAGCGTATTTAGGTGTGCCCCGGGTGT 27799
QY 1634 ----- 1633
Db 27800 CCTGTACGTTAGGGTAGTAGAGGCCCATCCCCGGGTGTCCCTGTACAGTGTAGGGT 27859
QY 1634 ----- 1633
Db 27860 GAGTAGCGGTGTCCCCGGGTGTCCCTGTCCCGTGCAGCGTATTTAGGTGTGCCCCC 27919
QY 1634 ----- 1633
Db 27920 GGGTGTCCCTGTACAGTGTAGGGTGAAGTAGGGCCATCCCCGGGTGTCCCTGTCCCGT 27979
QY 1634 ----- 1633
Db 27980 CAGGTTAGTAGAGCGCGCTCCCCGGGTGTCCCTGTCCCGTGCAGGGTAGTAGGCGTG 28039
QY 1634 ----- 1633
Db 28040 GCCCCGGGTTTCTCTGTCTACGTGCAGGGTGAAGTGAAGCACTGTCCCCGGGTGTCCCTGT 28099
QY 1634 ----- 1633
Db 28100 CACGTGAGGGTAGTAGAGCGCGGTCCCCGGGTGTCCCTGTACAGTGTAGGGTAGTGA 28159
QY 1634 ----- 1633
Db 28160 GGCATGTGCCCGGGTGTCCCTGTACAGTGTAGGGTAGAGGCGCTGTCCCCGGGTGT 28219
QY 1634 ----- 1633
Db 28220 CCCTGTACGTTAGGGTAGTAGAGCGCGGCCCCAGGGTGTCCCTGTACAGTGTAGGGT 28279
QY 1634 ----- 1633
Db 28280 GAGTAGAGCACCGTCCCTGGGTGTCCCTCCAGTATAGGGTAGTAGAGCACTGTCCCC 28339
QY 1634 ----- 1633
Db 28340 GGGTGTCCCTGTACAGTGCAGGGTAGTAGAGCGCGGTCCCAAGTGTCCCTGTACAGTG 28399
QY 1634 ----- 1633
Db 28400 TAGGGTAGTAGAGCACTGTCCCAAGTGTCCCTGTACAGTGCAGGGTAGTAGAGCGCG 28459
QY 1634 ----- 1633
Db 28460 GTCCCGAGTGTCCCTGTACAGTGCAGGGTAGTAGAGCGCGGTCCCGGGTGTCTGT 28519
QY 1634 ----- 1633
Db 28520 CACGTGAGGGTAGTAGAGCGCGGTCCCGGGTGTCCCTGTACAGTGCAGGGTAGTGA 28579
QY 1634 ----- 1633
Db 28580 GGGCGGTCCCGGGTGTCCCTGTCCCATGCAAGGTGAAGAGCGCCGTCCCGCATGT 28639
QY 1634 ----- 1633
Db 28640 CTCTGTACGTGAGGGTAGTAGAGCGCGGTCCCGGGTGTCCCTGTACAGTGCAGGGT 28699
QY 1634 ----- 1633
Db 28700 GAGTAGAGCGCGGTCCCGGGTGTCCCTGTCCCGTGCAGGGTAGTAGAGCACGCGCCCC 28759

D	b	30920	GGATTGAGCTCCAGGCCACAGGTGGAGTGCCTCCTGTCGTCTCCTGCTCGAGACCAGC	30979
O	y	1634	-----	1633
D	b	30980	TGGAGGCCGGGAGTCTCCGCCGCCCTTGCAACTTCCCTCTGGGCTTTAGTTTTGA	31039
O	y	1634	-----	1633
D	b	31040	TTTCACATTTACCTCTGACGTTTCTATCTCATATGATGATCTTTTCTGGTTAAT	31099
O	y	1634	-----	1633
D	b	31100	CTTTCATTCCTTTCTAGCTCTTAGTTAGTATGCTTCCCTTAAGTCTCTCTTA	31159
O	y	1634	-----	1633
D	b	31160	CCTGACCCTGTGTTTGATGTGAATATCATCATGACGACGACCTTTCAGTCTTA	31219
O	y	1634	-----	1633
D	b	31220	AAATACCTCAAGTGAATACTCTTTAAGTATCTTATCTGATTTTTTCTTGG	31279
O	y	1634	-----	1633
D	b	31280	TGCACGCTGCTTTTGACGTGAATCATTTGTATATCATGACTTTTAAGATCTTAG	31339
O	y	1634	-----	1633
D	b	31340	CTTATCTGTGATTTCTTTGACGAGTATTTTGAACACTGTTTATGTTCAAGATATG	31399
O	y	1634	-----	1633
D	b	31400	TAGAGTATCAAGTACGTAGATATTTAAGTATCATTTATATGATTTCTAATCA	31459
O	y	1634	-----	1633
D	b	31460	GTTGTGAGTGCCTATATATCAATTTATGAACTTTCGGAGCCTTGCTTGTGAT	31519
O	y	1634	-----	1633
D	b	31520	CTAGGTGTGATGTTTCCAGACTGTCATTTGAATTTGACATCTGTCAATATGG	31579
O	y	1634	-----	1633
D	b	31580	GCATGATTTCAATATCCAGCTTATTAAGTCCAGTCAAGCAAGCTTCTCTCTCT	31639
O	y	1634	-----	1633
D	b	31640	AGATGATGAATTCAGAAGAGAGCCATGCTCCACCTGGGGGATGGGTCTGTCA	31699
O	y	1634	-----	1633
D	b	31700	TTTCTTCTGCTTGGTACATTTATGTAGGCAATGTTAAGTGCATGACGTGTAGAA	31759
O	y	1634	-----	1633
D	b	31760	TTTATCTTCTGATAGTGAATCTTTTGAGACTTCTATGCTCTAGTAATCTAGTA	31819
O	y	1634	-----	1633
D	b	31820	TCTTTTAAAAATTCCTTAGTACTGCCCCACTGGGCTTTTGATAGTATTTTCT	31879
O	y	1634	-----	1633
D	b	31880	GCTGTCTGTTTCTGCTTAAATTAATATATATATATATATTTTGTGAGAC	31939
O	y	1634	-----	1633
D	b	31940	AGAGCTTGTGTCTGCCCCAGGCTAGTCACTGCTGTGATCACAGTCACTGAAT	31999
O	y	1634	-----	1633
D	b	32000	TTAACCTTGTGCCCAGACCGCTCTTCACCTCAGCTCTGTAGATAGCTGAATCAGAC	32059
O	y	1634	-----	1633

[illegible]

[illegible][illegible]

Db 35300 TGAGGTGCGCCAGGCCCTTGTTGGCTGGATGTGCCGTGCTCCGATGTCAGGTCGTGGG 35359
QY 1634 ----- 1633
Db 35360 TGAGGTGCGCCAGGCCCTTGTTGGCTGGATGTGCCGTGCTCCGATGTCAGGTCGTGGG 35419
QY 1634 ----- AGGGGTTGG 1642
Db 35420 TGAGGTGCGCCAGGCCCTTGTTGGCTGGATGTGCCGTGCTCCGATGTCAGGTCGTGGG 35479
QY 1643 CTGTTGTTCCGCGCCAGAGCAGCCGTCGTCGAGAGATGTCGAGCAGTTCCCTGCTG 1702
Db 35480 CTGTTGTTCCGCGCCAGAGCAGCCGTCGTCGAGAGATGTCGAGCAGTTCCCTGCTG 35539
QY 1703 GCTGATGAGTGTGATGCTGTCGAGCTGCTCAGGCTTTCTTTATATGTCAGGAGACCAC 1762
Db 35540 GCTGATGAGTGTGATGCTGTCGAGCTGCTCAGGCTTTCTTTATATGTCAGGAGACCAC 35599
QY 1763 GTTTCAAAAGAACAGGCTTTTCTACCGAGAGATGTCGAGCAGTTGCAAGCAT 1822
Db 35600 GTTTCAAAAGAACAGGCTTTTCTACCGAGAGATGTCGAGCAGTTGCAAGCAT 35659
QY 1823 TGGAAAT ----- 1828
Db 35660 TGGAAATGAGTGTGATGCTGTCGAGCTGCTCAGGCTTTCTGAAATGTCGAGCAGCAT 35719
QY 1829 ----- 1828
Db 35720 CCGGCGCTCAGCATGCGGCTGTCGCACTTGTGCTGCTCCGTCGTCGTCGAGCTG 35779
QY 1829 ----- 1828
Db 35780 GCTGGAGACCGAGGGGCCCTGTCAGAGCCTGTCGCAAGTGTGTCGCAAGCTCTGA 35839
QY 1829 ----- 1828
Db 35840 CTGCGTGGAGCTCAGCTTCTCTTCTGTAATCAGAGATTTGTGCCAAGTGTCTCTA 35899
QY 1829 ----- 1828
Db 35900 GGGTTTGAAGCAGAGAGGATTAATATGATGGAACACTTACCCTAGCCTCTGCC 35959
QY 1829 ----- 1828
Db 35960 TTCCCTGGAGATGAGGTGATGATCTCTCTCTTTTCTTTTCTTTTGTGAGATGAGT 36019
QY 1829 ----- 1828
Db 36020 CTCACCTGTGTCGCCAGGCTGGAGTGCAGTGGCATATCTTGCTCACTGCAACCTCCAC 36079
QY 1829 ----- 1828
Db 36080 CTCTGGGTTTAAGCAGATTCACAGCCTCAGCCTCCTAAGTACGAGGATTAACAGGCAC 36139
QY 1829 ----- 1828
Db 36140 TGCACACAGCCTGCTAATTTTGTACTTTTAGAGAGAGCGGGTTTACCAGATGTTGGC 36199
QY 1829 ----- 1828
Db 36200 CAGGCTGCTCGAATCTCATGATGATCCAGCCACCTTGCCCTCCCAAGTGTCT 36259
QY 1829 ----- 1828
Db 36260 GGGTTTACAGGCTAAGCAGCCGTCGCCAGCCCGGATTTCTTTAATTCATGCTGTTCT 36319
QY 1829 ----- 1828
Db 36320 GTATGATCTTCAATCTATTGATTTAGTATGAGAGATAAATCCACCACTTGGC 36379
QY 1829 ----- 1828
Db 36380 GACTCACTGACGAGAGACCTGTGACGAGGAGACCTGGGATAGAGAGTTCCACCATGA 36439

QY 1829 ----- 1828
Db 36440 GCTAATCTTAGTGTGCTGATTTGAATGCTGTGATTTTGTCTCAATGTTGCGCTG 36499
QY 1829 ----- 1828
Db 36500 ATGAGATGTGATTTGTGACAGATTCAGCTGATTTGATCATGAGTGGAGGAGCG 36559
QY 1829 ----- 1828
Db 36560 CTGCTGTGGAGATGCCAGCCTGCTGAGCCAGGCCATGATTTAGCTTCTCCGTGTC 36619
QY 1829 ----- 1828
Db 36620 CGCCAGGCTAGTGTGAGGGCTTTAGTCAGAAAGATGAGGGCTTCCACGCTCCCTGC 36679
QY 1829 ----- 1828
Db 36680 AACTCGAGTCCCTGGGGGGCTTGTGACACCCATGCCCCCAATCAGAGATGTGACAG 36739
QY 1829 ----- 1828
Db 36740 GGGAGCTGACAGACACCTGCTCAGAGTAAACAGCCTTGCGCTGGGGACCCGAGCT 36799
QY 1829 ----- 1828
Db 36800 GGTGCTGGGCCATTTCTTCATCTGAGGGAGGTCAGGGCTTCCCTGTGGAAACAG 36859
QY 1829 ----- 1828
Db 36860 TTAATACAAATGACCTTACTTAGACTTACAGTATTAATGATGTCGACCCAAACAT 36919
QY 1829 ----- 1828
Db 36920 GGTATTTGACCAGATTTTGAAGAAATTAATTTGGGTACCGGAAGACAGACAGA 36979
QY 1829 ----- 1828
Db 36980 CGTGTGTGCCCAAGATGCTCTTGTCACTACTGGGACTTGTGTCCTGGGGGGCC 37039
QY 1829 ----- 1828
Db 37040 TTGAGGCCCTCTCCCTGTCGACAGAGTACGTCCTTTCTACTGCTGGGCTGCGG 37099
QY 1829 ----- 1828
Db 37100 CCTGGGTGACAGGACACAGCTCCGAGACCCCGGCCAGTGTCCAGGATGCCAGG 37159
QY 1829 ----- 1828
Db 37160 CTGTACGACAGATGCCCCAGGTGTCAGGTGTGCGGCTCCAGCCCCGTCGCCCATGG 37219
QY 1829 ----- 1828
Db 37220 TGGTTTGGGGAAAAGGCCAAAGGACAGAGTGTACAGAGACTGTGGGCTATGAGAG 37279
QY 1829 ----- 1828
Db 37280 CTGATTTGCTCTTGGCTGAGTGCCTGACAGACCTCTCCGCGCTCTCATCTGAAG 37339
QY 1829 ----- 1828
Db 37340 GGATGTGCTCTTTCTAATCTGGGGTCTGCTGGGGCAGCCTTGGGCTACCCAGTGG 37399
QY 1829 ----- 1828
Db 37400 CTGTACAGAGGACAGCATCTGTGTGAGGGGCAATGAGTTCACGTGCCCCAGATGC 37459
QY 1829 ----- 1828
Db 37460 AGCTGGGACAGGCTCCCTGCTGATGTTGGAGACATCACCTGGGGGTTGACCGCC 37519

[illegible][illegible]

[illegible]

QY	2313	-----	2312
Db	40820	TGGGGTTGCTGGGTCACAGACGTCGTTTAGGGAATGTTGGAGATTTCAGGGGGGTGAC	40879/97
QY	2313	-----	2312
Db	40880	ACTGACACCCCGGCTGGCTTGCTTGTGAGGGCATGCTCCGGTGGCCGCTGGCCTGAAGG	40938/98
QY	2313	-----	2312
Db	40940	TGTCGAAGCCGCTCGTGGGATTGTGCAGGGGGCTCTTGATGCCACAGTGCCACACT	40999/99
QY	2313	-----	2312
Db	41000	GTTCCGCTGCGCCGCCCGGGGACTTTGCGGGAGTGCTGTCCGTCCTGCCCGCTC	41059/99
QY	2313	-----	2312
Db	41060	TGTATGGGGCGCCCTGCCCTCCATCATCGGCTTGCAAGAGCTCTTGTGTGTTCTGTCGA	41119/99
QY	2313	-----	2312
Db	41120	AGTGTGCATCACATGCTGTGCACGTGGAATCTGTGCGCGTGTCGTTGCTTTGTGC	41179/99
QY	2313	-----	2312
Db	41180	TCTCAAGTCAGCCTTTTGAGGACTGGAAAGATTGACTTCTATCCGACGTCCACTAACACA	41239/99
QY	2313	-----	2312
Db	41240	GTCACGTAACGAGAGTCACCTTATATCAGTGTGTTGCGCTAAAGCTGTTGTGTCTGC	41299/99
QY	2313	-----	2312
Db	41300	AGGAACCTCAGGATATTAGGTTGTGTGACGTTGCTTCTGTCCCTTCTTTAGAACAGTC	41359/99
QY	2313	-----	2312
Db	41360	TTTACTGTGTCAAGCTTGCAACCTGGGTGGGTTTTCATGTGTGAGTGTAGTGGAGATCTG	41419/99
QY	2313	-----	2312
Db	41420	TGAATTTGTTTTCATCCGTGGGCTAGGTGGGATCTGTGGAGATTGTTTTATGTGTGGG	41479/99
QY	2313	-----	2312
Db	41480	GTAAGTGGGATTGTTTTCATGTGCGGGGTAGGTGGGATCTGTGGGATTGTTTCTTG	41539/99
QY	2313	-----	2312
Db	41540	TGTGGGTAAGTGGGATCTGTGGATTGTTTTATGTGTGGGTAAGTGGGATATGT	41599/99
QY	2313	-----	2312
Db	41600	GAATTGTTTTCATCCGTGGGCTAGGTGGGATCTGTGGGATTGTTTTATGCTGGGG	41659/99
QY	2313	-----	2312
Db	41660	TAGTGGGATCTGTGAATTGTTTTCATCCGTGGGCTAGGTGGGTTCTGTGGGATTGG	41719/99
QY	2313	-----	2312
Db	41720	TTTTCATGTGTGAATAGTGGGATCTGTGAGATTGTTTTCATGTGTGTAGGTGG	41779/99
QY	2313	-----	2312
Db	41780	AGATCTGTGAATTGTTTTCATCCGTGGGCTAGGTGGGATCTGTGGGATTGTCTTCT	41839/99
QY	2313	-----	2312
Db	41840	ATGTGTGGGTAAGTGGGACCTGTGGATTGTTTTATGTGTGGGTAAGTGGGATC	41899/99

OY	2313	-----	2312	-----	2312
Db	41900	TGTGAATTGCTTTTCATCCCTGGGGTAGTGGGAGATCTGTGGAAATTGGTTTCATGTGTG	41959	-----	41959
OY	2313	-----	2312	-----	2312
Db	41960	GGGTAGTGGGGATCTGTGGAAATGGATTTCATGTGTGGGTAAGTGGGGATCTGTGGGA	42019	-----	42019
OY	2313	-----	2312	-----	2312
Db	42020	TTGGTTTCATGTGTGGGGTAGTGGGAGATCTGTGAGTTGGTTTTATGTGTGGGGTA	42079	-----	42079
OY	2313	-----	2312	-----	2312
Db	42080	GGTGGGATCTGTGAGATTGTGTTTCATGTGTAGGTAGTGGAGATCTGTGGATTGGT	42139	-----	42139
OY	2313	-----	2312	-----	2312
Db	42140	TTTCATGTGTGGGGTAGTGGGATCTGTGGAGTTGGTTTTCATGTGTGGGGTAGTGGG	42199	-----	42199
OY	2313	-----	2312	-----	2312
Db	42200	GATCTGTGGAGATTGGTTTCATGTGTGGGGTAGTGGGGATCTGTGAGTTGGTTCA	42259	-----	42259
OY	2313	-----	2312	-----	2312
Db	42260	GTTGGGGTAGTGGAGATCTGTGGAGTTGGTTTTCATGTGTGGATAGTGGGGATCTG	42319	-----	42319
OY	2313	-----	2312	-----	2312
Db	42320	TGGGATTGGTTTTATAGTAGTGGGGTACACAGAGTTCAAGCGAGGTTACTTCTGTAGT	42379	-----	42379
OY	2313	-----	2312	-----	2312
Db	42380	GGGTCTGCAGGTGCTCCAAAGCTTTATTGAGAGACCATTTCTTGTGACTATGGT	42439	-----	42439
OY	2313	-----	2312	-----	2312
Db	42440	CGGGTTTATAGTAGTGGGGTGTGAGGCCCTCCCTGGGCTCCCTGTCTTCTTC	42499	-----	42499
OY	2313	-----	2312	-----	2312
Db	42500	CACCTTGGGGTGTGTGTGTGCTCTGTGTGTGTGTGCGGTGGGAGAGGCTTCCAGGCC	42559	-----	42559
OY	2313	-----	2312	-----	2312
Db	42560	TCTTGTGTATTTAGGCTGTGATGTGGCTGTGCTACGTCGCTCTTGTGAATTCCTTG	42619	-----	42619
OY	2313	-----	2312	-----	2312
Db	42620	CGAGTTGAGAGCTTCTTCTTCTTTTCTTTTCTTTTCTTTTCTTTTGTGATACAGA	42679	-----	42679
OY	2313	-----	2312	-----	2312
Db	42680	GTTCTGCTTTTTTGGCCAGAGCTGAGAGGTTTGGGTATCTTGGCTACGTCAACT	42739	-----	42739
OY	2313	-----	2312	-----	2312
Db	42740	GTTCTTCTGAGTTTCAGCAATTCCTTGCCACAGCTCCCAAGTAGTGGAATTAAG	42799	-----	42799
OY	2313	-----	2312	-----	2312
Db	42800	CGGCCACACCATGCTACTAATTTTGTAAATTTAGTAAGACAGAGTTTCTCATGTT	42855	-----	42855
OY	2313	-----	2312	-----	2312
Db	42860	GGCCAGGCTGGTCTCGAACTCTGACTCTGAGTGTATCTCTCCACCTGGGCTCCCAAGT	42919	-----	42919
OY	2313	-----	2312	-----	2312
Db	42920	GCTGGATGACAGGTGTGAACCGCGCGCGCGCGAGACTGCTTCTCGAGCTTCGGT	42979	-----	42979
OY	2313	-----	2312	-----	2312

D	b	42980	GAGATCTGCAGCATACTGCTCCGACAGCCTTGGTGGACAACTCCGTTTCTCTCC	43093
O	y	2313	-----	2312
D	b	43040	AGGTCCTGATAGGGGCTCTTCCATTTCATGACTCTTCCACAGAAAGTTCCACGTGCG	43099
O	y	2313	-----	2312
D	b	43100	TGATTTCCCGGCTGTTCCGCGTAATGTGTCTGCTGTATGATGGCTCTTCCA	43159
O	y	2313	-----	2312
D	b	43160	TTTCTTAGGCTTTGTTATTTGTGTTTTCGGCTCTTGAAGAAAAGTTTCATTA	43219
O	y	2313	-----	2312
D	b	43220	TGATATTGTGAACTTCTTTTCAACAAGCATCTGAAGTGGCGTTTCCCTAAAG	43279
O	y	2313	-----	2312
D	b	43280	AGGGATCCGAGGCCCTGGCTGTGAGTGGCACCGCTCGGGGCTGTTAGAACCCGG	43339
O	y	2313	-----	2312
D	b	43340	CGCACAGCGGAGGCTAGGTGGGGTGGGGAGCGAGCTTCCCGCTGAGCCCCGCC	43399
O	y	2313	-----	2312
D	b	43400	TCTCAGATCAGCAGTGGCATGCGGTGCTCAGAGGCGACACACCTACTGAACTGTGC	43459
O	y	2313	-----	2312
D	b	43460	GTTAGAGGGGCTAGATTCTGTGCTCTTATGGGAATCTAATCCGATGATCTGAGGTG	43519
O	y	2313	-----	2312
D	b	43520	GAACGTTTGCTCCCAAAACCATCCCTTCCCGACTGCTGCTGTGGAAAATCGTCTT	43579
O	y	2313	-----	2312
D	b	43580	CCACGAACAACAGTCCCTGTATCCACAAATGTTGGGACCTGTGCTAAAGACTGTCA	43639
O	y	2313	-----	2312
D	b	43640	GCAGCCTCTGTCAGTGTGATATATGACTTTCTGTGTGATGCAGAAATATACGG	43699
O	y	2313	-----	2312
D	b	43700	ATTTCGTGATGCTTTCCGCCGACTCAGACCCATGGGCTATTGTGGGCGTGTGCTG	43759
O	y	2313	-----	2312
D	b	43760	CTCCTGAGTTGGGAAGGAGTCCAGGCCCATGTACCTTCTGTACTGCCCTTCAGGTTGG	43819
O	y	2313	-----	2312
D	b	43820	TTTCTCAGGGTTGAATCGTACGTGATGATGTTTAAACCCAGGCCCTGCCGACCTCTG	43879
O	y	2313	-----	2312
D	b	43880	GGGGCTGGGGAACATGCTGAAGACAGATCAGCTCGCGCTCTTTGATGCTCACAG	43939
O	y	2313	-----	2312
D	b	43940	CTGAGAGCCTCCTGTGTCCGTGTAGTGTGTGTCACGTCGCTCCTACATCCTGTTGG	43999
O	y	2313	-----	2312
D	b	44000	GGACGAGGGGCTTAGCAGGTCCTCGTAGTAATGACAAAGCGTCTGGGAGGTCTGCAGA	44059
O	y	2313	-----	2312

Db 44060 ATAGAGGTGGGGTGGCGGTCTCTCTCCGCTTTCAGACTCTCTCTGCTGCT 44119
QY 2313 ----- 2312
Db 44120 GTGGCTGACCTGCATCCCTGCAATCCCTCCAGACTGGGCTGAGAGGCCGGAGCTC 44179
QY 2313 ----- 2312
Db 44180 GAGTGCACCTTGTGCCAGTACTGTGGATGGAGTCCGCTACAGGGGCTGATGTGTG 44239
QY 2313 ----- 2312
Db 44240 TGACTGTGATGGCGGTGCTGGGCGCTGATGTGACTGTGATGGCGGTCTGAGGCTC 44299
QY 2313 ----- 2312
Db 44300 TGATGTGTGACTGTGATGAGGGGCTGCTGGGCTGTGATGTGTGACTGTGATGTG 44359
QY 2313 ----- 2312
Db 44360 TCGTGGATCTGATGTGTGACTGTGATGGCGGTGCTGGGCTGATGTGTGATC 44419
QY 2313 ----- 2312
Db 44420 TGTGATGGCGGTGCTGGGCTGTGATGTGTGACTGTGATGGCGGTCTGGGCTCTG 44479
QY 2313 ----- 2312
Db 44480 ATGTGTGTGACTGTGATGGCGGTCTGGGCTGTGATGTGTGACTGTGATGTG 44539
QY 2313 ----- 2312
Db 44540 GTGGGCTGTGATGTGTGACTGTGATGGCGGTCTGGGCTGTGATGTGTGACTG 44599
QY 2313 ----- 2312
Db 44600 TCGATGGCGGTCTGGGCTGTGATGTGTGACTGTGATGGCGGTCTGGGCTGTGAT 44659
QY 2313 ----- 2312
Db 44660 GTGCTGACTGTGATGTGATGGCTACAGGGCTGTGATGTGTGACTGTGATGGCG 44719
QY 2313 ----- 2312
Db 44720 GTGGTGGGCTGTGATGTGTGACTGTGATGGCTACAGGGCTGTGATGTG 44779
QY 2313 ----- 2312
Db 44780 GTGACTGTGATGGCGGTCTGGGCTGTGATGTGTGACTGTGATGGCGGTCTG 44839
QY 2313 ----- 2312
Db 44840 GGTCTGATGTGTGACTGTGATGGCGGTCTGGGCTGTGATGTGTGACTGTGATG 44899
QY 2313 ----- 2312
Db 44900 GCGGTGTAGGCTGTGATGTGTGACTGTGATGGCGGTCTGGGCTGTGATGTG 44959
QY 2313 ----- 2312
Db 44960 TGACTGTGATGGCGGTCTGGGCTGTGATGTGTGACTGTGATGGCGGTCTG 45019
QY 2313 ----- 2312
Db 45020 TGTGATGTGTGACTGTGATGGCGGTCTGGGCTGTGATGTGTGACTGTGATG 45079
QY 2313 ----- 2312
Db 45080 GCGGTGTGGGCTGTGATGTGTGACTGTGATGGCTACAGGGCTGTGATGTG 45139
QY 2313 ----- 2312
Db 45140 TGTGACTGTGATGGCTACAGGGCTGTGACTGTGACTGTGCTGGCGCCCG 45199

QY 2313 ----- 2312
Db 45200 GCGCCCGTTTCCAAACAGAACTTCCAGCGCTCTGTGGGCTTCAATCCGCCATGGG 45259
QY 2313 ----- 2312
Db 45260 CTTGGCGCAGTCCACACGTCGTGATGGAGAAACAGTGGCCAGCTGTGGCGGGG 45319
QY 2313 ----- 2312
Db 45320 AGGCCAATTTGTGGCTCATCCCTCTCTGCGCGGAGTCTTACCTTGACAGACT 45379
QY 2313 ----- 2312
Db 45380 CCAGCCGTACATGGCAGAGTTCTGTGGCTCACCTGACAGAGACCGCCGCTGAGGATGC 45439
QY 2393 CGTGTGATGCA ----- 2404
Db 45440 CGTGTGATGCAAGAGTCTGGGCACTGCCCTGACAGGTTGGGACGAGTCCAGAGT 45499
QY 2405 ----- 2404
Db 45500 GGTCTCTCCCTGGGCAATCACTGGGCTCATGACCGAGACTGTTGGCCCTGGGGG 45559
QY 2405 ----- 2404
Db 45560 AGTGGGGGAATGAGCTGTGATGGGGCATGATGAGCTGTGTGCTTGGGAAATCTGAG 45619
QY 2405 ----- 2404
Db 45620 CTGGGCAATGCAAGGCTGCGACAGCTGTGATGCAAGCACTGTGATGACTGG 45679
QY 2405 ----- 2404
Db 45680 CGGCTCTCTCCAGTTCGAGTCCGCTTGTTCATGATTTGCTAATGCTTCTGTGCCA 45739
QY 2405 ----- 2404
Db 45740 GTTTGATCTTGAAGCAAGAAAGGTGTCCTCTTGAAGAGGCAAGCCATGTT 45799
QY 2405 ----- 2404
Db 45800 GAGCGTGTCTGCCAGTGGCCCTCAGTGTGTGGCTGAGGCCAAAGAAAGCTGTC 45859
QY 2405 ----- 2404
Db 45860 CCCCTTCTTGAAGAGAGCGGCGGTGTTGAGCCAGCCCGCTGAGCGGCGCTCAGTG 45919
QY 2405 ----- 2404
Db 45920 CTGGGTGTGTCACAGTGGCCCTGTGGCCCTTGGAGATGTGTGTCACAGTGGCCCTG 45979
QY 2405 ----- 2404
Db 45980 TGGCTTCTTGCAGATGCTTGAACACTGTGCTGCTGAGGGAGACAGTGTCCACCG 46039
QY 2405 ----- 2404
Db 46040 CATGAGGCTAGAGACTCTGGGCGAATTCCTTGGCTCCAGGGTGGGGGTGAGGTG 46099
QY 2405 ----- 2404
Db 46100 CTTGGGCTGTGGAGCCAGACCTGTGCGCGGAGCTGGGCAAGCACTCTGATCACA 46159
QY 2405 ----- 2404
Db 46160 TATGCCATCCGGGCAAGTGGGCTGTGTGGGTGAGCCAGCTGAGCCACAGGTGGG 46219
QY 2405 ----- 2404
Db 46220 CAGAGGAGAGTCTGTGTGACACACTGTGCTTAAGCCATGTGTGTGACAGAGACTC 46279

OY	2405	-----	2404	-----	2404
Dp	46280	GGCCCGGACAGCCACGATGGCCCTGCAATTCACACCCAGCCCGCACTTACATCAAAACA	46339	-----	46339
OY	2405	-----	2404	-----	2404
Dp	46340	CTGACCCCAAAAAGGACGAGAGGTCTTGGCCACGTGGTCTCGCTGTCTCAGACACCAC	46399	-----	46399
OY	2405	-----	2404	-----	2404
Dp	46400	GGCTCACTCCACTGTGTCTCCGCTGCTCTTTCGAGAGCTCTCTCCCTGAATGAGCCAGC	46459	-----	46459
OY	2433	AGTGGCTCTTTCGACGCTTCTCTACGCTTCATGTGCCACACGCGGTGGCATCAGGGGC	2492	-----	2492
Dp	46460	AGTGGCTCTTTCGACGCTTCTCTACGCTTCATGTGCCACACGCGGTGGCATCAGGGGC	46519	-----	46519
OY	2493	AA-----	2494	-----	2494
Dp	46520	AAGTAGTCAGGTGGCCAGGTGCATGTCCCTGCGGGTGCTGGCGGGCTGCAGGGCT	46579	-----	46579
OY	2495	-----	2494	-----	2494
Dp	46580	TCGTCACTCTCTCTCCGCTCCCTCCCACTGCTTTCGCCGGGGCCACAGAGCT	46639	-----	46639
OY	2495	-----	2494	-----	2494
Dp	46640	CTTTTCTGGCCCCCGCCCCCTCCGGTCTTGGGCTGCAGGCTCCGAGGCCCGGAAC	46699	-----	46699
OY	2495	-----	2494	-----	2494
Dp	46700	ATGGCTCGGCTTGGGGACGCCGAGCGAGCAGAGTGCCACACGAGGCTGGAAATGGCAA	46759	-----	46759
OY	2495	-----	2494	-----	2494
Dp	46760	GCGGGGTGGAGTTGCTCCTCGCTGAGAGACAGAGGGGGGGGTGTGTGGTCAAG	46819	-----	46819
OY	2495	-----	2494	-----	2494
Dp	46820	TGTGCGCGAGCGTTTGTAGCTGCAGCTTGTCAGCTCAAGTTACTGAGCTGGACA	46879	-----	46879
OY	2495	-----	2494	-----	2494
Dp	46880	CCCGGCTCTCACAGCTTGTATCTCTCTCCGATACAAAGATTTTATCCGATTC	46939	-----	46939
OY	2495	-----	2494	-----	2494
Dp	46940	ATTCTGTCTCTGTGTGTGATCCCCGAGAGGCGCGGCTTCTCTGTGTGACTGAT	46999	-----	46999
OY	2495	-----	2494	-----	2494
Dp	47000	TTCCATCTGGAAGTGCGGGGTTGACGGTGTAGTTTGTCTCTCGGGGGCTGTGGT	47059	-----	47059
OY	2495	-----	2494	-----	2494
Dp	47060	GGCCATGGGGCAGCGGCTTGGAGAGCGCGGTACACAGCACCACTGGGTAGACCACT	47119	-----	47119
OY	2495	-----	2494	-----	2494
Dp	47120	CAGGTGTAGAGCACAAGTGCCTGTGTGCACATCAGTCTCTGGATTTTAAGTAAAC	47179	-----	47179
OY	2495	-----	2494	-----	2494
Dp	47180	CACACACTCCCGGACAGCACTGCTGCGACCTGTGTGCTTGGGAGAGTGTGAGC	47239	-----	47239
OY	2495	-----	2494	-----	2494
Dp	47240	ACGAGAAATTCGTGCACACTCAGAGTCAACGAAGTCAATCGCATCAGTGTGAAC	47299	-----	47299
OY	2495	-----	2494	-----	2494
Dp	47300	GTTGAGGCTCTCTGTGGATGTCTCAACGCGATTAAGAGCTGTGACAGCTTCGAAG	47359	-----	47359
OY	2495	-----	2494	-----	2494

D	47360	CTTTTATTTAAAAATATAACTATTATTAATGCAATTAAGTAAATACCAATATGATACAG	47419
OY	2495	-----	2494
D	47420	CAATTATATATTATTTAAAGTATAATTAGAAATTTAAGTAACTACACACTTCGAAA	47479
OY	2495	-----	2494
D	47480	ACACAAATTGCACATGAGCAGAGACTGAATTTTGGCCAGGAGCACGTGTGCATGTG	47539
OY	2495	-----	2494
D	47540	TGTAAAGGAGCCCCAGAGCCACAGAAATTGGTGACAAAAGTCACTCCACAGAGAAGCAC	47599
OY	2495	-----	2494
D	47600	CAGGGCCCTCTGTGTGTGTGTAATTTTATTAGATGATCAAGTCAAGTACGTCCAC	47655
OY	2495	-----	2494
D	47660	GTTGTGCAGGGCTTTGGGAATGTAGGTGATGATCGCTTCATGCCCTGCACAGACAG	47719
OY	2495	-----	2494
D	47720	GAGTGACTGTGTCTGTCTCTCCCTAGAGACAGGACAGGCCGGAAGCTTAGTCCCAT	47779
OY	2495	-----	2494
D	47780	CGTGTCCAGTTTGCCCTGTGAATAAAAAGTCTCAAAACGTGTGCCCAAAACTAA	47839
OY	2495	-----	2494
D	47840	GAAACAGAGAGATTTCCCATCCCATGTGCTCACAGGGGCGTATCTCTTGGTTGACTCG	47899
OY	2495	-----	2494
D	47900	CTGGCTGAGCGGACCTCTAGAGTTGTGTGTCTGTGTGTCGAAAAAGTGCAGTCTC	47955
OY	2495	-----	2494
D	47960	TTCGCCATCACTGTGATATCTGCACACAGAGAAAGCTCTTTCTTTCTTTCTTTT	48019
OY	2495	-----	2494
D	48020	TTTTTTTGTAGACGGAAGTCACTGTTGTCTGCTGGGCTTGAGTGCAGTGGCGGATCT	48079
OY	2495	-----	2494
D	48080	CAACTACTGCACACTCCGCTCCGGGTTCCAGATTTCTCCTGCTCAGCTCCGAG	48139
OY	2495	-----	2494
D	48140	CAGCTGAGTTACAGGACCCACCCTGCGCTGGCTAAATTTTGTATTTTAACTAGAG	48199
OY	2495	-----	2494
D	48200	AGGGGTTTTTGCACATGTTGGCCAGGCTGGTCTCGAAGTCTCTGACCTCAAGTATACACC	48259
OY	2495	-----	2494
D	48260	ACCTGGCTCCCAAGAGTGCGGATTTACAGGTGTGAGCATTACAGCCAGCCGGAAGC	48319
OY	2495	-----	2494
D	48320	CTCTTTTAAAGTGACCACTATAGCGTTCGCCAAAATAACAGGCTTTGTTTGCAGT	48379
OY	2495	-----	2494
D	48380	AGGCTCAAGCGCTCTTTACCAACAGAGATGGCGTCTGTGGGCTGTGGGATGGCTAG	48439
OY	2495	-----	2494

D	48440	GGCGCGTGGCAGCCATGCTCTTGTCACCTTTAGGTTCCAGGGGCTATTCTGCTC	48499
OY	2495	-----	2494
D	48500	TCACGTGTTGTCGAAAAAGCACACCTTGGCATCTTGTTGGAGAGTTTCTGCTTCGT	48559
OY	2495	-----	2494
D	48560	TGCTCATGCTGAACCTAGGGGCAAGGTGTATCCGTGGCGGCAGCGCTACATGAGG	48619
OY	2495	-----	2494
D	48620	GTCATGAGTCTTTCACCGCGTGCACAAATTCCTTGAAAAAAGAGTCCGGTTAAC	48679
OY	2495	-----	2494
D	48680	ATTCAATCCGGGTCAAGTGTCTGTTCTGTGAATAAAGCTAAGATTTAAGAACTTAA	48739
OY	2495	-----	2494
D	48740	TGAAAGAAACCTTATGATTCAGAGCAAGATGTGTACACCTGTGGCTGGATCTGT	48799
OY	2495	-----	2494
D	48800	TGACGGCGCCCGATGATGTGAGAGTGGGGAGCAGGGAATTGTTGTTACAGAGTCTCAT	48859
OY	2495	-----	2494
D	48860	CTGTATGTTTCTGAGGTGTGTTGCCGCTGAATGATAGACGTGCTGTTGTGTATGAG	48919
OY	2495	-----	2494
D	48920	GTTCTGTGTCGTGTGTGTGGCTCGTTTGAGTGTACGATGTCCAGACATGCTGCCCG	48979
OY	2495	-----	2527
D	48980	TCTCACCCTGTGTCTTCCCGCCAGGCTCTACGTCCAGTCCAGGGGATCCCGCAGGG	49039
OY	2528	CTCCATCCTCTTCACAGCTGTCTGTGACGCTGTGTTACGCGCAGCATGAGAACAGCTGTT	2587
D	49040	CTCCATCCTCTTCACAGCTGTCTGTGACGCTGTGTTACGCGCAGCATGAGAACAGCTGTT	49099
OY	2588	TGCGGGGAGTTGCGGGGAGCG-----	2607
D	49100	TGCGGGGAGTTGCGGGGAGCGGGGTGAGGCTCTCTTCCACAGGGGCTTGGGTGGGGGT	49159
OY	2608	-----	2607
D	49160	TGATTTGCTTTGATGCAATCAGTGTAAATATTCCTGTTGCTCTGGAGACATGACTGCT	49219
OY	2608	-----	2607
D	49220	CTGTCTGAGAACACAGACAAGTTGACAGCCCTCTTGTTATGAACCGCACGGGAGGG	49279
OY	2608	-----	2607
D	49280	GTTGCACAGCCTGAGAGCTGCGGGCTCCACAGCAGGCTGTTCACAGCGCATGTCCAGAG	49339
OY	2608	-----	2607
D	49340	GCCTAAGGGCTTCAGCAGCGCGGAGGGCGCGTGCCTGCATGATGAGCATGTGAATTTCAAC	49399
OY	2608	-----	2607
D	49400	ACCGAGGAAGCACACACACCTTCTGTACGTACACAGGTTCCGTTAAGGTTCTTTGGGGAG	49459
OY	2608	-----	2607
D	49460	ATGGGGCTGTGTACAGCTTAGAGGCCACACATTTCCAGCAGGGCCTTCAGAGGTGGCTTGG	49519
OY	2608	-----	2607
D	49520	ACTGGGCGCTTTCAGCCCATTTGCCCATCCCACTTGATGGGGCTTACACCCAAAGAGCG	49579

[illegible]

QY 2608 ----- 2607
Db 50660 ACAGTCACACAGCCAGCTTCCTGTGATAGATCTGGGTCCTGATCATGCTGAGAC 50719
QY 2608 ----- 2607
Db 50720 CACAGTCACATGCTGTAAAGGACACAGCTGCTCAGAGGGGCGAGGTTCCAGCCC 50779
QY 2608 ----- 2607
Db 50780 CAGCTTCTACCGCTTCAGTATTTTCCCTAAGAGCTGAGAGTGGGGCGGCGCT 50839
QY 2608 ----- 2607
Db 50840 GATGGCTTCGTTGCTTCAGCTGCACAGATTGCACAACTGATGTAACACTGAG 50899
QY 2608 ----- 2607
Db 50900 TACTTATATGATGAGAAATGCTGTAGAGTTAACTGTAGAGAGCTCGTCTGTGAA 50959
QY 2608 ----- 2607
Db 50960 AGAAATTAAGTTTTCATTAAACCGCTTGGAGAAATGTAATTATTTATGCTGTGA 51019
QY 2608 ----- 2607
Db 51020 AATTGTTGACATTCAGTCCCTCGTAGACAGATTAAGTAAAGTTAAAGTTAACT 51079
QY 2608 ----- 2643
Db 51080 TCGTGTGATTTTCCCTTATTTTAGCTGCTCGCTGGTGTGATGATTTCTTTTG 51139
QY 2644 TGAACCTACCTGACAGGCGGAAACCTTCCTC----- 2678
Db 51140 TGAACCTACCTGACAGGCGGAAACCTTCCTCAGTGAAGGCCCGGCTGTCTG 51139
QY 2679 ----- 2678
Db 51200 TGGGACCTCCACAGCTGTGGGCTTTCAGTTGAGCCCGGCTGCTGCCCCGACAC 51239
QY 2679 ----- 2678
Db 51260 CGCAGCGTGTCTTCGCAAGTCTCTCTCTGCGCGTCTGGATCCGCAAGACAGAG 51319
QY 2679 ----- 2678
Db 51320 GCGCTTGGCCGTGCACCCAGGCTGGGGGCGAGGGGACCTTCGGAGAGGAGTGGTAC 51379
QY 2679 ----- 2678
Db 51380 CGTCAGGCGCTGTCTGTGCAGAGACGACCGATTACACAGTGTGAGTGCAGGCG 51439
QY 2679 ----- 2678
Db 51440 TGAACCGGCTCCTGCTGCTTTTGGAAAGTCAGAGATGGCGGCTCTGGGGCCCCAGTGA 51499
QY 2679 ----- 2678
Db 51500 GACCCCAAGAGCTGTGCACAGGGCTTCGGGGCGAGGGGACGCTCCTCCCAAGGCT 51559
QY 2679 ----- 2678
Db 51580 GCACTGAGCTGCGAGAGAGAGAGCTGCTGAGTGAAGCTGCGCCACAGCGTTGCTGCG 51619
QY 2679 ----- 2678
Db 51620 GTCACGTTCTGCGTGGGGTTGTTGGATCGGTGGAGAAATTGAGATTGCTGAGTGTCT 51679
QY 2679 ----- 2678
Db 51680 GCTGCTTGAACAGAGAGATGCTAGAGTGGGTTTCAGATGATTTTGTGAATCAA 51739
QY 2679 ----- 2678

Db 51740 ACTAAATCAGGACAGGGGACCTTGGCTTCACACAGGGGATTGTCCAAATGTGTCGCC 51799
QY 2679 ----- 2678
Db 51800 TCAAGGGCCCCACAGAGCTGTGGCTTTGTTTAAAGTCGATTGACAGAGACAG 51859
QY 2679 ----- 2678
Db 51860 AAACCTTGAACGTGTAAGGGAACCCCTGAAATATGTGCCCGCAGGGGTGTTTCAG 51919
QY 2679 ----- 2678
Db 51920 TGCTTGTCTGGCTGTGTTGTGAAACCATTTTGGACCCCGCTCCAAATCCACCTCC 51979
QY 2679 ----- 2678
Db 51980 AGTCCACCTCCAGGGCCCGCTGGGCTGGGGGTATGCTGCGCTTCTTGACCCGAG 52039
QY 2679 ----- 2678
Db 52040 CCGGAGACAGCAGGCTGTGCACATTTAAATCCACTAATTCACTCGCGGGGAGCCCA 52099
QY 2679 ----- 2678
Db 52100 GGTCCCAAGCACTGAGGGCTCAGAGATCTGAGGCTGTGAGGGGACAGAGACGAG 52159
QY 2679 ----- 2678
Db 52160 GAACGCTGCTGTGTGTCGAATTCCTGAGGGTGTGCGCAGGAGAGTGGCTCAGAGTG 52219
QY 2679 ----- 2678
Db 52220 TATGTTGGGTTCCACCGGGGGGAGAACTGTCTGTATGATGTCGACACCTGTAA 52279
QY 2679 ----- 2678
Db 52280 GGAAGGTTGGCCACAGGAGCTGGAAATGCACACAGGGAGCTCCGACGTGGCCGAGT 52339
QY 2679 ----- 2678
Db 52340 CCCAGGCGCAGGCCACAGAGAGGAGGAGGAGCGCCGGGCTACACAGAGCGCAGG 52399
QY 2679 ----- 2678
Db 52400 AAGGAAAGGGATGCCACAGCCAGAGAGGCTACCCGCGCACAGGGGGCTCCCTGAGC 52459
QY 2679 ----- 2678
Db 52460 TGGATGAGCGAGCTCATGACTCGGAGGAACTCCTTGAAGTGAAGCTGACACTGG 52519
QY 2679 ----- 2678
Db 52520 TGTGGCCAGCTCAGAGCCAGCAGGTCCACAGCTGAGCAGGAACCTCAGAACCTGCC 52579
QY 2679 ----- 2678
Db 52580 CTTTGTCTAAACACAGCAGATGCTTCAGGGCATCTAGGAAACAGGCAAAATGCTGT 52639
QY 2679 ----- 2678
Db 52640 GAGAAAGCTTAAAGAGGTGGATGTGCAATTTCTTGTCCAGATTTAGTCTGCC 52699
QY 2679 ----- 2678
Db 52700 CCGGACACAGATGATCTATTAACGGATTTGTGTTGTCATGGGACACATGAGATGG 52759
QY 2679 ----- 2678
Db 52760 ACCATCAGAGGCACTGGGGCTGCACCTCCCATCTGATGATGCTGTGCTCCGGGTCCA 52819
QY 2679 ----- 2678

Db 52820 GCGCAGTTCTTGACATCTACCTACCTGTCTGCCCCGGGAGACAGGAGGAAAAGCACCCCCGA 52879
QY 2679 ----- 2678
Db 52880 AGTCTGAGACAGGCTGGGTCCAGAGCTCTCAGAGCTCTGCGCCAGGCCACACCTCTGCT 52939
QY 2679 ----- 2678
Db 52940 CCAATACACACTCTCTGGGGTTTTCAAAGCATTTAAAGAGGGTGTCAAGTTACCTCC 52999
QY 2679 ----- AGACCCCTGCTCCG 2692
Db 53000 TTGGGTACGGCCCCCGCATCTCTGGGGCTGACATTTGCCCTCTGCTTACGACCTCTGCTCCG 53059
QY 2693 AGGTCTCCCTGAGTATGCTGCGTGTGTAAGTTGCGGAGAGACAGATGCTGTAACCTCTCTGCT 2752
Db 53060 AGGTCTCCCTGAGTATGCTGCGTGTGTAAGTTGCGGAGAGACAGATGCTGTAACCTCTCTGCT 53119
QY 2753 AGAAGACGAGGCTCTGGGTGCGACAGGCTTTTGTTCAGATGCGGCGCCAGCGCTATTCC 2812
Db 53120 AGAAGACGAGGCTCTGGGTGCGACAGGCTTTTGTTCAGATGCGGCGCCAGCGCTATTCC 53179
QY 2813 CTGGTGGGCTCTGCTGCTGATACCCGACCTGTGAGCTGACAGCAGCTACTC----- 2866
Db 53180 CTGGTGGGCTCTGCTGCTGATACCCGACCTGTGAGCTGACAGCAGCTACTCAGGTG 53239
QY 2867 ----- 2866
Db 53240 AGGCGACCTGGCGGAGTGTGAGCTGTGCCCGCTGGGGCAGGTGCTGCTGCAGGGCCG 53299
QY 2867 ----- 2866
Db 53300 TTGCTGTCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCAAAGGTCAGAGGC 53359
QY 2867 ----- 2866
Db 53360 CACAGGCTGCCCTCGTCCACTGTGGGGCTGAGCAGAGAAATGATCTTTCTGTGGAGTGA 53419
QY 2867 ----- 2866
Db 53420 GGGTGTCTCAACAGGGGAGCAGTTTCTGTCTATTTTGGTAAAGAAATGTGTCACCAG 53479
QY 2867 ----- 2866
Db 53480 ACCTGGGTGACTGAGTGTCTTCAGAAAGCAGTGTGATCCGAACCCAGAGCCCGGG 53539
QY 2867 ----- 2866
Db 53540 CCCTGTGGGCTGAGTCTCTCCAAACCCGAAACAGAGGGCCCTGCTGGCATGAGTCC 53599
QY 2867 ----- 2866
Db 53600 CTCCGAACCCGAAACCTCTGGGGCCCTGCTGGGGTGTGCTCTCCGACCCAGAGACTTC 53659
QY 2867 ----- 2866
Db 53660 AGGGCCCTTTTGGGCGTGAAGTCTCTCCACTGTAGCCCCACACTCCAAAGGCTATCCACA 53719
QY 2867 ----- 2866
Db 53720 GTCTACAGATGCCATGAGTTGATGATCAGTGTGACCCATCAGGGGACAGGGCCATGAT 53779
QY 2867 ----- 2866
Db 53780 GTGGGGGGGGTCTCTACAAATCTCTGGGCTTGTGTTCCCCAGAGCCGAGAGCTCAAG 53839
QY 2867 ----- 2866
Db 53840 CCCGCTCTCAGGCTCAGACACAATGAAATGAGATGACACAGATGACAGAAATCTGTGC 53899
QY 2867 ----- 2866
Db 53900 TGTCTCTTTTATGAAATAAAAAGTATCAACATTCAGAGCAGGGCAGGTGGCTCACACTA 53959

QY 2867 ----- 2866
Db 53960 TAATCCAGACATTTGGGAGGCCAGGTGGGTGATCATCTTGAGCCAGAGTTTGAGGC 54019
QY 2867 ----- 2866
Db 54020 CAACCTAACCAATAGTAATTCATTTCTACTTAAAAAATCAAAAAATTAGCTGGC 54079
QY 2867 ----- 2866
Db 54080 CTGGTGACACAGGCTGTAGTCCCGCTATGCGGGAGGCTGAGGACAGAGAAATCATTTGA 54139
QY 2867 ----- 2866
Db 54140 ACCGAGAGCAGAGTTGACAGTACGCCAGATCACACACATGCACTCCAGCTGGGCA 54199
QY 2867 ----- 2866
Db 54200 CAGAGTACACTTCATCTTAAAAAATAAAGATACGATTCCAAAACCATAGTG 54259
QY 2867 ----- 2866
Db 54260 GACAGTGTGTTTTTATTTCTGCTCTGATTAATATTACTGTGTGCTGTAGAGCCGG 54319
QY 2867 ----- 2866
Db 54320 AACTGGGGGTGCTTCTCTGTAAAGCACACTTCATGGGAGAGAAATAAGTGTGAT 54379
QY 2867 ----- 2866
Db 54380 GGTGTAAACAGAGSTTTAAACTGGGGTCTGTCTGTGATTAACATCCAGATCT 54439
QY 2867 ----- 2866
Db 54440 GGACTTTGCTCTTCCAGAAATGCTCCGTGGGTTGCTTCATGAGGGGACAGCAGGTGT 54499
QY 2867 ----- 2866
Db 54500 GGACACCTCTGTATGGGGGAGCAGCAGGTGACAGCGCCCTCATGATGGGGAGTGGCAG 54559
QY 2867 ----- 2866
Db 54560 GTGACAGACACCTTGTGTCATGTGCCAGCATGTCCTGTGTGAGTCCCTCCACAG 54619
QY 2867 ----- 2866
Db 54620 GATGCCGTCTCTGTGCTCCCAACAGTCCCTGCTCTCAGACCTTACCTGTCC 54679
QY 2867 ----- 2866
Db 54680 TGGCTCTCACTGGCTTTGTGTGATGATTTCCACATTTCTGGGGTCCCAACACTCTTC 54739
QY 2867 ----- 2866
Db 54740 GCCTTCCAGGACCTCTGACGTGTGCCATACAGTACGTGTAACGTGCACACTGC 54799
QY 2867 ----- 2866
Db 54800 TTATTTGCTCCCAAGAAATGATTTTAAAGACAGGACCCCTGCTCCAGCTCTGG 54859
QY 2867 ----- 2866
Db 54860 CACAGCATCAGTAATGTTATTGAGGACAAAGAGACAGCAAAATCAGAAAAATGGG 54919
QY 2867 ----- 2866
Db 54920 TTCTCTAAACACATTTCAAGCCACAGAGCTAGTGACGATGGGTGGCATCAGGTC 54979
QY 2867 ----- 2866
Db 54980 ATCAGATGTGGTCCAAATGCCAGAAATATCTGTGCTCCAAAGGCCACTTGTGACAGTGT 55039

QY	2867	-----	2866	-----
Db	55040	TGTGCTTGACAGGTGGCTCTAAAAGCTCAGCAGTGGAGGCAGTGGTTGCCATCTCAG	55099	-----
QY	2867	-----	2866	-----
Db	55100	GGTGAACATCACATCCCTCTGTGTCTGTAGATATACGACAGAGGCTTTGAAGGGCATCTGGAG	55155	-----
QY	2867	-----	2866	-----
Db	55160	AAGAAAACAGCAAAATGATTAGAAAAGCTAAAAAGAAAAAGTGTAGATGGAAATTT	55219	-----
QY	2867	-----	2866	-----
Db	55220	TCTTTCAGATTTTACTCTCCCAACACACAGCTCAGATGTAATGTGTCAGAACTG	55279	-----
QY	2867	-----	2866	-----
Db	55280	ATGACAGACGAAATAGAAACAAAAGGAAGCCCATCTCTCAGAAACGTGTGTAATGTG	55333	-----
QY	2867	-----	2866	-----
Db	55340	TATGTGCACAGCTGATGAAAAAGAGTGTGTGTGTAATTTTTTTTTCTGAGAAAAC	55399	-----
QY	2867	-----	2866	-----
Db	55400	ACTGAGCAATTAAGTTGTGTCTTTACAGCATATACGACGACATTTCTAGTAGAAGA	55455	-----
QY	2867	-----	2866	-----
Db	55460	GGAGACATGCAAAACACACACGACACGAAATTAACAAAAGACTCAAAAGGAAAGGA	55519	-----
QY	2867	-----	2866	-----
Db	55520	GGTGAACGTTCCTCTGTTTGTGTGTGTGGGAGGACACACAGGAGGGGATGAACCA	55577	-----
QY	2867	-----	2866	-----
Db	55580	GAGGCAAGGGCATGCTTCTACTGCAGAAACTCAGTTGCTGAGCCACAGTGA	55639	-----
QY	2867	-----	2866	-----
Db	55640	TGGCAATTCCTGGAGCGTTTGTGCACGTGATTTATTAAGGCCCTGTGAGTCTGC	55699	-----
QY	2867	-----	2866	-----
Db	55700	ACATTCATCTCTCATTGTTGTTCTCTAACCACTGAGAGTGAAGAGAAAGCTCCA	55759	-----
QY	2867	-----	2866	-----
Db	55760	GGGAGACAGCCGCTTGTGTACACCCAGCTGGCAAAAGGCATGATGTCAGCCTGGC	55819	-----
QY	2867	-----	2866	-----
Db	55820	TCTGTCCGGGGCCCTTGCTGTGCCGAGGCCACACAACTGACGCCCATAGCTCA	55879	-----
QY	2867	-----	2866	-----
Db	55880	GGGTAGCGCGAGGCCAAGTCTGTTTGGGAGTGTCTTAAGAAAGAAATGACGCTG	55939	-----
QY	2867	-----	2866	-----
Db	55940	ATGCACTTGGGAAGTCTCTACGACGACGCTCAAAAGAAATGATGTAAACTGACAGC	55999	-----
QY	2867	-----	2866	-----
Db	56000	AGACCATCTCTCAAGAAAGCAGTGAAACTGATGGCAGACCTGTCCCATCTCTCA	56059	-----
QY	2867	-----	2866	-----
Db	56060	TGCTGTGCTCTTTTGTGGCTTGCCAAAGACCAACATCAGTTGAGCGCAGCTGAAAGA	56119	-----
QY	2867	-----	2866	-----

Db	56120	CTTTTGTGGAAGACGCTGTTGTTCATGAGAGTCCCTCAATGTCCTGTGCTTCCAGT	56179
OY	2867	-----	2866
Db	56180	AATTCCATCTTGAAGTGAACCAACATTAATGAGGGCTTATTTACATTTTCAGTGTTC	56239
OY	2867	-----	2866
Db	56240	CAGCAGGGGACTTGGCAACAGCAATGCACGACCTGCCCAATACAGGGCTAAGAGAT	56299
OY	2867	-----	2866
Db	56300	ATTATGATCAACAAAATTGCTGCTGGCATTAACATTTTCAMAAGATTTTGAAGATG	56359
OY	2867	-----	2866
Db	56360	TTTAATGCAACAAAAGCTTTATTTCATGATGACAGTGTTCAAAGCTGGATGTAAAGAAC	56419
OY	2867	-----	2866
Db	56420	ACACCCAGGAGCCTGCCGTGATGTCATGTGTTCATCTTTTGACATGAGATACATG	56479
OY	2867	-----	2866
Db	56480	GAGCAGTAGTGTGTGTGAGGCCCTGAGAGACATCGTGGATCCCTCATCCTGCCCTC	56539
OY	2867	-----	2866
Db	56540	TGAGAGCACCATGATGTGSCACAGTGCACACTGAGGCCGCTTACGTGTGTCCACTGG	56599
OY	2867	-----	2866
Db	56600	CTTCTTCATCCCTGAGATTAAACACAGTGAATTTCCACGCCCACTCACTGTTCTCC	56659
OY	2867	-----	2866
Db	56660	CACAAAAAAGCTGAGTCAACACCTGTGTTCACTCGAGGAGCCCGGAGACCAAGGGCTCCA	56719
OY	2867	-----	2866
Db	56720	CAGTTTATATGTGTTTTGGCTGAGATTATGTGCATCTCATCAGGCGAGATGATGATG	56779
OY	2867	-----	2866
Db	56780	GCACAAACACGCGCGTGCAGAGTTTGATACACTCAACATCACTAGCCAGGTCCTGGTGG	56839
OY	2867	-----	2866
Db	56840	AGTTTGTGATGCAGAGTCTGATGTGCATGTAGCATTTTGGAGTCCATGAGTGAACCC	56899
OY	2867	-----	2866
Db	56900	AGCCCTCTGGGCTGCAGGCCATGCCCCAGGCAGGAGGAAGCGGAGAGAGGACAGA	56959
OY	2867	-----	2866
Db	56960	GACCTTTTGGAGCAAGCTTTTGCAGGAGGGGCTGGGTGTGGGGCAGGCACTGTGTCTGA	57019
OY	2867	-----CAGCTATGCCGAGACCTCACTCAAGACCAAGTCTCACTTCAAC	2909
Db	57020	CATTCCCCCTGTGTGCACACTATATGCCGGAAGCTTCATCAGAGCCAGTCTCACTTCAAC	57079
OY	2910	CGCGGCTTCAAGGCTGGGAGGAACATCGCTGCMAACTCTTTTGGGGCTCTGGCGCTAAG	2969
Db	57080	CGCGGCTTCAAGGCTGGGAGGAACATCGCTGCMAACTCTTTTGGGGCTCTGGCGCTAAG	57139
OY	2970	TGTACACAGCTGTTCCTGATTTGC-----	2994
Db	57140	TGTACACAGCTGTTCCTGATTTGCAGGCTGAGGCTGATGTGTCAGACAGAGTTCAAG	57199
OY	2995	-----	2994

Db	57200	GTTCAGAGAGTGTGTGGCCGAAGTATGTGTGTGTGTGTGGCCGGGTGCTCCAAAGGCTG	57259
QY	2995	-----	2994
Db	57260	ATGTGACTGTGCTGCACGTATGAGATGTACATATGTACGATATACAGGTGACATATATG	57319
QY	2995	-----	2994
Db	57320	TGTGCATGTGTATCATGAAAGCATGGCAGTGTGTGCACAGGTGTGCAAGGCGCAATGTG	57379
QY	2995	-----	2994
Db	57380	TGTGCATGCGAATGACACACTGAATCATGTGTGTGTGTGTGCAAGTGTGTGGCAT	57439
QY	2995	-----	2994
Db	57440	TCACGTGAGGTGCATGCGTGTGGGTGTGCAGTGTAGTATGTGTGCACATATATGT	57499
QY	2995	-----	2994
Db	57500	ATTGAGGGGTCTCGTGTTCACCCCGCTAGTCTCAGACACGATGCCACTTCCTTACAGG	57559
QY	2995	-----	2994
Db	57560	GTGAGACGGGGTCCAGGCTTGTGTGGGTGTAGGCTGTGAAGCTGCAGCCCTGAGGGCAT	57619
QY	2995	-----	2994
Db	57620	TGTCCCATGTGGGACATCCGCGTCCACCTCCCTCTCGTGTGGCTTGTGTCCACTCCCCC	57679
QY	2995	-----	2994
Db	57680	TCTCTGTGGCGGTCCACACCCCTCTCTGTGGCATCCGATCCACTCCCTCTCTGT	57739
QY	2995	-----	2994
Db	57740	GGGCATCTGTGTCCACTCCCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	57799
QY	2995	-----	2994
Db	57800	GCGGTCCGCGTCCACTCCCTCTCTGTGGCATGTGCATCCACTCCCTCTCTGTGGG	57859
QY	2995	-----	2994
Db	57860	CGTCTGTGTCCACTCCCTCTCTGTGGCATCCGCGTCCACTCCCTCTCTGTGGCA	57919
QY	2995	-----	2994
Db	57920	TCTGCATCCACTCGTCTCTCTGTGGGCGTCCGTGTCCACTCCCTCTCTGTGGCAT	57979
QY	2995	-----	2994
Db	57980	CTGCGTCCACTCCCTCTCTGTGGGATCCGTGTCCACTCCCTCTCTGTGGCAT	58039
QY	2995	-----	2994
Db	58040	CCATGTCCACTCCCTCTCTGTGGGATCCGTGTCCACTCCCTCTCTGTGGGATCTGC	58099
QY	2995	-----	2994
Db	58100	GTCCTGTCCCTCTCTCTGTGGGCGTCCGTGTCCACTCCCTCTCTGTGGGCGTCCGG	58159
QY	2995	-----	2994
Db	58160	TCCACTCCCTCTCTGTGGGATCTGCGTCCCTCTCTCTGTGGGCGTCCGTGTGC	58219
QY	2995	-----	2994
Db	58220	CACCTCCCTCTCTGTGGGCGTCCGATCCGATCCCTCTCTGTGGGATCTGCGTGTGC	58279
QY	2995	-----	2994
Db	58280	TCCCTCTCTCTGTGGGCGTCCATGTCCACTCCCTCTCTGTGGGATCTGCGTCCACTC	58339

[illegible]

```
QY 3056 ----- 3055
Db 59420 TTGGGGCTCAGCAAGAGGGCCGAGGTGGTGCAAGTGAAGGCTGCTGGCCCCACCCCC 59479
QY 3056 ----- 3055
Db 59480 GGGAAAGTGCACAGAGCTGTGGCTCCCAACAGCCCGGCGACACCTGTGCTGGGC 59539
QY 3056 ----- 3055
Db 59540 ATGGCTGTGCTCTTGGAAAGCTTCCCTGTCTGTGGCTGTGACAGGGGTCCCTCCAGAA 59599
QY 3056 ----- 3055
Db 59600 TCGACAATTATTACAGAGGGAAGGCCAATCTGTGAGGCCACAGGCCAGCTTCTGC 59659
QY 3056 ----- 3055
Db 59660 CTGAGATCAGGGCAGGTGGTGCAAGACCTCGGGGCTGTACAAAGGCGAGTCGGGCAC 59719
QY 3056 ----- 3055
Db 59720 CAGAGCCCGGGCTCCACCTCAACAGGCTCCGAGCCACTGGAGCTGAATGCCAGA 59779
QY 3056 ----- 3055
Db 59780 GGCGAAGCCCTCGCCCATGAGGGCTGAGAAGAGATGTGAGCATTTGTGTACCCAGG 59839
QY 3056 ----- 3055
Db 59840 CCGAGGCTCGGGAATTACCGTGCACATTGATGTAAATGAGTCTGCTATATGTGG 59899
QY 3056 ----- 3055
Db 59900 AAACCCAGAGGCTCAGGGAGATTTCATTACAGAGTCTGTACCAATAAATGTT 59959
QY 3056 ----- 3055
Db 59960 TTTAACCCAGTGTTCGCCCTTCATGCTGTGCAAGGAGGGCAGAGCCACAGCTGCATG 60019
QY 3056 ----- 3055
Db 60020 TTACCGCTTTGACACAGCTCAGAGGCTTGAGCCAGGCTGTCTCATTTCCAGGGTGG 60079
QY 3056 ----- 3055
Db 60080 TCCGGCTCAGACCGCCCTCTCTCTGCTCTCTCTGCTCAAAATCTTCCTTGTGG 60139
QY 3056 ----- 3055
Db 60140 CATCTCCCTGACGCTGCTGGGCCCTCGTGAAGCTGCTTGACTCCTTCCGGAACCC 60199
QY 3056 ----- 3055
Db 60200 TTGGGGTGTGCTGATACAGGTGCCACTGAGACTGAGGTGTCTGACACTGTGTTGAC 60259
QY 3056 ----- 3055
Db 60260 CCCAGGCTCCAGCTGCGTGTGTTGGGCCCTCTTGAGCCATGATAGGTGAGAGATT 60319
QY 3056 ----- 3055
Db 60320 TCCAGGTAAACTCTGGAAACTCCAGGCCATGTGACCTGCACTGCTCTCTCC 60379
QY 3056 ----- 3055
Db 60380 ATATTAGCTCAGTCTTGTCTCATTTCCCAACAGGGTCTAGTCTGAGAGAGTCCC 60439
QY 3056 ----- 3055
Db 60440 GTAGAGGCTTGGGCTCAGGGGAGGGGAGTTTCCCAACCAGTATGGGACCTTGG 60499
QY 3056 ----- 3055

Db 60500 GTAGTCCGTTGATTGGGTAGCCCTGAGAGGCCGAGATGCAATGGGCCACGGCCGTTT 60559
QY 3056 ----- 3055
Db 60560 CCAACACAGATCAGGACAGTGGAAAGGCCAGAAATCCCTTCCCTGAGGCAGAGTG 60619
QY 3056 ----- 3055
Db 60620 GGAGAACGAGAGCTGGGCCCGATTTTCAGGCAAGCAGCTGCAATGGGGCAGGCTGTG 60679
QY 3056 ----- 3055
Db 60680 GTGTTCACGTGGCGCTGGGGCGGGGTCTGATTCAATCCGCTGGGGCTCGGCTTCT 60739
QY 3056 ----- 3055
Db 60740 GGCCCGTGTGGCCGCCCTCCACAGGGCTTGGGTGACGCCCGACCTTACAGAGT 60799
QY 3056 ----- 3055
Db 60800 GGCTATTCTCCTTTGGAAGAGAGCCCTCACCCATGTAAGTGTTCCTCTCGGGTC 60859
QY 3056 ----- 3055
Db 60860 AGGAGCGTGGCGGTGGCAACCCCGGACCTTAGGCTATTATTGTTAAACATT 60919
QY 3056 ----- 3055
Db 60920 CTGGGCTGTGGCTTCCGTTTGTCTAAATGGGAAAGACATCCACCTCAGCAGATTAC 60979
QY 3056 ----- 3055
Db 60980 TGAGAGCTGAACCGGGGGTGTGCTTACTGTGTGATCTAGTCAATTCAGAGATG 61039
QY 3056 ----- 3055
Db 61040 GCTCAGAAATCAGTGAACACAGTACATGGGGGCTCAGCAGTGGTGAGATAGGTA 61099
QY 3056 ----- 3055
Db 61100 CACGGGGGCTCAGCAGTGGGTGAGGCCAGTACATGGGGGCTCAGCAGCTGGGTAG 61159
QY 3056 ----- 3055
Db 61160 ATGAGTACATGGGGGCTCAGGCAGAGGGTCAAGCAAGTACACGGGGGCTGTGATCAC 61219
QY 3056 ----- 3055
Db 61220 ACGCATATGACCATGTGCAATGTGCTGTTTCATGTAGCCAGTCTGTGCACAC 61279
QY 3056 ----- 3055
Db 61280 TGCCCCAAGTCCAGGAAGCTGAGAGGCCAAAGATGAGGCTGACAGGGCTGGCGCGT 61339
QY 3056 ----- 3055
Db 61340 GGCTCACCTGTAGTCCAGCACTTTGGAGGCCGAGGCGAGAGATCCTTGAGCCCA 61399
QY 3056 ----- 3055
Db 61400 GGAGTTTAAGACAGCCTGAGCAACATAGTAACCCATCTATGAAAAATTAACA 61459
QY 3056 ----- 3055
Db 61460 AAATTTAGCTGAGATGTGTGTGGCTGTAGTCCAAATACTTGGAGGCTGAAGTG 61519
QY 3056 ----- 3055
Db 61520 GAGGATCACTTGAGCCAGAGAGGTGAAGCTCAGTGAAGCTTGAGATTGCACCACTGTACT 61579
QY 3056 ----- 3055
```


D	b	61580	GCAGCCTGGGTGTCACAGATGTGAAGGCCCATCTCTAACACACACAAAGAGACTGACAAATGC	61639
O	y	3056	-----	3055
D	b	61640	AGTTTCTTGGAAGAACAATTTAGTAGAAGCTTAACCTACACAGAAAGCAAGTCGGTG	61699
O	y	3056	-----	3055
D	b	61700	TCTCGGTGTCAGTGAGATGAGATGATGGGTCTCTACACCATCACCACCCAGAGCGTTT	61759
O	y	3056	-----	3055
D	b	61760	ATGCACACAGAGGGGGGTGGCTCAGAAAGGATGCGCAGAGAGCTTGATATACATGACAT	61819
O	y	3056	-----	3055
D	b	61820	CAAGTTGTCAGCAAGAGGCGAGATTCATATGATAGTACCTCTGGTACACAAGAACAA	61879
O	y	3056	-----	3055
D	b	61880	TGGATTAACCTGGAACCTTAGAGCCTTCCGGAACAGGGGCTAATCAGAACCCAGCATG	61939
O	y	3056	-----	3055
D	b	61940	GGGGGCTGGCATCCAGATGGAGCTGCTTCAGCTCCACATCCGTGTTTATACATGATGT	61999
O	y	3056	-----	3055
D	b	62000	GCACAGAAACGAGTGTACCTGTGCACACACAGACAGCAGCTACTCGCACACACAAAGA	62059
O	y	3056	-----	3055
D	b	62060	CACACAGACATGCATGCATGCATCCGTGTGTGTGCACCTGTGCCATGAGAAACCA	62119
O	y	3056	-----	3055
D	b	62120	TGCATGTGATTCATGACAGCAGCACACAGGACCCGGTGGGCCATGCCACACCAGAGCA	62179
O	y	3056	-----	3069
D	b	62180	CCGTCTGATTAGAGAGCCTTCTCTGACGGCTGTCCCGCATCTCTCAGGTTTACGCGAT	62239
O	y	3070	GTGTCTGAGTCTCCCATTTTCATCAGCAAGTTTGGAAAGAACCCCATTTTCTGCGCG	62299
D	b	62240	GGTCTCTGAGCTCCCATTTTCATCAGCAAGTTTGGAAAGAACCCCATTTTCTGCGCG	62299
O	y	3130	TCATCTGACAGCGGCTCCCTCCCTCTCTCTCATCTGAAAGCCAAAGCAAG-----	3180
D	b	62300	TCATCTGACAGCGGCTCCCTCTCTCTCATCTGAAAGCCAAAGCGAGGTATGT	62359
O	y	3181	-----	3180
D	b	62360	GCAGGTGCTGGCTTCAGTGGCAGCAGAGTGGCTGGCTGGTGTAGTGTGCAGAGAGC	62419
O	y	3181	-----	3180
D	b	62420	TGAGTAATCTGGGCTTAGAGAGTCTTAACCCCTTTTGCATCAGGAAGTGGTTAAACC	62479
O	y	3181	-----	3180
D	b	62480	AACCATGTCAAGGCTGCTGTGCGCCGCTCTCTGTGGGTGAGCAGAGACCTGATGAAG	62539
O	y	3181	-----	3180
D	b	62540	GGACAGAGAGCTGTGGGAGCTGCCATCCTTCCACCTTGGCTCTGCGCTGGGGAAGCGCTG	62599
O	y	3181	-----	3180
D	b	62600	GGGGGCTGAGTCTCTCTGTTTGGCCCAAGGAGGAGTTTGGGGGGCTGGGCTCTCTGT	62659
O	y	3181	-----	3180
D	b	62660	TTGCCCTGTGTGGAGTTGGGCTGTCTCCGTCATGCGACATTAGGCCCTTGTGCAAC	62719

QY	3181	-----	3180
Dp	62720	CCAGGCCAAGGGCTTTAGAGAGAGCCAGGCCAGGCTTACCACCCCTCTCAGAGACAGA	62779
QY	3181	-----	3180
Dp	62780	GGCCCGGTATCACACACAGACAGAGAGCCCGCGGCTCTTGCTTCCAGTACCGTCTCT	62839
QY	3181	-----	3180
Dp	62840	GGCCCTGACACTTTGTCTCCAGCATCAGGAGGTTTCTGATCCGTGGAATTCAGACCAT	62899
QY	3181	-----	3180
Dp	62900	GTCGAACCTCGCGCTCTGAGCTTAACAGCTTCTACTTCTGTCTTCTGTGTGGAA	62955
QY	3181	-----	3180
Dp	62960	ATTTCACCTGGAGAGAGCCGAGAAAAATTTCTGTCTGATCTCTGCGGTGGGTGCG	63019
QY	3181	-----	3180
Dp	63020	GGACAGCCAGAGATGGAGGCCACCCCGCAGACCGTGGGTGTGGGACATTTCCGGTCT	63079
QY	3181	-----	3188
Dp	63080	CCTGGGAGGGGAGCTGGGGCTGGGCGCTGTGACTCCTCAGCTCTGTTTTCCCCAGGAGTG	63139
QY	3189	TGGCTGGGGGCCAAGAGGGCCCGCGGCTCTTGCCCTCCGAGGCGGTGATGGCTGTGC	3248
Dp	63140	TGGCTGGGGGCCAAGAGGGCCCGCGGCTCTTGCCCTCCGAGGCGGTGATGGCTGTGC	63199
QY	3249	CACCAAGCATTTCTGCTCAAGCTGATGACTGACACCGTGTCACTACGTGCGCATCTCGGGG	3308
Dp	63200	CACCAAGCATTTCTGCTCAAGCTGATGACTGACACCGTGTCACTACGTGCGCATCTCGGGG	63255
QY	3309	TCACTCAGGA-----	3318
Dp	63260	TCACTCAGAGACAGCAAGTGTGGTGGAGGCCAGTGGCGGGCCACCTTCCAGGGGTCA	63319
QY	3319	-----	3318
Dp	63320	TCTTTGAACGCCCTGTGTGGGGCGAGACGCTCAGATGCTGCTGAAGTGCAGACGCCCC	63379
QY	3319	-----	3318
Dp	63380	GGGCTGACCTTGGGGGCTTGAGGACAGCTGGACGCTATGTGATTAACGCTGTGT	63439
QY	3319	-----	3318
Dp	63440	CCCCAGCCACGGAGCCTGGCAGGGTCCACAACATTTGTGAACCCCTGTTCCCATCTCAG	63499
QY	3319	-----	3318
Dp	63500	GGGCGATGGCTCCCAACGCTTGGAGGCTTCTGACCCCTGACCTGTGTCTCTCAAGGC	63559
QY	3319	-----	3318
Dp	63560	TCTTCCCTGGCTGTGCCCTGTAGCTCTGGGGTCTGTGACAGATTTCTTCCCGCCCGC	63619
QY	3319	-----	3318
Dp	63620	CGCTCAGCGTCACTGGGCTCGCTGTGTCTGTCCCGGTGGAGGGGTGTCTGTCCCTTC	63679
QY	3319	-----	3318
Dp	63680	ACTGAGTTCCACACAGCCAGGGCCACGAGGTGACAGGCCCTGTGCGCGGCCACCCACA	63739
QY	3319	-----	3318
Dp	63740	CGTCTAGAGGGTTGAGAGATCCACCTCTGCGCTTCTTGTGAACGAGTCTGATTTTG	63799

QY	3319	----	-CAGGCCAGACGAGCGTGTATGTCATGTCGAGAGCTCCGGGGAGACGACGCTGATCGCTCGG	3372
Db	63800	GGCCCCGACGCCAGACGACGCTGATGCTGGAAGACTCCGGGGAGACGACGCTATCGCTCGG		63855
QY	3373	AGCCCGAGGCAACCCGGGCAACATCGCTGACACTTCAGAACACATCTCTGACTGATGAGCCAC	3432	
Db	63860	AGGCGCAGCCAAACCCGGACATGCTGCTCAAGACTTCAGAACACATCTCTGACTGATGAGCCAC	63911	
QY	3433	CCGCCCAACAGCGCGGAGAGGACACACAGACGCCCTGTACAGCGCGGCTCTACGTCC	3492	
Db	63920	CCGCCCAACAGCGCGGAGAGGACACACAGACGCCCTGTACAGCGCGGCTCTACAGGTCC	63977	
QY	3493	CAGGAGGAGGAGGGGGCGGCCACACCCAGGGCCCGACCGCTGGAGTCTGAGGCGCTGAGTG	3552	
Db	63980	CAGGAGGAGGAGGGGGCGGCCACACCCAGGGCCCGACCGCTGGAGTCTGAGGCGCTGAGTG	64033	
QY	3553	AAGTGTGGGGCCAGAGCCCTGCATGTCTCCGGCTAAAGCTGAGTGTCCGGGTGAGGCGCTGAGC	3612	
Db	64040	AAGTGTGGGGCCAGAGCCCTGCATGTCTCCGGCTAAAGCTGAGTGTCCGGGTGAGGCGCTGAGC	64099	
QY	3613	GAGTGTCCACCCAAAGGGGTGAGTGTCCACACACACTTCCGGCTTACTACATTCGCCACAGGT	3672	
Db	64100	GAGTGTCCACCCAAAGGGGTGAGTGTCCACACACACTTCCGGCTTACTACATTCGCCACAGGT	64155	
QY	3673	GGCGGTGGGTCTCCACCCAGGGGGCACTTTTCTCCACAGAGGCCGGGTCTTCACATCCC	3732	
Db	64160	GGCGGTGGGTCTCCACCCAGGGGGCACTTTTCTCCACAGAGGCCGGGTCTTCACATCCC	64211	
QY	3733	ACATPAGAAATAGTCATATCCCAATTCGCAATGTCTACCCCTGGCCCTCTGCTCCTTTTG	3792	
Db	64220	ACATPAGAAATAGTCATATCCCAATTCGCAATGTCTACCCCTGGCCCTCTGCTCCTTTTG	64277	
QY	3793	CGTTTCACCCCCACCATTCAGGTGTGAGACCTTGAGAAAGACCTTGGAGCTCTGGGAATT	3852	
Db	64280	CGTTTCACCCCCACCATTCAGGTGTGAGACCTTGAGAAAGACCTTGGAGCTCTGGGAATT	64333	
QY	3853	TGAGATGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCCTGCACCTGGANTGGGGGTCC	3912	
Db	64340	TGAGATGACCAAAGGTGTGCCCTGTGTACACAGGCGAGGACCCCTGCACCTGGANTGGGGGTCC	64399	
QY	3913	CTGTGGGTCAAAATTTGGGGGAGGTGCTGTGGAGATTAATAATCTAGTAATATATGATTTTTC	3972	
Db	64400	CTGTGGGTCAAAATTTGGGGGAGGTGCTGTGGAGATTAATAATCTAGTAATATATGATTTTTC	64455	
QY	3973	ACTTTTAAAAAAA-----	3986	
Db	64460	ACTTTTAAAAAAA-----	64511	
QY	3987	-----	3986	
Db	64520	CAATTTAGAGAGCCTGTGAGTGAAGACGGGGGTGTGTGATGGGGGCCCATATGGCTGTGGTG	64577	
QY	3987	-----	3986	
Db	64580	TGCATTTAGAGGAAGCTATGAGTGAATGGGGGTGTGTGTACATGTGCGGGCCCATATGGCTGTGGC	64633	
QY	3987	-----	3986	
Db	64640	TGGGCGCTGGAGATTTCTGATGCTGTGTGAGGACGAGAGGGAGGAGAGGATGAGGAGATATGACA	64699	
QY	3987	-----	3986	
Db	64700	GTGGGAGCCCCCACCCTTGAAAGACATTAACATGAATGTCAAGGCCGAGAGGGCGACAGGAT	64755	
QY	3987	-----	3986	
Db	64760	GCTGGGGGCCCACTTGGGCGGGCGGAGATGATGAGAGGGCTGTGGCCGGGTGTGCAGGAGTG	64811	
QY	3987	-----	3986	
Db	64820	ATGGGGGCCCACTTGGGCGGGCGGAGATGATGAGAGGGCTGTGGCTGTGGCTGTGGCGGAGA	64877	
QY	3987	-----	3986	

[illegible]

Thu Apr 17 08:21:56 2003

us-09-424-686b-1del.rmpb

Page 1

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 16, 2003, 23:08:30 ; Search time 610 Seconds
(Without alignments)
6597.172 Million cell updates/sec

Title: US-09-424-686b-1DEL
Perfect score: 4006
Sequence: 1 gttcagcagcagcgtcgtc.....aaaaaaaaaaaaaaaaaaaa 4006

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.0

Searched: 639749 segs, 502280978 residues

Total number of hits satisfying chosen parameters: 1279498

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubna/PTCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3969	99.1	4015	9	US-09-843-676-224
2	3969	99.1	4015	9	US-09-953-052-1
3	3969	99.1	4015	9	US-10-033-758-224
4	3969	99.1	4015	9	US-10-034-295-224
5	3969	99.1	4015	9	US-10-208-243-1
6	3969	99.1	4015	9	US-10-054-611-173
7	3969	99.1	4015	9	US-10-105-963-1
8	3969	99.1	4015	10	US-09-733-294A-3
9	3969	99.1	4015	10	US-09-990-080-1
10	3969	99.1	4015	10	US-09-733-294A-30
11	3969	99.1	4015	9	US-09-843-676-173
12	3969	99.1	4015	9	US-09-438-486-173
13	3969	99.1	4015	9	US-10-053-758-173
14	3969	99.1	4015	9	US-10-054-295-173
15	3969	99.1	4015	9	US-10-054-611-173
16	3969	99.1	4015	9	US-10-205-629-1
17	3969	99.1	4015	9	US-09-749-728B-32
18	3969	99.1	4015	9	US-09-843-676-100
19	3969	99.1	4015	9	US-09-766-253-100

20	2039.2	50.9	2171	9	US-09-438-486-100	Sequence 100, App
21	2039.2	50.9	2171	9	US-10-053-758-100	Sequence 100, App
22	2039.2	50.9	2171	9	US-10-054-295-100	Sequence 100, App
23	2039.2	50.9	2171	9	US-10-054-611-100	Sequence 100, App
24	1777.4	44.4	1866	9	US-10-294-778-11	Sequence 11, Appl
25	1635.4	40.8	15418	9	US-09-995-419A-1	Sequence 1, Appl
26	1635.4	40.8	15418	9	US-10-111-220-1	Sequence 1, Appl
27	1635.4	40.8	15418	10	US-09-783-203-1	Sequence 1, Appl
28	1635.4	40.8	15418	10	US-09-994-427A-1	Sequence 1, Appl
29	1224.4	30.6	1314	9	US-10-284-778-9	Sequence 1, Appl
30	1211.4	30.2	1311	9	US-10-294-778-1	Sequence 1, Appl
31	457.4	11.4	88421	9	US-09-976-059-1	Sequence 1, Appl
32	449.4	11.2	88421	9	US-09-976-059-1	Sequence 1, Appl
33	425.6	10.6	68750	9	US-10-014-717-1	Sequence 1, Appl
34	410.6	10.2	53522	9	US-09-904-968A-1	Sequence 1, Appl
35	403.8	10.1	155074	9	US-10-026-188-6	Sequence 6, Appl
36	399.4	10.0	36778	9	US-09-860-846-5	Sequence 5, Appl
37	399.4	10.0	36778	10	US-09-861-289-5	Sequence 1, Appl
38	397.6	9.9	68750	9	US-09-808-880-1	Sequence 1, Appl
39	394	9.8	50937	9	US-09-808-880-1	Sequence 1, Appl
40	391.8	9.8	174424	10	US-09-967-768A-314	Sequence 314, App
41	387.8	9.7	50937	9	US-09-808-880-1	Sequence 1, Appl
42	387.6	9.7	53522	9	US-09-904-968A-1	Sequence 1, Appl
43	385.8	9.6	389	9	US-09-843-676-62	Sequence 62, Appl
44	385.8	9.6	389	9	US-09-766-253-62	Sequence 62, Appl
45	385.8	9.6	389	9	US-09-438-486-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-09-843-676-224
Sequence 224, Application US/09843676
Patent No. US20020164786A1
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-843-676-224

Query Match 99.1%; Score 3969; DB 9; Length 4015;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;
QY 8 GCAGCGCTGCTCTGCTGCGACGTGGAAAGCCCTGGCCCGCCGCGATGCC 67
DB 1 GCAGCGCTGCTCTGCTGCGACGTGGAAAGCCCTGGCCCGCCGCGATGCC 60
QY 68 GCGGCGTCCCGCGTCCCGACGCGTGGCCCTCTGCTGCGACGCTACCGGAGTCT 127
DB 61 GCGGCGTCCCGCGTCCCGACGCGTGGCCCTCTGCTGCGACGCTACCGGAGTCT 120
QY 128 GCGGCGTCCCGCGTCCCGACGCGTGGCCCTCTGCTGCGACGCTACCGGAGTCT 187
DB 121 GCGGCGTCCCGCGTCCCGACGCGTGGCCCTCTGCTGCGACGCTACCGGAGTCT 180
QY 188 GGACCGCGGCGCTTTCGCGCGTGGTGGCCAGTGGCTGGTGGTGGTGGTGG 247
DB 181 GGACCGCGGCGCTTTCGCGCGTGGTGGCCAGTGGCTGGTGGTGGTGGTGG 240
QY 248 ACGGCG 307
DB 241 ACGGCG 300
QY 308 CCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGCGAGAGTGTGCTTGGCTTGC 367
DB 301 CCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGCGAGAGTGTGCTTGGCTTGC 360
QY 368 GCTGCTGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 427
DB 361 GCTGCTGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 428 CCTGCGCCAAACAGGTGACGACGACTGCGGGGAGCGGGCGTGGGGCTGCTCTCG 487
DB 421 CCTGCGCCAAACAGGTGACGACGACTGCGGGGAGCGGGCGTGGGGCTGCTCTCG 480
QY 488 CCGCGTGGGCGACGAGCTGTGTGTACCTCTGCGACGCTGCGCGCTTGTGTGCTGT 547
DB 481 CCGCGTGGGCGACGAGCTGTGTGTACCTCTGCGACGCTGCGCGCTTGTGTGCTGT 540
QY 548 GCGTCCCAAGCTGCGCTACAGGTGTGTGGGCGCGCGCTGTACAGCTTGGCGCTGCAC 607
DB 541 GCGTCCCAAGCTGCGCTACAGGTGTGTGGGCGCGCGCTGTACAGCTTGGCGCTGCAC 600
QY 608 TCAGAGCG 667
DB 601 TCAGAGCG 660
QY 668 CTGGAACCATAGCTGACGAGAGCGCGGGGTCCCTTGGGCTTGGCGCTGGTGGAG 727
DB 661 CTGGAACCATAGCTGACGAGAGCGCGGGGTCCCTTGGGCTTGGCGCTGGTGGAG 720

QY 728 GAGCGCGCGGCGAGTGGCCAGCCGAGTCTCCCTGTCGCCAAGAGGCCAGCGCTGGCGC 787
DB 721 GAGCGCGCGGCGAGTGGCCAGCCGAGTCTCCCTGTCGCCAAGAGGCCAGCGCTGGCGC 780
QY 788 TGCCCCGTAGCGGAGGAGGAGCGCGCGTGGGAGGAGGTCGAGGGCCACCGCGGAGGAGC 847
DB 781 TGCCCCGTAGCGGAGGAGGAGCGCGCGTGGGAGGAGGTCGAGGGCCACCGCGGAGGAGC 840
QY 848 GCGTGGACGAGTGAACCGTGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
DB 841 GCGTGGACGAGTGAACCGTGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 908 CACCTCTTTGAGAGGTGGCGTCTGTGAGCGCGCACCTTCCCAACCATCCGTGGCGCGCA 967
DB 901 CACCTCTTTGAGAGGTGGCGTCTGTGAGCGCGCACCTTCCCAACCATCCGTGGCGCGCA 960
QY 968 GCACACGCGGGGCG 1027
DB 961 GCACACGCGGGGCG 1020
QY 1028 CCGCGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCTCAGGCGCAAGAGAGAGAGTGGC 1087
DB 1021 CCGCGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCTCAGGCGCAAGAGAGAGTGGC 1080
QY 1088 GCGCT 1147
DB 1081 GCGCT 1140
QY 1148 GACCATCTTCTGAGTGTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1207
DB 1141 GACCATCTTCTGAGTGTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1200
QY 1208 GCGCGAGCGCTACTGTGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1267
DB 1201 GCGCGAGCGCTACTGTGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
QY 1268 GTGCCCTTACGCGGCTGTCT 1327
DB 1261 GTGCCCTTACGCGGCTGTCT 1320
QY 1328 AGCGGAGTGTGTGCGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1387
DB 1321 AGCGGAGTGTGTGCGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
QY 1388 CACAGACCCCGTGTGCTGT 1447
DB 1381 CACAGACCCCGTGTGCTGT 1440
QY 1448 GCGCTGT 1507
DB 1441 GCGCTGT 1500
QY 1508 CAAGCAAGCGCGCTTCTCTCAGAGAACCAAGTATCTCTCTCTCTCTCTCTCTCTCTCTCT 1567
DB 1501 CAAGCAAGCGCGCTTCTCTCAGAGAACCAAGTATCTCTCTCTCTCTCTCTCTCTCTCTCT 1560
QY 1568 GCTCTGCTGAGAGCTGTGAGT 1627
DB 1561 GCTCTGCTGAGAGCTGTGAGT 1620
QY 1628 GAGCCCAAGGAGT 1687
DB 1621 GAGCCCAAGGAGT 1680
QY 1688 CAAGTCTCTGACTGT 1747
DB 1681 CAAGTCTCTGACTGT 1740
QY 1748 TGTACGAGAGACAGTGTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1807
DB 1741 TGTACGAGAGACAGTGTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1808 CAAGTGTCAAGCATTTGGAATCAGACAGCACTTGAAGAGGAGTGCAGCTGCGGAGCTGTCT 1867

Db 1801 CAAGTTGGCAAAAGCATTTGAAATTCAGACAGCATTTGAAAGGGGTGAGTCCGGAGACTCTGC 1860
Qy 1868 GGAAGCAGAGGTCAAGGCAGCATGCGGAAAGCCAGGCCCCCTGCTGACGTCAGACTCCG 1927
Db 1861 GGAAGCAGAGGTCAAGGCAGCATGCGGAAAGCCAGGCCCCCTGCTGACGTCAGACTCCG 1920
Qy 1928 CTTTCATCCCAAGGCGTGCAGGGGCTGCGGCGATTGTGAACATGGACATGACGTGTGGAGAGC 1987
Db 1921 CTTTCATCCCAAGGCGTGCAGGGGCTGCGGCGATTGTGAACATGGACATGACGTGTGGAGAGC 1980
Qy 1988 CAGAACGTTCCGCAAGAGAAAAGAGGGCGAGGCTGCACCTCCAGGGGTGAAGCACTGTT 2047
Db 1981 CAGAACGTTCCGCAAGAGAAAAGAGGGCGAGGCTGCACCTCCAGGGGTGAAGCACTGTT 2040
Qy 2048 CAGCGTCTCAACTACAGAGCGGGCGCGGCGCTCTGAGGGCGCTGTGCTGTGG 2107
Db 2041 CAGCGTCTCAACTACAGAGCGGGCGCGGCGCTCTGAGGGCGCTGTGCTGTGG 2100
Qy 2108 CCTGGACGATTCACAGAGGCGCTGGCGACCTTTCGTGCTGTGTGTGGGCGCCAGGAGACC 2167
Db 2101 CCTGGACGATTCACAGAGGCGCTGGCGACCTTTCGTGCTGTGTGTGGGCGCCAGGAGACC 2160
Qy 2168 GCCGCGCTGAGCTGTA-----CATCCCCCA 2191
Db 2161 GCCGCGCTGAGCTGTA-----CATCCCCCA 2220
Qy 2192 GGACAGAGCTCAAGAGGTCAATCCGACATCATCAAACCCAGAACACGATCGGTGCG 2251
Db 2221 GGACAGAGCTCAAGAGGTCAATCCGACATCATCAAACCCAGAACACGATCGGTGCG 2280
Qy 2252 TCGGTATGCGCGGTTCAGAGAAAGCGCGCCATGAGGAGCTCCGCAAGGCGCTTCAAGAGCA 2311
Db 2281 TCGGTATGCGCGGTTCAGAGAAAGCGCGCCATGAGGAGCTCCGCAAGGCGCTTCAAGAGCA 2340
Qy 2312 CGTTCCTACCTTTGACACACTCCAGCGGCTACATGAGAGAGTGTGGTCTACCTGACAGA 2371
Db 2341 CGTTCCTACCTTTGACACACTCCAGCGGCTACATGAGAGAGTGTGGTCTACCTGACAGA 2400
Qy 2372 GACAGAGCGCTGAGAGGATGCGTGTCTCATGAGACAGAGCTCTCCCTGATGAGGCGAG 2431
Db 2401 GACAGAGCGCGCTGAGAGGATGCGTGTCTCATGAGACAGAGCTCTCCCTGATGAGGCGAG 2460
Qy 2432 CAGTGGCGCTTCGACGCTCTTCTTACGCTTCAATGTGCCACACCGCGTGCAGTCAAGGGG 2491
Db 2461 CAGTGGCGCTTCGACGCTCTTCTTACGCTTCAATGTGCCACACCGCGTGCAGTCAAGGGG 2520
Qy 2492 CAAGTCTACGTCACAGTGCCAGGGGATCCCGCAGGGGCTCATCTCTCCACGCTGCTCG 2551
Db 2521 CAAGTCTACGTCACAGTGCCAGGGGATCCCGCAGGGGCTCATCTCTCCACGCTGCTCG 2580
Qy 2552 CAGCCCTGTGTACGCGACATGGAAGAAAGCTGTTTCCGGGGATTCCGGGGAGGGGCT 2611
Db 2581 CAGCCCTGTGTACGCGACATGGAAGAAAGCTGTTTCCGGGGATTCCGGGGAGGGGCT 2640
Qy 2612 GCTCCGCGTTTGGTGGATGATTTCTTGTGGTGAACACCTACCTACCCAGCGGCAAAAC 2671
Db 2641 GCTCCGCGTTTGGTGGATGATTTCTTGTGGTGAACACCTACCTACCCAGCGGCAAAAC 2700
Qy 2672 CTTTCCTCAGAGACCTGGTCCGAGGTTCCCTGAGTATGCTGCGTGTGAACCTGCGGAA 2731
Db 2701 CTTTCCTCAGAGACCTGGTCCGAGGTTCCCTGAGTATGCTGCGTGTGAACCTGCGGAA 2760
Qy 2732 GACAGTGTGAATCTCCCTGTAGAGAGAGGCGCTGGGTGGCAAGGCTGTTTGTTCAGAT 2791
Db 2761 GACAGTGTGTGAATCTCCCTGTAGAGAGAGGCGCTGGGTGGCAAGGCTGTTTGTTCAGAT 2820
Qy 2792 GCCGGGCCACGAGCCTATTCCTGTGTGCGGCTGCTGTGTGATACCCGAGACCTGTGAGAGT 2851
Db 2821 GCCGGGCCACGAGCCTATTCCTGTGTGCGGCTGCTGTGTGATACCCGAGACCTGTGAGAGT 2880
Qy 2852 GCAGAGCAGTACTACGATATGCCCGGAGCTCCATCGAGACAGTCTGACCTTGAACCG 2911

Db 2881 GCAGAGCAGTACTCCAGTATGCCCGGAGCTCCATCGAGAGCCAGTCTACCTTGAACCG 2940
Qy 2912 CGGCTTCAAGGCTGGGAGGAACATGTGTGCGAAACTTTTGGGGTCTTTCGGCTGAAGTG 2971
Db 2941 CGGCTTCAAGGCTGGGAGGAACATGTGTGCGAAACTTTTGGGGTCTTTCGGCTGAAGTG 3000
Qy 2972 TCAGACCGCTTTTGTGATTTGATGAGTGAAGAGGCTCCAGAGGCTGTGACCAATCA 3031
Db 3001 TCAGACCGCTTTTGTGATTTGATGAGTGAAGAGGCTCCAGAGGCTGTGACCAATCA 3060
Qy 3032 CAAATCTCTCTGCTGAGAGCGTACAGGTTTTCAGGCAATGTGTCTGAGCTCCATTTCA 3091
Db 3061 CAAATCTCTCTGCTGAGAGCGTACAGGTTTTCAGGCAATGTGTCTGAGCTCCATTTCA 3120
Qy 3092 TCAGCAAGTTTGGAGAAACCCACATTTTTCCTGCGGTATCTGTGACAGGCGCTCCCT 3151
Db 3121 TCAGCAAGTTTGGAGAAACCCACATTTTTCCTGCGGTATCTGTGACAGGCGCTCCCT 3180
Qy 3152 CTGCTACTTCATCTCTGAAAGCCAAAGAACCCAGAGGATGTGCTGGGGGCCAAGGGCGCGC 3211
Db 3181 CTGCTACTTCATCTCTGAAAGCCAAAGAACCCAGAGGATGTGCTGGGGGCCAAGGGCGCGC 3240
Qy 3212 CGGCGCTCTGCGCTCCGAGGCGCTGAGGCTGTGCAACCAAGCATTTCTCTCAAGCT 3271
Db 3241 CGGCGCTCTGCGCTCCGAGGCGCTGAGGCTGTGCAACCAAGCATTTCTCTCAAGCT 3300
Qy 3272 GACTGACACCGGTGTCACTACGTTGCACTGCTGAGGCTGCACTGAGGAGACGCCAGAGGCA 3331
Db 3301 GACTGACACCGGTGTCACTACGTTGCACTGCTGAGGCTGCACTGAGGAGACGCCAGAGGCA 3360
Qy 3332 GCTGAGTGGGAAGCTCCCGGGGAGCAGACGCTGACATGCTGAGGCGCGCAGCCAGACCGCGC 3391
Db 3361 GCTGAGTGGGAAGCTCCCGGGGAGCAGACGCTGACATGCTGAGGCGCGCAGCCAGACCGCGC 3420
Qy 3392 ACTGCCCTCAACTTCAAAACCATCTCTGAGTGAATGGCCACCGCCACAGCAGCGCGA 3451
Db 3421 ACTGCCCTCAACTTCAAAACCATCTCTGAGTGAATGGCCACCGCCACAGCAGCGCGA 3480
Qy 3452 GAGCAGACACCAAGCAGCGCTGTACAGCGGGGCTCTACGTCCTCAGGAGGAGGAGGGCGCC 3511
Db 3481 GAGCAGACACCAAGCAGCGCGTGTACAGCGGGGCTCTACGTCCTCAGGAGGAGGAGGGCGCC 3540
Qy 3512 CACACCAGGGCCGACACCGCTGAGAGTGTGAGAGGCTGAGTGTGTTGGCGAGGCGTG 3571
Db 3541 CACACCAGGGCCGACACCGCTGAGAGTGTGAGAGGCTGAGTGTGTTGGCGAGGCGTG 3600
Qy 3572 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGAGTGTCCAGCAAGGGCT 3631
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGAGTGTCCAGCAAGGGCT 3660
Qy 3632 GAGTGTCCAGACACCTGCGGCTTTCACCTCCACAGAGGCTGAGGCTGAGGCTCCACCCCA 3691
Db 3661 GAGTGTCCAGACACCTGCGGCTTTCACCTCCACAGAGGCTGAGGCTGAGGCTCCACCCCA 3720
Qy 3692 GGGCCAGCTTTTCTGACGAGAGCCCGGCTTCCACATCCGCAATATGGAATATGTCATCC 3751
Db 3721 GGGCCAGCTTTTCTGACGAGAGCCCGGCTTCCACATCCGCAATATGGAATATGTCATCC 3780
Qy 3752 CCAGATTCGCCATTTGTACCCCTGCGGCTGCGCTCTTGTGCTTCCACCCGCAACATCC 3811
Db 3781 CCAGATTCGCCATTTGTACCCCTGCGGCTGCGCTCTTGTGCTTCCACCCGCAACATCC 3840
Qy 3812 AGGTGAGAACCTGAGAAAGACCTGTGAGGCTGTGGAAATTTTGAAGTGAACCAAGAGTGTG 3871
Db 3841 AGGTGAGAACCTGAGAAAGACCTGTGAGGCTGTGGAAATTTTGAAGTGAACCAAGAGTGTG 3900
Qy 3872 CCCTGTACACAGGCGAGAGCCCTGTACCTGATGAGGAGTCCGTGTGGTCAAAATTTGGGGG 3931
Db 3901 CCCTGTACACAGGCGAGAGCCCTGTACCTGATGAGGAGTCCGTGTGGTCAAAATTTGGGGG 3960
Qy 3932 GAGGTGCTGTGGAGTAAATTAATGATATGATTTTCACTTTTGAATTTGAAAAA 3986
Db 3961 GAGGTGCTGTGGAGTAAATTAATGATATGATTTTCACTTTTGAATTTGAAAAA 4015


```
Db 901 CACCTTTGGAGGGGTGCGCTCTGTGGACGCGCACCTCCACCCATCCGTTGGGCCGCCCA 960
QY 968 GCACACACGCGGGGCCCCCATTCACATTCGCGGCCACACAGTCCCTGGGAGACAGCCTTGTCC 1027
Db 961 GCACACACGCGGGGCCCCCATTCACATTCGCGGCCACACAGTCCCTGGGAGACAGCCTTGTCC 1020
QY 1028 CCGGGGTAGCCGAGACCAACAGCACTTCTTACTCTCTCAGGCGACAGAGAGAGAGCTGCGC 1087
Db 1021 CCGGGGTAGCCGAGACCAACAGCACTTCTTACTCTCTCAGGCGACAGAGAGAGAGCTGCGC 1080
QY 1088 GCCCTCCCTTCCACTAGCTCTGTAGGCCAGCCTGACTGCGGCTCGAGAGGCTCGTGGGA 1147
Db 1081 GCCCTCCCTTCCACTAGCTCTGTAGGCCAGCCTGACTGCGGCTCGAGAGGCTCGTGGGA 1140
QY 1148 GACCATCTTCTGGTTCCAGAGCCCTGGATGCGAGGAGCTCCCGAGAGTTGCCCGCCCT 1207
Db 1141 GACCATCTTCTGGTTCCAGAGCCCTGGATGCGAGGAGCTCCCGAGAGTTGCCCGCCCT 1200
QY 1208 GCCCAGCGCTACTGGCAAAATCGGGCCCTTCTTCTGTGAGCTGTGGGAACACAGCGCA 1267
Db 1201 GCCCAGCGCTACTGGCAAAATCGGGCCCTTCTTCTGTGAGCTGTGGGAACACAGCGCA 1260
QY 1268 GTGCCCCAGCGGGTCTCTCAAGACGCACTGCCCCGCTCGAGCTGCGTCAACCCAGC 1327
Db 1261 GTGCCCCAGCGGGTCTCTCTCAAGACGCACTGCCCCGCTCGAGCTGCGTCAACCCAGC 1320
QY 1328 ACCCGGTGTCTGTGCCCGGAGAGAGCCCAAGGGCTGTGTGGCGGCCCGCGAGAGAGGA 1387
Db 1321 ACCCGGTGTCTGTGCCCGGAGAGAGCCCAAGGGCTGTGTGGCGGCCCGCGAGAGAGGA 1380
QY 1388 CACAGACCCCGCTGCGCTGATGCTGCTGCTCGGCACACACAGAGAGCCCTGGCAGGGTGA 1447
Db 1381 CACAGACCCCGCTGCGCTGATGCTGCTGCTCGGCACACACAGAGAGCCCTGGCAGGGTGA 1440
QY 1448 CGGCTGTGTGGGGGCGGCTGCGCGGGCTGTGGTCCCGCAGGCTCTGGGGAGCATGCCAA 1507
Db 1441 CGGCTGTGTGGGGGCGGCTGCGCGGGCTGTGGTCCCGCAGGCTCTGGGGAGCATGCCAA 1500
QY 1508 CACAGACGCCGCTTCTCTAGAGAACACAGAGATCATCTCCCTGGGAGAGCATGCCAA 1567
Db 1501 CACAGACGCCGCTTCTCTAGAGAACACAGAGATCATCTCCCTGGGAGAGCATGCCAA 1560
QY 1568 GCTCTGCTGACAGAGTACGTGAGAGANTGAGCGTGGGAGCTGGCTGTGGCTGCCAG 1627
Db 1561 GCTCTGCTGACAGAGTACGTGAGAGANTGAGCGTGGGAGCTGGCTGTGGCTGCCAG 1620
QY 1628 GAGCCACAGGGGTGGCTGTGTTCCGGCCGACAGAGACCTCTGCTGAGAGATCTGGC 1687
Db 1621 GAGCCACAGGGGTGGCTGTGTTCCGGCCGACAGAGACCTCTGCTGAGAGATCTGGC 1680
QY 1688 CAAGTTCCTGACAGGCTGATGATGATGTGTAGCTGTGAGCTGCTAGGCTCTTTCTTTA 1747
Db 1681 CAAGTTCCTGACAGGCTGATGATGATGTGTAGCTGTGAGCTGCTAGGCTCTTTCTTTA 1740
QY 1748 TGTCCAGAGACCAAGCTTTCAAAAGACAGGCTTTTCTACCGAGAGAGTGTGGAG 1807
Db 1741 TGTCCAGAGACCAAGCTTTCAAAAGACAGGCTTTTCTACCGAGAGAGTGTGGAG 1800
QY 1808 CAAGTTCGAAAGCATTTGGAATCAGACACACTTGAAGAGGGTGTGAGCTGTGGAGCTGTG 1867
Db 1801 CAAGTTCGAAAGCATTTGGAATCAGACACACTTGAAGAGGGTGTGAGCTGTGGAGCTGTG 1860
QY 1868 GGAAGCAGAGGTGAGCAGCATCGGAAAGCAGGCGCCGCTGCTGAGCTCAAGCTCG 1927
Db 1861 GGAAGCAGAGGTGAGCAGCATCGGAAAGCAGGCGCCGCTGCTGAGCTCAAGCTCG 1920
QY 1928 CTTTCATCCCAAGCTGACGGGCTGCGGCGCATTTGTGAACATGAGTACGTGTGGAGC 1987
Db 1921 CTTTCATCCCAAGCTGACGGGCTGCGGCGCATTTGTGAACATGAGTACGTGTGGAGC 1980
QY 1988 CAGAACGTTCCGAGAGAAAAAGAGGCGCAGAGCTGTACCTCAGAGGTGAAGGCACTGTT 2047
Db 1981 CAGAACGTTCCGAGAGAAAAAGAGGCGCAGAGCTGTACCTCAGAGGTGAAGGCACTGTT 2040
```

```
QY 2048 CAGGCTCTCACTACGAGCGGCGCGGCGCCCGGCTCTCTGGGCGCTCTGTGTGG 2107
Db 2041 CAGGCTCTCACTACGAGCGGCGCGGCGCCCGGCTCTCTGGGCGCTCTGTGTGG 2100
QY 2108 CCTGAGATATCCAGAGGGCTGGCGACCTTGTGTGCTGTGGCGGCCAGAGACC 2167
Db 2101 CCTGAGATATCCAGAGGGCTGGCGACCTTGTGTGCTGTGGCGGCCAGAGACC 2160
QY 2168 GCCGCTGAGCTGTA-----CATGCCCA 2191
Db 2161 GCCGCTGAGCTGTA-----CATGCCCA 2220
QY 2192 GGAACGCTCAGAGAGATACAGCAGATCATCAACCCGAAACATGATGCTGGG 2251
Db 2221 GGAACGCTCAGAGAGATACAGCAGATCATCAACCCGAAACATGATGCTGGG 2280
QY 2252 TCGGATGCGGTGTCCAGAGAGCCCGCATGGGCACTGCCAAGGCTTTCAAGAGCA 2311
Db 2281 TCGGATGCGGTGTCCAGAGAGCCCGCATGGGCACTGCCAAGGCTTTCAAGAGCA 2340
QY 2312 GGTCTTACCTTACAGACCTTCAGCCGTACATGCGACAGTTCTGTGCTCACTGACAGA 2371
Db 2341 GGTCTTACCTTACAGACCTTCAGCCGTACATGCGACAGTTCTGTGCTCACTGACAGA 2400
QY 2372 GACCAGCCCGCTGAGGAGATGCGTGTATCAGAGAGAGCTCTCCTGATGAGGCCAG 2431
Db 2401 GACCAGCCCGCTGAGGAGATGCGTGTATCAGAGAGAGCTCTCCTGATGAGGCCAG 2460
QY 2432 CAGTGGGCTCTTGACAGTCTTCTACGCTTCATGTGTCACACAGCGCGTGGCATGAGGG 2491
Db 2461 CAGTGGGCTCTTGACAGTCTTCTACGCTTCATGTGTCACACAGCGCGTGGCATGAGGG 2520
QY 2492 CAAGTCTACGTCAGATGCGAGAGGATCCGCGAGGGCTGCACTCTCTCAGCGCTGCG 2551
Db 2521 CAAGTCTACGTCAGATGCGAGAGGATCCGCGAGGGCTGCACTCTCTCAGCGCTGCG 2580
QY 2552 CAGCCTGTGCTACGCGGACATGAGAGAACAGCTGTTTGGCGGAGTTGGCGGACGGGCT 2611
Db 2581 CAGCCTGTGCTACGCGGACATGAGAGAACAGCTGTTTGGCGGAGTTGGCGGACGGGCT 2640
QY 2612 GCTCCTGCGTTTGGTGGATGATTTCTTGTGGTACACCTCACTCAACCCACGGGAAAC 2671
Db 2641 GCTCCTGCGTTTGGTGGATGATTTCTTGTGGTACACCTCACTCAACCCACGGGAAAC 2700
QY 2672 CTTCCCTAGAGACCCTGTGTCGAGGTGTCCTGAGTATGGCTACGTTGTAATTTGGGAA 2731
Db 2701 CTTCCCTAGAGACCCTGTGTCGAGGTGTCCTGAGTATGGCTACGTTGTAATTTGGGAA 2760
QY 2732 GACAGTGTGAATTCCTGTTGAAGAGACGAGGCCCTGGGTGGACAGGCTTTTGTTCAGAT 2791
Db 2761 GACAGTGTGAATTCCTGTTGAAGAGACGAGGCCCTGGGTGGACAGGCTTTTGTTCAGAT 2820
QY 2792 GCCGGCCACAGGCTATTCCTCGGTGGCGCTGCGTGTGATATCCCGAGACCTGGAGGT 2851
Db 2821 GCCGGCCACAGGCTATTCCTCGGTGGCGCTGCGTGTGATATCCCGAGACCTGGAGGT 2880
QY 2852 GCAGAGGACTACTCCAGCTATATGCCCGGACCTGCATCAGAGCAAGTCTCACCTTCAACG 2911
Db 2881 GCAGAGGACTACTCCAGCTATATGCCCGGACCTGCATCAGAGCAAGTCTCACCTTCAACG 2940
QY 2912 CGGCTTAAAGCTGGGAGAGACATGCTGCAAACTCTTTGGGGTCTTGGCGGTGAAGTG 2971
Db 2941 CGGCTTAAAGCTGGGAGAGACATGCTGCAAACTCTTTGGGGTCTTGGCGGTGAAGTG 3000
QY 2972 TCACAGGCTGTTTCTGATTTTCAAGTGAACAGCTTCACAGAGGTTGTCACCAACATCTA 3031
Db 3001 TCACAGGCTGTTTCTGATTTTCAAGTGAACAGCTTCACAGAGGTTGTCACCAACATCTA 3060
QY 3032 CAAGTCTCTCTCTCAGAGGCTACAGGTTTCAAGGATGTGTGTGAGCTCCCATTTCA 3091
Db 3061 CAAGTCTCTCTCTCAGAGGCTACAGGTTTCAAGGATGTGTGTGAGCTCCCATTTCA 3120
```


Db 2401 GACCAGCCCGCTGAGGATGCGCTGTCATCAGACAGACTCTCTGTAATGAGGCCAG 2460
 QY 2432 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 2491
 Db 2461 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 2520
 QY 2492 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 2551
 Db 2521 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 2580
 QY 2552 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 2611
 Db 2581 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 2640
 QY 2612 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 2671
 Db 2641 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 2700
 QY 2672 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 2731
 Db 2701 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 2760
 QY 2732 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 2791
 Db 2761 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 2820
 QY 2792 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 2851
 Db 2821 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 2880
 QY 2852 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 2911
 Db 2881 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 2940
 QY 2912 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 2971
 Db 2941 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3000
 QY 2972 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3031
 Db 3001 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3060
 QY 3032 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3091
 Db 3061 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3120
 QY 3092 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3151
 Db 3121 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3180
 QY 3152 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3211
 Db 3181 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3240
 QY 3212 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3271
 Db 3241 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3300
 QY 3272 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3331
 Db 3301 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3360
 QY 3332 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3391
 Db 3361 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3420
 QY 3392 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3451
 Db 3421 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3480
 QY 3452 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3511
 Db 3481 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3540

QY 3512 CACACCCAGGCGCCGACCGCTGGAGTCTGAGGCGCTGAGTGTGTTGGCCGAGGCGTG 3571
 Db 3541 CACACCCAGGCGCCGACCGCTGGAGTCTGAGGCGCTGAGTGTGTTGGCCGAGGCGTG 3600
 QY 3572 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3631
 Db 3601 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3660
 QY 3632 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3691
 Db 3661 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3720
 QY 3692 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3751
 Db 3721 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3780
 QY 3752 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3811
 Db 3781 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3840
 QY 3812 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3871
 Db 3841 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3900
 QY 3872 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3931
 Db 3901 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3960
 QY 3932 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 3986
 Db 3961 CAGTGGCCCTCTTGCAGCTCTCTTACGCTTCATGTGCGACACCGCGTGCATCAGAGG 4015

RESULT 4

US-10-054-295-224
 Sequence 224, Application US/10054295
 Publication No. US20030044953A1

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: No. US20030044953A1el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESSES:

ADDRESS: Two Embarcadero Center, 8th Floor

City: San Francisco

STATE: California

COUNTRY: United States of America

Zip: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/054,295

FILING DATE: 18-Jan-2002

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00293005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hprt"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-054-295-224

Query Match 99.1%; Score 3969; DB 9; Length 4015;
Best Local Similarity 99.1%; Prog No. 0;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 8 GAGAGCGCTGCTCTCTCTGCGACGTGGAAAGCCCTGGCCGACCCCGCGATGCC 67
DB 1 GAGAGCGCTGCTCTCTCTGCGACGTGGAAAGCCCTGGCCGACCCCGCGATGCC 60
QY 68 GCGGCTCCCGCTGCCGAGCCGTGCTCTCTCTGCGACGTGGAAAGCCCTGGCCG 127
DB 61 GCGGCTCCCGCTGCCGAGCCGTGCTCTCTCTGCGACGTGGAAAGCCCTGGCCG 120
QY 128 GCGGCTCCCGCTGCCGAGCCGTGCTCTCTCTGCGACGTGGAAAGCCCTGGCCG 187
DB 121 GCGGCTCCCGCTGCCGAGCCGTGCTCTCTCTGCGACGTGGAAAGCCCTGGCCG 180
QY 188 GGACCCGCGGCTTTCCGCGCGCTGGTGGCCAGTGGCTGGTGGCCCTGGGAGCG 247
DB 181 GGACCCGCGGCTTTCCGCGCGCTGGTGGCCAGTGGCTGGTGGCCCTGGGAGCG 240
QY 248 AGGCG 307
DB 241 AGGCG 300
QY 308 CCGAGTGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 367
DB 301 CCGAGTGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 360
QY 368 GGTGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 427
DB 361 GGTGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 420
QY 428 CCGTCCCAACAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 487
DB 421 CCGTCCCAACAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 480
QY 488 CCGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 547
DB 481 CCGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 540
QY 548 GGTGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 607
DB 541 GGTGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 600
QY 608 TCAGGCG 667
DB 601 TCAGGCG 660
QY 668 CTGAGACATAGCTCAGAGAGCGCGGAGTCCCTTGCGGCTGCGACCCCGGAG 727

DB 661 CTGAGACATAGCTCAGAGAGCGCGGAGTCCCTTGCGGCTGCGACCCCGGAG 720
QY 728 GAGCG 787
DB 721 GAGCG 780
QY 788 TGCCCTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 847
DB 781 TGCCCTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 840
QY 848 GCGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 907
DB 841 GCGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 900
QY 908 CACCTCTTTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 967
DB 901 CACCTCTTTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 960
QY 968 GCACCGAGCG 1027
DB 961 GCACCGAGCG 1020
QY 1028 CCGGCTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 1087
DB 1021 CCGGCTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 1080
QY 1088 GCGCT 1147
DB 1081 GCGCT 1140
QY 1148 GACCATCTTCTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAG 1207
DB 1141 GACCATCTTCTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAG 1200
QY 1208 GCCCGAGCGCTACTGCAAAATGCGGCGCGCTCTCTCTCTCTCTCTCTCTCTCT 1267
DB 1201 GCCCGAGCGCTACTGCAAAATGCGGCGCGCTCTCTCTCTCTCTCTCTCTCTCT 1260
QY 1268 GTGCCCTAGCGGAGGTGTCTCTCAAGACGACTGCGCGAGCTGCGGTCACCCAGC 1327
DB 1261 GTGCCCTAGCGGAGGTGTCTCTCAAGACGACTGCGCGAGCTGCGGTCACCCAGC 1320
QY 1328 AGCGGAGTGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAG 1387
DB 1321 AGCGGAGTGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAG 1380
QY 1388 CAGAGACCCCGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAG 1447
DB 1381 CAGAGACCCCGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAG 1440
QY 1448 CGGCTGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 1507
DB 1441 CGGCTGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 1500
QY 1508 CAGAGACCGCGCTCTCTCAAGACGACTGCGCGAGCTGCGGTCACCCAGC 1567
DB 1501 CAGAGACCGCGCTCTCTCAAGACGACTGCGCGAGCTGCGGTCACCCAGC 1560
QY 1568 GCTCTGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 1627
DB 1561 GCTCTGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 1620
QY 1628 GAGCCAGAGGTTGAGCTGTGTTCCGCGCGAGAGACCGTCTGAGAGGATCTGCGC 1687
DB 1621 GAGCCAGAGGTTGAGCTGTGTTCCGCGCGAGAGACCGTCTGAGAGGATCTGCGC 1680
QY 1688 CAAGTCTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 1747
DB 1681 CAAGTCTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTG 1740
QY 1748 TGTCTGAGAGACGAGCTTCAAGAGAGGCTTTTCTACCGAGAGATGTCTGAG 1807

Db 1741 TGTACGGAGACCACTTTTCAAAAGACAGGCTTTTCTTACCGGAAGACTGTCTGGAG 1800
Qy 1808 CAAGTTGCAAGACATTGGAAATCAGACAGCACTTGAAGAGGTGACGTGCGGAGACTGTC 1867
Db 1801 CAATTCGAAGACATTGGAAATCAGACAGCACTTGAAGAGGTGACGTGCGGAGACTGTC 1860
Qy 1868 GGAAGCAGAGGTGACAGCAGCATGCGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCG 1927
Db 1861 GGAAGCAGAGGTGACAGCAGCATGCGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCG 1920
Qy 1928 CTTATCCCCCAAGGCTGACGGGGCTGCGGGCGATTGTGAACATGGACTACGTGCGGGAGC 1987
Db 1921 CTTATCCCCCAAGGCTGACGGGGCTGCGGGCGATTGTGAACATGGACTACGTGCGGGAGC 1980
Qy 1988 CAGAAGCTTCCGACAGAGAAAAGAGGGCGAGCGTCTACCTCGAGAGGTGAAGGCACTGTT 2047
Db 1981 CAGAAGCTTCCGACAGAGAAAAGAGGGCGAGCGTCTACCTCGAGAGGTGAAGGCACTGTT 2040
Qy 2048 CAGCGTGTCACTACGAGCGGGCGGGCGCCCGGCTCTCTGGGCGCTGTGTCTGGG 2107
Db 2041 CAGCGTGTCACTACGAGCGGGCGGGCGCCCGGCTCTCTGGGCGCTGTGTCTGGG 2100
Qy 2108 CCGTAGAGATATCCACAGGGGCTGGCGACCTGTGCTGGGTGCGGGGGCCAGAGACC 2167
Db 2101 CCGTAGAGATATCCACAGGGGCTGGCGACCTGTGCTGGGTGCGGGGGCCAGAGACC 2160
Qy 2168 GCCGCTGAGCTGTA-----CATCCCCCA 2191
Db 2161 GCCGCTGAGCTGTA-----CATCCCCCA 2220
Qy 2192 GGACAGGCTCAGGAGGTATGCGCAGCATATCAAAACCCAGAGACAGTACTGCTGCG 2251
Db 2221 GGACAGGCTCAGGAGGTATGCGCAGCATATCAAAACCCAGAGACAGTACTGCTGCG 2280
Qy 2252 TCGGTATGCGGTGTCAGAGAGGGCGCCATGGGACGTCCGGAAGGCTTCAAGAGCA 2311
Db 2281 TCGGTATGCGGTGTCAGAGAGGGCGCCATGGGACGTCCGGAAGGCTTCAAGAGCA 2340
Qy 2312 CGTCTTACCTTGAACAGACCTCCAGCCGTACATGCGACAGTTCGTGGTCACTGACAGA 2371
Db 2341 CGTCTTACCTTGAACAGACCTCCAGCCGTACATGCGACAGTTCGTGGTCACTGACAGA 2400
Qy 2372 GACCAGCCCGGTGAGGATGCGGTGTCATGAGCAGAGTCTTCCCTGAATGAGGCCAG 2431
Db 2401 GACCAGCCCGGTGAGGATGCGGTGTCATGAGCAGAGTCTTCCCTGAATGAGGCCAG 2460
Qy 2432 CAGTGGGCTTTCAGACGTCCTACGCTCATGTCATGTCACACAGCGCGGCATCAGGGG 2491
Db 2461 CAGTGGGCTTTCAGACGTCCTACGCTCATGTCATGTCACACAGCGCGGCATCAGGGG 2520
Qy 2492 CAAGTCTTACGTCCAGTGCAGAGGGATCCGACAGGGCTCATCTCTCCAGCTGCTG 2551
Db 2521 CAAGTCTTACGTCCAGTGCAGAGGGATCCGACAGGGCTCATCTCTCCAGCTGCTG 2580
Qy 2552 CAGGCTGTGTCAGGGCAGACATGGAGAACAGCTGTTGCGGGGAGTTCGGCGGGAGCGGCT 2611
Db 2581 CAGGCTGTGTCAGGGCAGACATGGAGAACAGCTGTTGCGGGGAGTTCGGCGGGAGCGGCT 2640
Qy 2612 GCTTCTCGTTGGTGTGATGATTTCTTGTGTTGTTGACACCTACCTCACCACCGGAAAAC 2671
Db 2641 GCTTCTCGTTGGTGTGATGATTTCTTGTGTTGTTGACACCTACCTCACCACCGGAAAAC 2700
Qy 2672 CTTCTTACAGACCTGTGTCGAGGTGTCTGAGTATGCTGCGTGTGAATTTGGCGAA 2731
Db 2701 CTTCTTACAGACCTGTGTCGAGGTGTCTGAGTATGCTGCGTGTGAATTTGGCGAA 2760
Qy 2732 GACAGGTGTGAATTTCCCTGTGAAGAGAGAGCCCTGGGTGGACGCGTTTGTTCAGAT 2791
Db 2761 GACAGGTGTGAATTTCCCTGTGAAGAGAGAGCCCTGGGTGGACGCGTTTGTTCAGAT 2820
Qy 2792 GCCGAGCCACAGGCTATTTCCCTGCTGCGGCTCTGCTGATATACCGGACCTGAGAGT 2851
Db 2821 GCCGAGCCACAGGCTATTTCCCTGCTGCGGCTCTGCTGATATACCGGACCTGAGAGT 2880

Qy 2852 GCAGAGGCACTACTCCACCTATGCCCGGACCTCCATCAGAGCCAGTCTACCTTCAACCG 2911
Db 2881 GCAGAGGCACTACTCCACCTATGCCCGGACCTCCATCAGAGCCAGTCTACCTTCAACCG 2940
Qy 2912 CGGCTTCAAGGCTGGAGGAACATGCGTCCGAACCTCTTTGGGGCTTGGCGCTGAAGT 2971
Db 2941 CGGCTTCAAGGCTGGAGGAACATGCGTCCGAACCTCTTTGGGGCTTGGCGCTGAAGT 3000
Qy 2972 TCACAGGCTGTTTGGATTGGATTGAGGTGAACAGCTCCAGACGGGTGTCACCAATCTA 3031
Db 3001 TCACAGGCTGTTTGGATTGGATTGAGGTGAACAGCTCCAGACGGGTGTCACCAATCTA 3060
Qy 3032 CAAGATCCCTCTGCTGACAGGCGTACAGGTTTCACGATGTGTGCTGACGTCCCATTTCA 3091
Db 3061 CAAGATCCCTCTGCTGACAGGCGTACAGGTTTCACGATGTGTGCTGACGTCCCATTTCA 3120
Qy 3092 TCAGCAATTTGGAAGAACCCACATTTTCTCGCGCTCATCTCTGACAGGCTCCCT 3151
Db 3121 TCAGCAATTTGGAAGAACCCACATTTTCTCGCGCTCATCTCTGACAGGCTCCCT 3180
Qy 3152 CTGCTACTCCATCCGTAAGAGCCAGAAACGACAGGGATGTGCGTGGGGGCGCAAGGGCGCG 3211
Db 3181 CTGCTACTCCATCCGTAAGAGCCAGAAACGACAGGGATGTGCGTGGGGGCGCAAGGGCGCG 3240
Qy 3212 CGGCTCTCTGCTCCGAGGCGTGCAGTGTGCTGTCACCAAGCATTCCTGCTCAAGCT 3271
Db 3241 CGGCTCTCTGCTCCGAGGCGTGCAGTGTGCTGTCACCAAGCATTCCTGCTCAAGCT 3300
Qy 3272 GACTGACACCGGTGTACCTACGTGCCACTCTCTGGGGTCACTCAGAGACGCCAGAGCA 3331
Db 3301 GACTGACACCGGTGTACCTACGTGCCACTCTCTGGGGTCACTCAGAGACGCCAGAGCA 3360
Qy 3332 GCTGAGTGGGAAGTCCCGGGGAGAGAGCTGACTGCTTGGAGGCGCGGCAACCCGCG 3391
Db 3361 GCTGAGTGGGAAGTCCCGGGGAGAGAGCTGACTGCTTGGAGGCGCGGCAACCCGCG 3420
Qy 3392 ACTGCGCTCAGACTTCAAGACATCTGAGTGTGAGTGGCCACCGCCACAGCCAGGCGCA 3451
Db 3421 ACTGCGCTCAGACTTCAAGACATCTGAGTGTGAGTGGCCACCGCCACAGCCAGGCGCA 3480
Qy 3452 GAGCAGACACGAGAGCCCTTCAAGCGCGGGCTCTAGCTCCCAAGGAGAGGGGGCGCC 3511
Db 3481 GAGCAGACACGAGAGCCCTTCAAGCGCGGGCTCTAGCTCCCAAGGAGAGGGGGCGCC 3540
Qy 3512 CACACCCAGGCGCCAGCGCTGGAGTGTGAGGCTGAGTGTGAGTGTGGCGGAGGCTG 3571
Db 3541 CACACCCAGGCGCCAGCGCTGGAGTGTGAGGCTGAGTGTGAGTGTGGCGGAGGCTG 3600
Qy 3572 CATGTCGGGTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGAGTGTCCAGCCAAAGGCT 3631
Db 3601 CATGTCGGGTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGAGTGTCCAGCCAAAGGCT 3660
Qy 3632 GAGTGTCCAGACACCTGCGGCTTCACTTCCACAGGCGGGGCGTGGCTCCACCCCA 3691
Db 3661 GAGTGTCCAGACACCTGCGGCTTCACTTCCACAGGCGGGGCGTGGCTCCACCCCA 3720
Qy 3692 GGGCGAGCTTTCCTACACAGAGCGCGGCTTCCACTCCCAATAGAAATAGTCAATCC 3751
Db 3721 GGGCGAGCTTTCCTACACAGAGCGCGGCTTCCACTCCCAATAGAAATAGTCAATCC 3780
Qy 3752 CCAGATTCGCCATTGTTCACCCCTGCGCTGCTCTTTCCTTCCACCCCAACATCC 3811
Db 3781 CCAGATTCGCCATTGTTCACCCCTGCGCTGCTCTTTCCTTCCACCCCAACATCC 3840
Qy 3812 AGGTGGAGACCTGTGAAGAGACCCCTGGGAGTGTGGGAATTTGGAGTACCAAGGTGTG 3871
Db 3841 AGGTGGAGACCTGTGAAGAGACCCCTGGGAGTGTGGGAATTTGGAGTACCAAGGTGTG 3900
Qy 3872 CCCTGTACACAGGGAGAGACCTGACCTGATGAGGGTTCCTGTTGGGTCAAAATTTGGGG 3931
Db 3901 CCCTGTACACAGGGAGAGACCTGACCTGATGAGGGTTCCTGTTGGGTCAAAATTTGGGG 3960

QY 3932 GAGCTCTGTGGAGATAAATAGTATATATGATTTTTCAGTTTGAAGAAAA 3986
Db 3961 GAGGTCTGTGGAGATAAATAGTATATATGATTTTTCAGTTTGAAGAAAA 4015

RESULT 5

US-10-208-243-1
: Sequence 1, Application US/10208243
: Publication No. US20030044394A1
: GENERAL INFORMATION:
: APPLICANT: Gaeta, Federico C. A.
: APPLICANT: Genon Corporation
: TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
: TITLE OF INVENTION: Response to a Telomerase Antigen
: FILE REFERENCE: 015389-003500PC
: CURRENT APPLICATION NUMBER: US/10/208, 243
: CURRENT FILING DATE: 2002-07-30
: PRIOR APPLICATION NUMBER: US/09/675, 321
: PRIOR FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: US 60/112, 006
: PRIOR FILING DATE: 1998-03-31
: PRIOR APPLICATION NUMBER: WO PCT/US99/06898
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 4015
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (56)..(3454)
: OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
US-10-208-243-1

Query Match 99.1%; Score 3969; DB 9; Length 4015;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 8 GCAGCGTCTGCTCTGTCGCAAGTGGAGAACCTTGGCCCGCCGACCCCGGATGCC 67
Db 1 GCAGCGTCTGCTCTGTCGCAAGTGGAGAACCTTGGCCCGCCGACCCCGGATGCC 60
QY 68 GCGCGTCTGCTCTGTCGCAAGTGGAGAACCTTGGCCCGCCGACCCCGGATGCC 127
Db 61 GCGCGTCTGCTCTGTCGCAAGTGGAGAACCTTGGCCCGCCGACCCCGGATGCC 120
QY 128 GCGCGTCTGCTCTGTCGCAAGTGGAGAACCTTGGCCCGCCGACCCCGGATGCC 187
Db 121 GCGCGTCTGCTCTGTCGCAAGTGGAGAACCTTGGCCCGCCGACCCCGGATGCC 180
QY 188 GCGCGTCTGCTCTGTCGCAAGTGGAGAACCTTGGCCCGCCGACCCCGGATGCC 247
Db 181 GCGCGTCTGCTCTGTCGCAAGTGGAGAACCTTGGCCCGCCGACCCCGGATGCC 240
QY 248 GCGCGTCTGCTCTGTCGCAAGTGGAGAACCTTGGCCCGCCGACCCCGGATGCC 307
Db 241 GCGCGTCTGCTCTGTCGCAAGTGGAGAACCTTGGCCCGCCGACCCCGGATGCC 300
QY 308 GCGAGTCTGTCAGAGGCTGTGCGAGCGCGCGCAAGAACGTGCTGCTGCGCTTGGC 367
Db 301 CCGAGTCTGTCAGAGGCTGTGCGAGCGCGCGCAAGAACGTGCTGCTGCGCTTGGC 360
QY 368 GCTGTGTCAGAGGCG 427
Db 361 GCTGTGTCAGAGGCG 420
QY 428 CCGGCCAACAGAGTGAACGACGACTGCGGAGGAGCGGCGCGCGCGCGCGCGCGCG 487
Db 421 CCGGCCAACAGAGTGAACGACGACTGCGGAGGAGCGGCGCGCGCGCGCGCGCGCG 480
QY 488 CCGCGTGGGCGACGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547

Db 481 CCGCGTGGGCGACGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 548 GCGTCTGTCAGAGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
Db 541 GCGTCTGTCAGAGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 608 TCAGGCG 667
Db 601 TCAGGCG 660
QY 668 CCGAGCAATAGCGTCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
Db 661 CCGAGCAATAGCGTCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 728 GAGGCGCGGCG 787
Db 721 GAGGCGCGGCG 780
QY 788 TCGCCCTGAGCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
Db 781 TCGCCCTGAGCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 848 GCGTGAACGAGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 907
Db 841 GCGTGAACGAGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 908 CACCTCTTGGAGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 967
Db 901 CACCTCTTGGAGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 968 GCG 1027
Db 961 GCG 1020
QY 1028 CCGGCTGACCGCGAGCAACGACGACTTCTCTACTCTCTGAGCGAGCAAGGAGCTGCG 1087
Db 1021 CCGGCTGACCGCGAGCAACGACGACTTCTCTACTCTCTGAGCGAGCAAGGAGCTGCG 1080
QY 1088 GCGCTCTTCTACTGACTGCTGCTGAGCGCGAGCGTACGAGCGTCTGAGGCTCTGGA 1147
Db 1081 GCGCTCTTCTACTGACTGCTGCTGAGCGCGAGCGTACGAGCGTCTGAGGCTCTGGA 1140
QY 1148 GACCATCTTCTGAGGCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1207
Db 1141 GACCATCTTCTGAGGCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1200
QY 1208 GCGCGAGGCTACTGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1267
Db 1201 GCGCGAGGCTACTGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
QY 1268 GCGCGCTAGCGGCTGCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1327
Db 1261 GCGCGCTAGCGGCTGCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
QY 1328 AGCGGTGCTGTGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1387
Db 1321 AGCGGTGCTGTGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
QY 1388 CACAGACCGCGGTGCTGCTGAGCGTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1447
Db 1381 CACAGACCGCGGTGCTGCTGAGCGTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1440
QY 1448 CCGCTCTGTCGCGGCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1507
Db 1441 CCGCTCTGTCGCGGCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1500
QY 1508 CAAAGCAAGCGCGCTTCTCTGAGCAACCAAGCAATGATCTCTCTGAGGAGCAATGCA 1567
Db 1501 CAAAGCAAGCGCGCTTCTCTGAGCAACCAAGCAATGATCTCTCTGAGGAGCAATGCA 1560
QY 1568 GCTCTGCTGTCAGAGAGTGAACGAGTGAAGATGAGCGTGTGCGGAGTGTGCTGCGCAG 1627
Db 1561 GCTCTGCTGTCAGAGAGTGAACGAGTGAAGATGAGCGTGTGCGGAGTGTGCTGCGCAG 1620

QY	1638	GACCCAGGGGGTGGCGTGGTTCGGGGCCGACAGACCGTCTGGCTGAGGAGATCTCGGC	1687
Dp	1621	GAGCCACAGGGGGTGGCGTGGTTCGGGGCCGACAGACCGTCTGGCTGAGGAGATCTCGGC	1680
QY	1688	CAAGTTCCTGACACTGGGCTGATGAGTGTGATACGTCTGCGAGTGCCTCAAGTCTTTCTTTA	1747
Dp	1681	CAAGTTCCTGACACTGGGCTGATGAGTGTGATACGTCTGCGAGTGCCTCAAGTCTTTCTTTA	1740
QY	1748	TGTACAGGAGACCAAGCTTTCAAAAACAGGCTCTTTTTCATACGGGAAGAGTGTCTGGAG	1807
Dp	1741	TGTACAGGAGACCAAGCTTTCAAAAACAGGCTCTTTTTCATACGGGAAGAGTGTCTGGAG	1800
QY	1808	CAAGTTCGAAGCAATTGGAAATCAGACAGACTTGAAGAAGGGGCGACGTGCGAGAGCTGTGTC	1867
Dp	1801	CAAGTTCGAAGCAATTGGAAATCAGACAGACTTGAAGAAGGGGCGACGTGCGAGAGCTGTGTC	1860
QY	1868	GGAAGCAGAGGTACAGGCAGCATGCGGAGAACCAAGGCCCGGCTGCTGACGTCCAGACTCCG	1927
Dp	1861	GGAAGCAGAGGTACAGGCAGCATGCGGAGAACCAAGGCCCGGCTGCTGACAGTCCAGACTCCG	1920
QY	1928	CTTCATCCCAAGCTGACGGGGGCTGGGGCGAATTGGAACATGAGACTGTACGTGCGGGAGC	1987
Dp	1921	CTTCATCCCAAGCTGACGGGGGCTGGGGCGAATTGGAACATGAGACTGTACGTGCGGGAGC	1980
QY	1988	CAGAACGTTCCGAGAGAAAAAGAGGGCCGACGGCTCTCAACTCTGAGAGGTGAAGGCACTGTT	2047
Dp	1981	CAGAACGTTCCGAGAGAAAAAGAGGGCCGACGGCTCTCAACTCTGAGAGGTGAAGGCACTGTT	2040
QY	2048	CAGGCTGCTCAACTACGAGAGGGGGCGGGGGCCCGGCTCTCTGGGGGCTCTGTGCTGGG	2107
Dp	2041	CAGGCTGCTCAACTACGAGAGGGGGCGGGGGCCCGGCTCTCTGGGGGCTCTGTGCTGGG	2100
QY	2108	CCTTGACGATATCTACAGAGGGCTGCGGCGCACTTCTGTGCTGTGCGGGGCCAGAGAACCC	2167
Dp	2101	CCTTGACGATATCTACAGAGGGCTGCGGCGCACTTCTGTGCTGTGCGGGGCCAGAGAACCC	2160
QY	2168	GCGCGCTGACCTGTA-----CATCCCCA	2191
Dp	2161	GCGCGCTGACCTGTA-----CATCCCCA	2220
QY	2192	GGAAGAGCTCAGAGAGGTCTATCCGCAAGATCATCAAAACCCCAAGACAGTACTCGTGGCG	2251
Dp	2221	GGAAGAGCTCAGAGAGGTCTATCCGCAAGATCATCAAAACCCCAAGACAGTACTCGTGGCG	2280
QY	2252	TCGGATATGCGTGGTCCAGAAAGGCGGCCCATGAGGCACTGTCGCAAGGCGTTCAAGAGCCA	2311
Dp	2281	TCGGATATGCGTGGTCCAGAAAGGCGGCCCATGAGGCACTGTCGCAAGGCGTTCAAGAGCCA	2340
QY	2312	CGTCTACCTGACAGACCTCCAGGCGGATGAGAGAGAGGAGAGGTCGAGGCTCACGTGACAGGA	2371
Dp	2341	CGTCTACCTGACAGACCTCCAGGCGGATGAGAGAGAGGAGAGGTCGAGGCTCACGTGACAGGA	2400
QY	2372	GACCAGCCGCTGAGGAGATCCCTCTCTCATGACAGCAGAGAGCTCTCCGAATGAGGGCAG	2431
Dp	2401	GACCAGCCGCTGAGGAGATCCCTCTCTCATGACAGCAGAGAGCTCTCCGAATGAGGGCAG	2460
QY	2432	CAGTGGCTCTTGAGAGTCTTCTATAGCTTCATGTGCCACACAGCGCTGCGCATACAGGG	2491
Dp	2461	CAGTGGCTCTTGAGAGTCTTCTATAGCTTCATGTGCCACACAGCGCTGCGCATACAGGG	2520
QY	2492	CAATCTCTACGTCCAGTGCAGGAGGAGATCCCGAGGGGCTCATCTCTCCACAGCTGCTGTG	2551
Dp	2521	CAATCTCTACGTCCAGTGCAGGAGGAGATCCCGAGGGGCTCATCTCTCCACAGCTGCTGTG	2580
QY	2552	CAGGCTTGGCTACGGCGACATGTGAGAAACAAGCTGTTTGGCGGGATTCGGCGGGACGGGCT	2611
Dp	2581	CAGGCTTGGCTACGGCGACATGTGAGAAACAAGCTGTTTGGCGGGATTCGGCGGGACGGGCT	2640
QY	2612	GCCTCTCGCTTGGTGGATGATTTCTTGTGGTGACACTCATCTCACCACAGGGAAC	2671
Dp	2641	GCCTCTCGCTTGGTGGATGATTTCTTGTGGTGACACTCATCTCACCACAGGGAAC	2700

QY	2672	CTCCTCCAGAGACCCTGGTCCGAGGTCGCCGAGTATGTCGCGGGGAGCTTCGGGAA	2731
Db	2701	CTTCCTCCAGAGACCCTGGTCCGAGGTCGCCGAGTATGTCGCGGGGAGCTTCGGGAA	2760
QY	2732	GACAGTGGATGAACCTCCCTGTAGAAGACGAGAGCCCTGGGTGGACGAGCTTTTGTTCAGAT	2791
Db	2761	GACAGTGGATGAACCTCCCTGTAGAAGACGAGAGCCCTGGGTGGACGAGCTTTTGTTCAGAT	2820
QY	2792	GCCGGGCCACGAGGCTATTTCCTGGTGGCGGCTGCTGTCGTGATACCCGGACCTTGGAGT	2861
Db	2821	GCCGGGCCACGAGGCTATTTCCTGGTGGCGGCTGCTGTCGTGATACCCGGACCTTGGAGT	2880
QY	2852	GCAGAGCGACACTACTCCACTATGCCCCGAGACCTCCATCAGACGACAGTCCACCTTCAACCG	2911
Db	2881	GCAGAGCGACACTACTCCACTATGCCCCGAGACCTCCATCAGACGACAGTCCACCTTCAACCG	2940
QY	2912	CGGCTTCAAGGCTGGGAGAACATCTGTCGCAAACTCTTTGGGGTCTGTCGGCTGAAGTG	2971
Db	2941	CGGCTTCAAGGCTGGGAGAACATCTGTCGCAAACTCTTTGGGGTCTGTCGGCTGAAGTG	3000
QY	2972	TCACAGCCTGTATTTCGATTTTGCAGGTGAACAGCCTCCAGACGGGTGACACCAACATCTA	3031
Db	3001	TCACAGCCTGTATTTCGATTTTGCAGGTGAACAGCCTCCAGACGGGTGACACCAACATCTA	3060
QY	3032	CAAGTCTCTCTGCTGCGAGGGGTACAGGTTCACGCAATGTGCTGCGAGCTCCCATTTTCA	3091
Db	3061	CAAGTCTCTCTGCTGCGAGGGGTACAGGTTCACGCAATGTGCTGCGAGCTCCCATTTTCA	3120
QY	3092	TCAGCAAGTTTGGAAAGAACCCACATTTTTCCTGGGCTCACTCTCTGACAGGGCTCCCT	3151
Db	3121	TCAGCAAGTTTGGAAAGAACCCACATTTTTCCTGGGCTCACTCTCTGACAGGGCTCCCT	3180
QY	3152	CTGCTACTCCATCTCTGAAAAGCCAAAGACGACGAGGATGTGCTGGGGGCCAAAGGGCGCCG	3211
Db	3181	CTGCTACTCCATCTCTGAAAAGCCAAAGACGACGAGGATGTGCTGGGGGCCAAAGGGCGCCG	3240
QY	3212	CGGCGCTCTGCCCTCCGAGGGCCGTGACAGTGGCTGTGCGCACCAGATTCCTGCTCAAGCT	3271
Db	3241	CGGCGCTCTGCCCTCCGAGGGCCGTGACAGTGGCTGTGCGCACCAGATTCCTGCTCAAGCT	3300
QY	3272	GACTGCGACACCGTGCACACTACAGTGCACACTCTGCGGGTCACTCAGAGACGCCAGACGA	3331
Db	3301	GACTGCGACACCGTGCACACTACAGTGCACACTCTGCGGGTCACTCAGAGACGCCAGACGA	3360
QY	3332	GCTGAGTGGGAAGCTCCCGGGGACGACGCTGACTGCCCTGAGAGGCCGACGCCAACCCGGC	3391
Db	3361	GCTGAGTGGGAAGCTCCCGGGGACGACGCTGACTGCCCTGAGAGGCCGACGCCAACCCGGC	3420
QY	3392	ACTGCCCTCAGACTTCAAGACCATCTCTGGACTGATGAGCCACCCGCCACACGAGCCGA	3451
Db	3421	ACTGCCCTCAGACTTCAAGACCATCTCTGGACTGATGAGCCACCCGCCACACGAGCCGA	3480
QY	3452	GAGCAGACACCGACGACGCCCTGTACAGCGCGGCTCTACCTCCAGGAGAGGAGGGCGGC	3511
Db	3481	GAGCAGACACCGACGACGCCCTGTACAGCGCGGCTCTACCTCCAGGAGAGGAGGGCGGC	3540
QY	3512	CACACCCAGGCCGACACCGTGGGAGTCTGAAGCCCTGAAGTGTGTTGGCCGAGGCCGTG	3571
Db	3541	CACACCCAGGCCGACACCGTGGGAGTCTGAAGCCCTGAAGTGTGTTGGCCGAGGCCGTG	3600
QY	3572	CATGTCGGGCTGAAGGCTGATGTCTCCGCTGAAGCCTTAAGCGAGTGTCCACGCAAGGGCT	3631
Db	3601	CATGTCGGGCTGAAGGCTGATGTCTCCGCTGAAGCCTTAAGCGAGTGTCCACGCAAGGGCT	3660
QY	3632	GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGAGGTGGGGCTGCGGCTCCACCCCA	3691
Db	3661	GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGAGGTGGGGCTGCGGCTCCACCCCA	3720
QY	3692	GGGCGACGTTTTTCTCACCAGAGGCCGGCTTCCACTCTCCCAATAGAGAAATAGTCCATCC	3751
Db	3721	GGGCGACGTTTTTCTCACCAGAGGCCGGCTTCCACTCTCCCAATAGAGAAATAGTCCATCC	3780
QY	3752	CCAGATTTGGCCATTGTTCACCCCTTGCCCTGCTCTTGTGCTTCCACCCCAACATCC	3811

Db 3781 CCGAGATGCGCCATGTCACCCCTGCGCCCTGCTCCCTTGGCTCCACCCACCATCC 3840
 QY 3812 AGGTGAGACCCCTGAGAAGACCCCTGGAGCTCTGGGAATTTTGGAGTACCAAGCTGTG 3871
 Db 3841 AGGTGAGACCCCTGAGAAGACCCCTGGAGCTCTGGGAATTTTGGAGTACCAAGCTGTG 3900
 QY 3872 CCCCTAGACAGGCGAGACCCCTGACACCTGAGTATGGGGTCCCTGTGGTCAAAATTTGGGGG 3931
 Db 3901 CCCCTAGACAGGCGAGACCCCTGACACCTGAGTATGGGGTCCCTGTGGTCAAAATTTGGGGG 3960
 QY 3932 GAGGTGCTGTGGAGTAAATATGATATATGATTTTTCAGTTTGAAGAAAAA 3986
 Db 3961 GAGGTGCTGTGGAGTAAATATGATATATGATTTTTCAGTTTGAAGAAAAA 4015

RESULT 6

US-10-054-611-224
 : Sequence 224: Application US/10054611
 : Publication No. US20030059787A1
 : GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Langner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: No. US20030059787A1el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS: Townsend and Townsend and Crew LLP

ADDRESS: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/10/054,611

FILING DATE: 18-Jan-2002

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/846,017

FILING DATE: 23-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 224:

SEQUENCE CHARACTERISTICS:

LENGTH: 4015 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 56..3454

OTHER INFORMATION: /Product= "hprt"

; /note= "human telomerase reverse
 ; transcriptase (hprt) catalytic protein
 ; component"
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 224:
 US-10-054-611-224

Query Match 99.1%; Score 3969; DB 9; Length 4015;
 Best Local Similarity 99.1%; Pred. No. 0;
 Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 8 GCAGCGTGCCTCCCTGCTGCGACGTGGAGAGCCCTGGCCCGCCGACCCCGGATGCC 67
 Db 1 GCAGCGTGCCTCCCTGCTGCGACGTGGAGAGCCCTGGCCCGCCGACCCCGGATGCC 60
 QY 68 GCGGCTCCCGCGCGCGAGCCGCTGCTCCCTGCTGCGACGTGGAGAGCCCTGGCCCG 127
 Db 61 GCGGCTCCCGCGCGCGAGCCGCTGCTCCCTGCTGCGACGTGGAGAGCCCTGGCCCG 120
 QY 128 GCGGCTCCCGCGCGCGAGCCGCTGCTCCCTGCTGCGACGTGGAGAGCCCTGGCCCG 187
 Db 121 GCGGCTCCCGCGCGCGAGCCGCTGCTCCCTGCTGCGACGTGGAGAGCCCTGGCCCG 180
 QY 188 GCAGCGCGCGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 247
 Db 181 GCAGCGCGCGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 QY 248 ACAGCGCGCGCGCGCGCGCGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 307
 Db 241 ACAGCGCGCGCGCGCGCGCGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 QY 308 CCGAGTGTGTCAGAGAGGTGTGTCAGAGAGCGGCGCGAGAGAGAGAGAGAGAGAGAGAG 367
 Db 301 CCGAGTGTGTCAGAGAGGTGTGTCAGAGAGCGGCGCGAGAGAGAGAGAGAGAGAGAGAG 360
 QY 368 GCTGTGTCAG 427
 Db 361 GCTGTGTCAG 420
 QY 428 CCGTCCCAACAGAGGTGTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487
 Db 421 CCGTCCCAACAGAGGTGTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 QY 488 CCGTCCCAACAGAGGTGTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 547
 Db 481 CCGTCCCAACAGAGGTGTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 548 GCGTCCCAACAGAGGTGTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 607
 Db 541 GCGTCCCAACAGAGGTGTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
 QY 608 TCAGGCGCGCGCGCGCGCGAG 667
 Db 601 TCAGGCGCGCGCGCGCGCGAG 660
 QY 668 CTGGAACCATATGCTCAG 727
 Db 661 CTGGAACCATATGCTCAG 720
 QY 728 GAGGCGCGGCGCGAGTGTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 787
 Db 721 GAGGCGCGGCGCGAGTGTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 QY 788 TCAGGCGCGCGCGCGCGAG 847
 Db 781 TCAGGCGCGCGCGCGCGAG 840
 QY 848 GCGTGTGACGAGTGTGTCAG 907
 Db 841 GCGTGTGACGAGTGTGTCAG 900
 QY 908 CACCTCTTGGAGAGGTGCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 967
 Db 901 CACCTCTTGGAGAGGTGCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960

OY	1968	GACACAGCGGGGGCCCCCAATCCACATTCGGGGCCACACAGCTCCCTGGAGACGCTTGTGC	1027
Db	961	GCACACAGCGGGGGCCCCCAATCCACATTCGGGGCCACACAGCTCCCTGGAGACGCTTGTGC	1020
OY	1028	CCGGGTGACCCCGACAGACCAAGCACTTCCCTCTACTCTCTAGGCGACAGAGACAGCTGCG	1087
Db	1021	CCGGGTGACCCCGACAGACCAAGCACTTCCCTCTACTCTCTAGGCGACAGAGACAGCTGCG	1080
OY	1088	GCCTTCCTTCTACTCAGCTCTCTGAGGCCAGACTGACTGGCGCTCGAGAGCTCTGCGA	1147
Db	1081	GCCTTCCTTCTACTCAGCTCTCTGAGGCCAGACTGACTGGCGCTCGAGAGCTCTGCGA	1140
OY	1148	GACCATCTTCTGGGTTCAGAGGCCCTTGAGTGGCCAGAGGACTCCCGAGATTGCCCGGCT	1207
Db	1141	GACCATCTTCTGGGTTCAGAGGCCCTTGAGTGGCCAGAGGACTCCCGAGATTGCCCGGCT	1200
OY	1208	GCCCCAGCGCTACTGGCAAAATGGCGGCCCTGTATTGAGAGCTGCTTGGGAACACAGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAAAATGGCGGCCCTGTATTGAGAGCTGCTTGGGAACACAGCGCA	1260
OY	1268	GTGCCCCCTAGCGGGGTGCTCTCTCAAGACGCACTGCCGTGCGAGCTGGGGTACCCACAGC	1327
Db	1261	GTGCCCCCTAGCGGGGTGCTCTCTCAAGACGCACTGCCGTGCGAGCTGGGGTACCCACAGC	1320
OY	1328	AGCGGTGTCTGTCTGCCGGGAGAAAGCCCAAGGAGCTTGTGGGGGCCCCCGAGAGAGAGA	1387
Db	1321	AGCGGTGTCTGTCTGCCGGGAGAAAGCCCAAGGAGCTTGTGGGGGCCCCCGAGAGAGAGA	1380
OY	1388	CACAGACCCCGCTGCTGTGTCAGAGCTGCTCCGCGACAGACAGACCCCTGGAGGTGA	1447
Db	1381	CACAGACCCCGCTGCTGTGTCAGAGCTGCTCCGCGACAGACAGACCCCTGGAGGTGA	1440
OY	1448	CGGGTGTGTGGGGGCTGGCTGGGGCGGGGTGGGGGCCCGAGGCGTGTGGGGCTCCAGGCA	1507
Db	1441	CGGGTGTGTGGGGGCTGGCTGGGGCGGGGTGGGGGCCCGAGGCGTGTGGGGCTCCAGGCA	1500
OY	1508	CAAGGAAGCGCGCTTCTCTCAGAGAACACAAAGATTCATCTCCCTGGGGAAAGCATGCCAA	1567
Db	1501	CAAGGAAGCGCGCTTCTCTCAGAGAACACAAAGATTCATCTCCCTGGGGAAAGCATGCCAA	1560
OY	1568	GCTCTCGCTGACAGAGCTGACGCTGGAAGATGAGCGTGGCGGACTGCGCTTGGCTGCGAG	1627
Db	1561	GCTCTCGCTGACAGAGCTGACGCTGGAAGATGAGCGTGGCGGACTGCGCTTGGCTGCGAG	1620
OY	1628	GAGCCACAGGGGTGGCGTGTCCCGGCGGAGAGACGCTGCGGCGTGAAGAGATCTGTGC	1687
Db	1621	GAGCCACAGGGGTGGCGTGTCCCGGCGGAGAGACGCTGCGGCGTGAAGAGATCTGTGC	1680
OY	1688	CAAGTTCCTGTGACTGTGTGATGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTA	1747
Db	1681	CAAGTTCCTGTGACTGTGTGATGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTA	1740
OY	1748	TGTACAGGAGACACAGCTTTCAAAAAGACAGAGCTCTTTTCTACCGGAAGAGTGTGTGAG	1807
Db	1741	TGTACAGGAGACACAGCTTTCAAAAAGACAGAGCTCTTTTCTACCGGAAGAGTGTGTGAG	1800
OY	1808	CAAGTTCGAAGAAGCTTGAGTTCAGACAGCACTTGAAGAGGGGTGCAGCTGCGGAGACTGTC	1867
Db	1801	CAAGTTCGAAGAAGCTTGAGTTCAGACAGCACTTGAAGAGGGGTGCAGCTGCGGAGACTGTC	1860
OY	1868	GGAAGCAGAGAGTTCAGGAGCATCGGGAGCCAGAGGCCCGCGCTGCTGAGCTCCAGACTCG	1927
Db	1861	GGAAGCAGAGAGTTCAGGAGCATCGGGAGCCAGAGGCCCGCGCTGCTGAGCTCCAGACTCG	1920
OY	1928	CTTCATCCCCAAGCTGACGGGTGCGGCCGATTTGTGAACATGACTAGCTGTGGAGC	1987
Db	1921	CTTCATCCCCAAGCTGACGGGTGCGGCCGATTTGTGAACATGACTAGCTGTGGAGC	1980
OY	1988	CAGAAGCTTCCGCGAGAAAAAGAGGGCCGAGGCTCTACACTTGAGGGTGAAGGCACTGTT	2047
Db	1981	CAGAAGCTTCCGCGAGAAAAAGAGGGCCGAGGCTCTACACTTGAGGGTGAAGGCACTGTT	2040

[illegible]

```

Db 3121 TCAGCAAGTTGGAGAAAGCCCAATTTTCTGCGCTCTCTACACAGCCCTCCCT 3180
QY 3152 CTGCTACTCCATCTGAAAGCAAGACAGGATGTGCTGGGGGGCAAGGGCGCCG 3211
Db 3181 CTGCTACTCCATCTGAAAGCAAGACAGGATGTGCTGGGGGGCAAGGGCGCCG 3240
QY 3212 CGGCGCTGCGCTCCGAGGCGCTGCAAGTGTGCTGCACCAACATCTCTCAAGCT 3271
Db 3241 CGGCGCTGCGCTCCGAGGCGCTGCAAGTGTGCTGCACCAACATCTCTCAAGCT 3300
QY 3272 GACTGACACCGTGTACACAGTGTGCTGCTGGGGGCACTGACGACAGCCAGACGA 3331
Db 3301 GACTGACACCGTGTACACAGTGTGCTGCTGGGGGCACTGACGACAGCCAGACGA 3360
QY 3332 GCTGATGAGGAAAGCTCCGCGGGGAGACGCTGACTCCCTGGAGGCGACCCAGCCG 3391
Db 3361 GCTGATGAGGAAAGCTCCGCGGGGAGACGCTGACTCCCTGGAGGCGACCCAGCCG 3420
QY 3392 ACTGCCCTGACACTTCAAGACATCTGTGATGTGATGCGCACCGCCGACAGCCGCGA 3451
Db 3421 ACTGCCCTGACACTTCAAGACATCTGTGATGTGATGCGCACCGCCGACAGCCGCGA 3480
QY 3452 GAGCAGACACGACGAGCCCTGTACAGCCGCGGCTTACGCTCCAGAGGAGAGGGCGGCC 3511
Db 3481 GAGCAGACACGACGAGCCCTGTACAGCCGCGGCTTACGCTCCAGAGGAGAGGGCGGCC 3540
QY 3512 CACACCCAGAGCCCGACCGCTGGAGTCTGAGGCTGTGAGTGTGTTGGCCGAGGCTG 3571
Db 3541 CACACCCAGAGCCCGACCGCTGGAGTCTGAGGCTGTGAGTGTGTTGGCCGAGGCTG 3600
QY 3572 CATGTCCGGCTGAAGGCTGAGTGTCCGAGTGTGAGGCTGAGGAGTGTGACAGCAGGCT 3631
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGAGTGTGAGGCTGAGGAGTGTGACAGCAGGCT 3660
QY 3632 GAGTGTCAAGACACGCTGCTGTACCTTCCCAAGAGGAGGAGGCTGCTGACAGCCGA 3691
Db 3661 GAGTGTCAAGACACGCTGCTGTACCTTCCCAAGAGGAGGAGGCTGCTGACAGCCGA 3720
QY 3692 GGGCCACGCTTTCCTCACAGAGAGCCCGCTTCCACTCCCACTAGAAATAGTCATCC 3751
Db 3721 GGGCCACGCTTTCCTCACAGAGAGCCCGCTTCCACTCCCACTAGAAATAGTCATCC 3780
QY 3752 CCAGATTGGCCATTGTACCCCTGCGCCCTGCTCTTTCCTTCCACCCCCACCATCC 3811
Db 3781 CCAGATTGGCCATTGTACCCCTGCGCCCTGCTCTTTCCTTCCACCCCCACCATCC 3840
QY 3812 AGGTGAGAACCTTGAGAGAGACCTGGAGCTGTGGAATTTGGAGTGAACAAAGGTGTG 3871
Db 3841 AGGTGAGAACCTTGAGAGAGACCTGGAGCTGTGGAATTTGGAGTGAACAAAGGTGTG 3900
QY 3872 CCTGTACACAGAGGAGAGCCCTGACCTGATGGGGGTCCCTGTGGGCTCAAAATGGGGG 3931
Db 3901 CCTGTACACAGAGGAGAGCCCTGACCTGATGGGGGTCCCTGTGGGCTCAAAATGGGGG 3960
QY 3932 GAGTGTGCTGGAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 3986
Db 3961 GAGTGTGCTGGAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 4015

```

```

RESULT 7
US-10-105-963-1
: Sequence 1, Application US/10105963
: Publication No. US20030068618A1
: GENERAL INFORMATION:
: APPLICANT: Genon Corporation
: APPLICANT: Denning, Chris
: APPLICANT: Clark, A. John
: APPLICANT: Schif, J. Michael
: TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
: TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
: FILE REFERENCE: 731/002

```

```

: CURRENT APPLICATION NUMBER: US/10/105, 963
: CURRENT FILING DATE: 2002-03-21
: PRIOR APPLICATION NUMBER: US 60/277, 811
: PRIOR FILING DATE: 2001-03-21
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 4015
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (56) .. (3454)
: OTHER INFORMATION:
US-10-105-963-1

Query Match 99.1%; Score 3969; DB 9; Length 4015;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 8 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 67
Db 1 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 60
QY 68 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 127
Db 61 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 120
QY 128 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 187
Db 121 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 180
QY 188 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 247
Db 181 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 240
QY 248 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 307
Db 241 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 300
QY 308 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 367
Db 301 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 360
QY 368 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 427
Db 361 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 420
QY 428 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 487
Db 421 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 480
QY 488 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 547
Db 481 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 540
QY 548 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 607
Db 541 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 600
QY 608 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 667
Db 601 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 660
QY 668 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 727
Db 661 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 720
QY 728 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 787
Db 721 GCAGCGTGTGCTGCTGTGCGACGTTGGAGAGCCCTGACCCCGGACCCCGGATGCC 780
QY 788 TGCCCTGAGCGCGAGAGCGCCCTGTGGAGAGGCTGCTGGGCCACCCGGAGGAGC 847

```


Dh	2881	GCAGAGGACTATCTCCACTCTATGCCCCGAGACCTCATAGAGCCAGCTCACCTTCAACCG	2940
Qy	2912	CGGCTTCACAGCGCGGGAGAAACATGCTGCGCAAACTCTTGGGGGCTTGGCGCGGAAGTG	2971
Dh	2941	CGGGCTTCACAGCGCGGGAGAAACATGCTGCGCAAACTCTTGGGGGCTTGGCGCGGAAGTG	3000
Qy	2972	TCACAGCTCTTTCCTGAGATTGGACGGTGAACGGCTCCACAGGGTGTGCACCAACATCTCA	3031
Dh	3001	TCACAGCTCTTTCCTGAGATTGGACGGTGAACGGCTCCACAGGGTGTGCACCAACATCTCA	3060
Qy	3032	CAGATCT	3091
Dh	3061	CAGATCT	3120
Qy	3092	TCACAGATTGGAGAAACCCACATTTTTCCCTGGCGCTATCTCGACAGGCTCCCT	3151
Dh	3121	TCACAGATTGGAGAAACCCACATTTTTCCCTGGCGCTATCTCGACAGGCTCCCT	3180
Qy	3152	CTGCTACTCCATCTCTGAAGGCCAAGAACAGAGGATGTCCCTGGGGGCGCAAGGCCGCGC	3211
Dh	3181	CTGCTACTCCATCTCTGAAGGCCAAGAACAGAGGATGTCCCTGGGGGCGCAAGGCCGCGC	3240
Qy	3212	CGGGCTCTCTCCCTCCGAGGGCGGTGCAAGGGTGTGTCACACAAGATTCCTGCTCAAGCT	3271
Dh	3241	CGGGCTCTCTCCCTCCGAGGGCGGTGCAAGGGTGTGTCACACAAGATTCCTGCTCAAGCT	3300
Qy	3272	GACTGTGACACCGGTGACCTTACGTACGTGTCATCTCTGGGGTCACTAGAGAACCCGACAGCA	3331
Dh	3301	GACTGTGACACCGGTGACCTTACGTACGTGTCATCTCTGGGGTCACTAGAGAACCCGACAGCA	3360
Qy	3332	GCTGTGATCGGAACCTCCGGGGGAGAGAGCGTGTACCTCCCTGGAGCGCGGACAGCCAGCCGCG	3391
Dh	3361	GCTGTGATCGGAACCTCCGGGGGAGAGAGCGTGTACCTCCCTGGAGCGCGGACAGCCAGCCGCG	3420
Qy	3392	ACTGCGCTTCAGATTTCAGACACATCTGGACGTGAATGAGCCAGCCGCGCACACAGCGCGCA	3451
Dh	3421	ACTGCGCTTCAGATTTCAGACACATCTGGACGTGAATGAGCCAGCCGCGCACACAGCGCGCA	3480
Qy	3452	GAGCGAGACACAGAGAGCCGTGTACGCGCGGGCTCTACGTCCAGAGAGAGAGAGGGGGGCGC	3511
Dh	3481	GAGCGAGACACAGAGAGCCGTGTACGCGCGGGCTCTACGTCCAGAGAGAGAGAGGGGGGCGC	3540
Qy	3512	CACACCCAGGCGCCGACCGCTGGGAGTCTTGAGGCTGTGAGTGTGTTGGCCAGGCGCTG	3571
Dh	3541	CACACCCAGGCGCCGACCGCTGGGAGTCTTGAGGCTGTGAGTGTGTTGGCCAGGCGCTG	3600
Qy	3572	CATGCTCGGCTGAAGGCTGAGTGTCCGGGCTGAGGCGTGAACGAGTGTCCAGCCAAAGGCT	3631
Dh	3601	CATGCTCGGCTGAAGGCTGAGTGTCCGGGCTGAGGCGTGAACGAGTGTCCAGCCAAAGGCT	3660
Qy	3632	GAGTGTCCACACACACTCCGCTCTTCACTTCCCAACAGGTGGGCGTGGCTCCACCCCA	3691
Dh	3661	GAGTGTCCACACACACTCCGCTCTTCACTTCCCAACAGGTGGGCGTGGCTCCACCCCA	3720
Qy	3692	GGGCGACCTTTTCTGTACACAGAACCGCGGCTTCCACGCCCATATGAGAAATGTCATCC	3751
Dh	3721	GGGCGACCTTTTCTGTACACAGAACCGCGGCTTCCACGCCCATATGAGAAATGTCATCC	3780
Qy	3752	CCAGATTTCGCAATTGTGTACCCCTGCGCGCTCTCTTGGCTTCAACCCCAACATCC	3811
Dh	3781	CCAGATTTCGCAATTGTGTACCCCTGCGCGCTCTCTTGGCTTCAACCCCAACATCC	3840
Qy	3812	AGGTGAGACCCCGAGAAAGACCTGGAGCTTGTGGAAATTTGGAAATGACCAAGGCTGTG	3877
Dh	3841	AGGTGAGACCCCGAGAAAGACCTGGAGCTTGTGGAAATTTGGAAATGACCAAGGCTGTG	3906
Qy	3872	CCCTGTACACAGCGAGAGCCCTGTACCTGTGATGGGGGTCCCTGTGGTCAAAATTTGGGG	3931
Dh	3901	CCCTGTACACAGCGAGAGCCCTGTACCTGTGATGGGGGTCCCTGTGTGGTCAAAATTTGGGG	3960
Qy	3932	GAGTGTCTGTGGGATAAAATCTGAATATGAACTTTTCACTTTTGTGAAAAA 3986	

Db	3961	GAGGGCGCTGGAGTAAATCTGAATATATGAGTTTCAGTTTGAAAAA	4015
	RESULT 9		
	US-09-990-080-1		
	Sequence 1, Application US/09990080		
	Patent No. US20020102686A1		
	GENERAL INFORMATION:		
	APPLICANT: Morin, Gregg B		
	APPLICANT: Genent Corporation.		
	TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants		
	FILE REFERENCE: 018/2586		
	CURRENT APPLICATION NUMBER: US/09/990,080		
	CURRENT FILING DATE: 1998-08-03		
	PRIOR APPLICATION NUMBER: US 09/052,864		
	PRIOR FILING DATE: 1998-03-31		
	NUMBER OF SEQ ID NOS: 21		
	SOFTWARE: PatentIn Ver. 2.0		
	SEQ ID NO 1		
	LENGTH: 4015		
	TYPE: DNA		
	ORGANISM: Homo sapiens		
	FEATURE:		
	NAME/KEY: CDS		
	LOCATION: (56)..(3454)		
	OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA		
	US-09-990-080-1		
	Query Match	99.1%;	Score 3969; DB 10; Length 4015;
	Best Local Similarity	99.1%;	Pred. No. 0;
	Matches 3979; Conservative	0;	Mismatches 0; Indels 36; Gaps
Oy	8	GCAGGCGCTGCTCTGCTGGCGACGTGGGAAGCCCTGGGCCCGGACACCCCGCGCATGCC	67
Db	1	GCAGGCGCTGCTCTGCTGGCGACGTGGGAAGCCCTGGGCCCGGACACCCCGCGCATGCC	60
Oy	68	GGCGCGTCTCCCGCTGGCGGACGCTGCTCTGCTGGCGACGACCTAAGCGGAGGTGCT	127
Db	61	GGCGCGTCTCCCGCTGGCGGACGCTGCTCTGCTGGCGACGACCTAAGCGGAGGTGCT	120
Oy	128	GCCGCTGGCCACGTTGCTGGGCGCCCTTGGGGCCCAAGGCTGGCGGCTGGTGGACGGCG	187
Db	121	GCGCGTGGCCACGTTGCTGGGCGCCCTTGGGGCCCAAGGCTGGCGGCTGGTGGACGGCG	180
Oy	188	GGACCCGGCGGCTTTCCGCGACGCTGTGGGCCCAAGTGTGTGTGTGCTGGCGACGC	247
Db	181	GGACCCGGCGGCTTTCCGCGACGCTGTGGGCCCAAGTGTGTGTGTGCTGGCGACGC	240
Oy	248	ACGGCGCGCCCGCCCGCCCGCTCTCTCCGCGAAGTGTCTCTCTCGAAGAGCTGTGGC	307
Db	241	ACGGCGCGCCCGCCCGCCCGCTCTCTCCGCGAAGTGTCTCTCTCGAAGAGCTGTGGC	300
Oy	308	CCGAGTGTGTCAGAGAGGTGTGGAGCGGCGCGGAAGAACTGTGGCTTCCTGGCTTCGC	367
Db	301	CCGAGTGTGTCAGAGAGGTGTGGAGCGGCGCGGAAGAACTGTGGCTTCCTGGCTTCGC	360
Oy	368	GGTGGGACGGGGGCGCGGGGGGGCCCGCGAAGCCCTTACACACACACGTCGGCGACGTA	427
Db	361	GGTGGGACGGGGGCGCGGGGGGGCCCGCGAAGCCCTTACACACACACGTCGGCGACGTA	420
Oy	428	CCGCGCCCAACAGGTGTACGACGACATCGGGGGAGCGGGGGCGTGGCGTGGCGTGG	487
Db	421	CCGCGCCCAACAGGTGTACGACGACATCGGGGGAGCGGGGGCGTGGCGTGGCGTGG	480
Oy	488	CGCGGTGGGGCGACAGCTGTGTACCTCTGTGACGCTGTGCGCTCTTCTTGTGCTGGT	547
Db	481	CGCGGTGGGGCGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	540
Oy	548	GGCTCTCACTGCGCTACCAAGGTGTGGGGCGCGCGACTGTACAGCTGGCGCTGCAC	607
Db	541	GGCTCTCACTGCGCTACCAAGGTGTGGGGCGCGCGACTGTACAGCTGGCGCTGCAC	600
Oy	608	TCAAGGCGCGCGCGCGCGCGACACGCTAAGTGTGACCCCGAAGCGCTCTGGAGTGTGCAAGGGCG	667

Qy	2792	GGCGGCCACAGGCGATTTCCTCCCTGGTGGCGGCGCTGCTGGTAATACCGGACCCCTGGAGGT	2851
Db	2821	GGCGGCCACAGGCGATTTCCTCCCTGGTGGCGGCGCTGCTGGTAATACCGGACCCCTGGAGGT	2880
Qy	2852	GGAGAGGGAATACCTACACATCTGCCCCGACCCGTCATACAGAGCAATGCAACTCTTAACG	2911
Db	2881	GGAGAGGGAATACCTACACATCTGCCCCGACCCGTCATACAGAGCAATGCAACTCTTAACG	2940
Qy	2912	CGGCTTCAAGCTGGGAGGAACAATCGCTGGCAACTCTTTGGGAGCTTGGGGCTGAAGT	2971
Db	2941	CGGCTTCAAGCTGGGAGGAACAATCGCTGGCAACTCTTTGGGAGCTTGGGGCTGAAGT	3000
Qy	2972	TCACAGCCTGTTCTGGAATTTGAGAGTGAACAGCCTTCACAGCGGTGTCACCAACATCTA	3031
Db	3001	TCACAGCCTGTTCTGGAATTTGAGAGTGAACAGCCTTCACACGGGTGTCACCAACATCTA	3060
Qy	3032	CAGATCCTCTGCTGTCAGAGCGTACAGAGTTTTCACGCAATGTGTGTCGACAGTCCCATTTCA	3091
Db	3061	CAGATCCTCTGCTGTCAGAGCGTACAGAGTTTTCACGCAATGTGTGTCGACAGTCCCATTTCA	3120
Qy	3092	TCAGCAAGTTTGGAGAAGAACCCCAATTTTTCCTCGCGGTCAATCTGTGACAGCGCTCCCT	3151
Db	3121	TCAGCAAGTTTGGAGAAGAACCCCAATTTTTCCTCGCGGTCAATCTGTGACAGCGCTCCCT	3180
Qy	3152	CTGCTACTCCATCTCGAAGCAAGAACGAGGATCTGCTGGGGGGCAAGGGCGCGCG	3211
Db	3181	CTGCTACTCCATCTCGAAGCAAGAACGAGGATCTGCTGGGGGGCAAGGGCGCGCG	3240
Qy	3212	GGGGCGCTCTCCCTCGAGGGCGGTGAGAGTGGTGTGCACACAAGATTCCTGCTCAAGT	3271
Db	3241	GGGGCGCTCTCCCTCGAGGGCGGTGAGAGTGGTGTGCACACAAGATTCCTGCTCAAGT	3300
Qy	3272	GACCTGACACCCGTCGACATGACGTGCACTGCTGGGGTCACTCAGAGACCCAGACGA	3331
Db	3301	GACCTGACACCCGTCGACATGACGTGCACTGCTGGGGTCACTCAGAGACCCAGACGA	3360
Qy	3332	GCTGATGTCGAAGCTTCCGGGGAGACAGCTGACTGCTTGGAGGCCGACACCCGCG	3391
Db	3361	GCTGATGTCGAAGCTTCCGGGGAGACAGCTGACTGCTTGGAGGCCGACACCCGCG	3420
Qy	3392	ACTGCGCTCAGACTTCACAGCAATCTGTGAGTAGGTCACCCGCGCCACACAGCGACGA	3451
Db	3421	ACTGCGCTCAGACTTCACAGCAATCTGTGAGTAGGTCACCCGCGCCACACAGCGACGA	3480
Qy	3452	GAGCAGACACACAGCAGCCCTGTACCCCGGGCTCTAGCTCCAGGAGAGGAGGGCGGC	3511
Db	3481	GAGCAGACACACAGCAGCCCTGTACCCCGGGCTCTAGCTCCAGGAGAGGAGGGCGGC	3540
Qy	3512	CACACCCAGGCGCAGACCGCTGGGAACTGAGAGGCTGAGTGAATTTTGGCCAGGCGTG	3571
Db	3541	CACACCCAGGCGCAGACCGCTGGGAACTGAGAGGCTGAGTGAATTTTGGCCAGGCGTG	3600
Qy	3572	CATGTCGGGTGAAGCTGAGTGTCCGGGTGAGGCTGAGACGAGTGTCCACCAAGGGGT	3631
Db	3601	CATGTCGGGTGAAGCTGAGTGTCCGGGTGAGGCTGAGACGAGTGTCCACCAAGGGGT	3660
Qy	3632	GAGGTGTCCACACACCTGCGCTCTTACCTTCCACACAGGTGGGCGCTGGGTCTCACCCA	3691
Db	3661	GAGGTGTCCACACACCTGCGCTCTTACCTTCCACACAGGTGGGCGCTGGGTCTCACCCA	3720
Qy	3692	GGGCGACCTTTTCTACACAGAGAGCCGGGCTTCACATCCGACATAGGAATAGTCATCG	3751
Db	3721	GGGCGACCTTTTCTACACAGAGAGCCGGGCTTCACATCCGACATAGGAATAGTCATCG	3780
Qy	3752	CGAATTTCCGCAATGTGTACCCCTCGCGCTGCTCTTTGGCTTCACCCCAACATCG	3811
Db	3781	CGAATTTCCGCAATGTGTACCCCTCGCGCTGCTCTTTGGCTTCACCCCAACATCG	3840
Qy	3812	AGGTGAGACCCCTGAGAGAGACCCCTGGAGCTGTGGAAATTTGAGTGAACCAAGGTGTG	3871
Db	3841	AGGTGAGACCCCTGAGAGAGACCCCTGGAGCTGTGGAAATTTGAGTGAACCAAGGTGTG	3900

```

1 Oy 39372 CCCTGTACACAGCGAGACCCCTGCACCTGGAATGGGGGTCCTGTGGGCAAAATGGGGG 3931
2 Db 3901 CCCTGTACACAGCGAGACCCCTGCACCTGGAATGGGGGTCCTGTGGGCAAAATGGGGG 3960
3 Oy 39332 GAGGCGCTGGGGAGGATAAATATGATATATGAGTTTTCAGTTTGTAAAAA 3986
4 Db 3961 GAGGCGCTGGGGAGGATAAATATGATATATGAGTTTTCAGTTTGTAAAAA 4015
5
6 RESULT 10
7 US-09-733-294A-30
8 : Sequence 30, Application US/09733294A
9 : Patent No. US20020045588A1
10 : GENERAL INFORMATION:
11 : APPLICANT: Brett P. Monia
12 : APPLICANT: William Gaarde
13 : APPLICANT: Susan M. Freiler
14 : APPLICANT: Edward V. Wancowicz
15 : TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
16 : FILE REFERENCE: ISPH-0527
17 : CURRENT APPLICATION NUMBER: US/09/733,294A
18 : CURRENT FILING DATE: 2000-12-07
19 : PRIOR APPLICATION NUMBER: 09/572,423
20 : PRIOR FILING DATE: 2000-05-16
21 : NUMBER OF SEQ ID NOS: 108
22 : SEQ ID NO 30
23 : LENGTH: 51552
24 : TYPE: DNA
25 : ORGANISM: Homo sapiens
26 :
27 : FEATURE:
28 : NAME/KEY: exon
29 : LOCATION: (1) ..(11492)
30 : OTHER INFORMATION: exon 1
31 : NAME/KEY: intron
32 : LOCATION: (11493) ..(11566)
33 : OTHER INFORMATION: Intron 1
34 : NAME/KEY: exon
35 : LOCATION: (11597) ..(12950)
36 : OTHER INFORMATION: exon 2
37 : NAME/KEY: intron
38 : LOCATION: (12951) ..(21566)
39 : OTHER INFORMATION: Intron 2
40 : NAME/KEY: exon
41 : LOCATION: (21567) ..(21762)
42 : OTHER INFORMATION: exon 3
43 : NAME/KEY: intron
44 : LOCATION: (21763) ..(23851)
45 : OTHER INFORMATION: Intron 3
46 : NAME/KEY: exon
47 : LOCATION: (23852) ..(24032)
48 : OTHER INFORMATION: exon 4
49 : NAME/KEY: intron
50 : LOCATION: (24033) ..(24719)
51 : OTHER INFORMATION: Intron 4
52 : NAME/KEY: exon
53 : LOCATION: (24720) ..(24899)
54 : OTHER INFORMATION: exon 5
55 : NAME/KEY: intron
56 : LOCATION: (24900) ..(25393)
57 : OTHER INFORMATION: Intron 5
58 : NAME/KEY: exon
59 : LOCATION: (25394) ..(25549)
60 : OTHER INFORMATION: exon 6
61 : NAME/KEY: intron
62 : LOCATION: (25550) ..(30196)
63 : OTHER INFORMATION: Intron 6
64 : NAME/KEY: exon
65 : LOCATION: (30195) ..(30292)
66 : OTHER INFORMATION: exon 7
67 : NAME/KEY: intron
68 : LOCATION: (30293) ..(31272)
69 : OTHER INFORMATION: Intron 7
70 : NAME/KEY: exon

```

LOCATION: (31273)...(31358)
? OTHER INFORMATION: exon 8
? NAME/KEY: Intron
? LOCATION: (31359)...(33843)
? OTHER INFORMATION: Intron 8
? NAME/KEY: unsure
? LOCATION: 31450
? OTHER INFORMATION: unknown
? NAME/KEY: exon
? LOCATION: (33844)...(33957)
? OTHER INFORMATION: exon 9
? NAME/KEY: Intron
? LOCATION: (33958)...(35941)
? OTHER INFORMATION: Intron 9
? NAME/KEY: exon
? LOCATION: (35942)...(36013)
? OTHER INFORMATION: exon 10
? NAME/KEY: Intron
? LOCATION: (36014)...(37884)
? OTHER INFORMATION: Intron 10
? NAME/KEY: exon
? LOCATION: (37885)...(38073)
? OTHER INFORMATION: exon 11
? NAME/KEY: Intron
? LOCATION: (38074)...(41874)
? OTHER INFORMATION: Intron 11
? NAME/KEY: exon
? LOCATION: (41875)...(42001)
? OTHER INFORMATION: exon 12
? NAME/KEY: Intron
? LOCATION: (42002)...(42881)
? OTHER INFORMATION: Intron 12
? NAME/KEY: exon
? LOCATION: (42882)...(42943)
? OTHER INFORMATION: exon 13
? NAME/KEY: Intron
? LOCATION: (42944)...(46129)
? OTHER INFORMATION: Intron 13
? NAME/KEY: exon
? LOCATION: (46130)...(46254)
? OTHER INFORMATION: exon 14
? NAME/KEY: Intron
? LOCATION: (46255)...(47035)
? OTHER INFORMATION: Intron 14
? NAME/KEY: exon
? LOCATION: (47036)...(47173)
? OTHER INFORMATION: exon 15
? NAME/KEY: Intron
? LOCATION: (47174)...(47709)
? OTHER INFORMATION: Intron 15
? NAME/KEY: exon
? LOCATION: (47710)...(50544)
? OTHER INFORMATION: exon 16
US-09-733-294A-30

Query Match 95.98; Score 3843.4; DB 10; Length 51552;
Best Local Similarity 10.28; Pred. No. 0;
Matches 4004; Conservative 0; Mismatches 1; Indels 35347; Gaps 16;

QY 1 GTTTCAGGAGCGCTGCTCTGCTGGGCAAGTGGGAAGCCCTGGCCCGCCACCCCG 60
DB 11212 GTTTCAGGAGCGCTGCTCTGCTGGGCAAGTGGGAAGCCCTGGCCCGCCACCCCG 11271
QY 61 CGATGCGCGCGCTCCCGCTGCGAGCGCGCTCCCTGCTGCGAGCCACTACCGCG 120
DB 11272 CGATGCGCGCGCTCCCGCTGCGAGCGCGCTCCCTGCTGCGAGCCACTACCGCG 11331
QY 121 AGGTGCTGCGGTCGACGTTCTGTGCGGCGCTGGGGCCCGCAGGCGCTGGCGTGTGC 180
DB 11332 AGGTGCTGCGGTCGACGTTCTGTGCGGCGCTGGGGCCCGCAGGCGCTGGCGTGTGC 11391
QY 181 AGCGGGGAGACCGCGGCTTTCCGCGCGCTGTGGCCCACTGCTGCTGTGCTGCT 240

DB 11392 AGCGGGGAGACCGCGGCTTTCCGCGCGCTGTGGCCCACTGCTGCTGTGCTGCT 11451
QY 241 GGGAGCGACGGGCGCCCGCCCGCCCGCCCTGCTCCG----- 278
DB 11452 GGGAGCGACGGGCGCCCGCCCGCCCGCCCTGCTCCGCAAGTGAGCTCCCGGGTGC 11511
QY 279 ----- 278
DB 11512 GCGTCCGCTGGGGTTGAGGGGCGGGGGAACGACGATGCGGAGAGCGAGC 11571
QY 279 -----CAGGTGCTCTGCTTAAGAGCTGTGGCCGAGTGTCT 316
DB 11572 GCGACTAGGGCGCTTCCCGCCCGGCAAGTGTCTGCTGAAGAGCTGTGGCCGAGTGTCT 11631
QY 317 GCAGAGCTGTGCGAGCGCGCGGGAAGAGTGTGCTGCTGTGGCTTCCGGCTGTGGA 376
DB 11632 GCAGAGCTGTGCGAGCGCGCGGGAAGAGTGTGCTGCTGTGGCTTCCGGCTGTGGA 11691
QY 377 CGGGGCGCGCGGGGCGCCCGCCGAGGCTTTCACCAACGAGCTGTGCGAGCTACCTGCCCCA 436
DB 11692 CGGGGCGCGGGGGGCGCCCGCCGAGGCTTTCACCAACGAGCTGTGCGAGCTACCTGCCCCA 11751
QY 437 CACGCTACCGACGCACTGCGGGGAGCGGGGCTGTGGGCTGCTGCTGCGCCGCTGCG 496
DB 11752 CACGCTACCGACGCACTGCGGGGAGCGGGGCTGTGGGCTGCTGCTGCGCCGCTGCG 11811
QY 497 CGACGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 556
DB 11812 CGACGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 11871
QY 557 CTGCGCTTACGAGTGTGCGGGGCGCGCTGTACAGCTGTGCGCTGCTGCTGCTGCTGCTGCT 616
DB 11872 CTGCGCTTACGAGTGTGCGGGGCGCGCTGTACAGCTGTGCGCTGCTGCTGCTGCTGCTGCT 11931
QY 617 GCGCCCGCGACACGCTAGTGAACCCCGAAGCGCTGTGGATGCGCAAGGGGCTGGAACCA 676
DB 11932 GCGCCCGCGACACGCTAGTGAACCCCGAAGCGCTGTGGATGCGCAAGGGGCTGGAACCA 11991
QY 677 TAGGTCAGGAGGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 736
DB 11992 TAGGTCAGGAGGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 12051
QY 737 GGGCAGTGCACGCGAAGTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 796
DB 12052 GGGCAGTGCACGCGAAGTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 12111
QY 797 GCGGAGCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 856
DB 12112 GCGGAGCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 12171
QY 857 GAGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 916
DB 12172 GAGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 12231
QY 917 GGAAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 976
DB 12232 GGAAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 12291
QY 977 GGGGCGCGCGACATCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1036
DB 12292 GGGGCGCGCGACATCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 12351
QY 1037 CGCGGAGACCAAGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1096
DB 12352 CGCGGAGACCAAGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 12411
QY 1097 CCTACTAGCTCTGAGGCGCGACGCTGAGCTGCGCTGCGAGGCTGCTGAGACCATCTT 1156
DB 12412 CCTACTAGCTCTGAGGCGCGACGCTGAGCTGCGGCTGCGAGGCTGCTGAGACCATCTT 12471
QY 1157 TCTGGTTCCAGGCGCTGAGTGCAGGAGCTCCCGCAGTGTGCTGCTGCTGCTGCTGCTGCT 1216
DB 12472 TCTGGTTCCAGGCGCTGAGTGCAGGAGCTCCCGCAGTGTGCTGCTGCTGCTGCTGCTGCT 12531

```
QY 1217 CTACTGCAAAATGCGGCCCTGTTTCGTGAGCTCTTGGGAACCAACGCGACGTGCCCTTA 1276
    |||||
Db 12532 CTACTGCAAAATGCGGCCCTGTTTCGTGAGCTCTTGGGAACCAACGCGACGTGCCCTTA 12591
QY 1277 CCGGGTGCCTCTCAAGACGACACTGCCCGCTGAGCTGCGGTACCCAGCAGCCGGTGT 1336
    |||||
Db 12592 CCGGGTGCCTCTCAAGACGACACTGCCCGCTGAGCTGCGGTACCCAGCAGCCGGTGT 12651
QY 1337 CTGTGCCCCGAGAACGCCAGGAGCTGTGTGGCGGCCCGGAGAGAGACACAGAACCC 1396
    |||||
Db 12652 CTGTGCCCCGAGAACGCCAGGAGCTGTGTGGCGGCCCGGAGAGAGACACAGAACCC 12711
QY 1397 CCGTGGCTGTGAGCTGTCCGCCACAGACAGAGCCCTGCGAGAGTGTACGGTTTGT 1456
    |||||
Db 12712 CCGTGGCTGTGAGCTGTCCGCCACAGACAGAGCCCTGCGAGAGTGTACGGTTTGT 12771
QY 1457 GCGGGCTGCTGCGCGCGGTGTGTGCCCAAGCCCTTGGGGCTCCAGGCACACGAACG 1516
    |||||
Db 12772 GCGGGCTGCTGCGCGCGGTGTGTGCCCAAGCCCTTGGGGCTCCAGGCACACGAACG 12831
QY 1517 CCGCTTCTCTAGAAACCAACCAAGTTCATCTCCTGGGGAACATGCCAAGCTCTGCT 1576
    |||||
Db 12832 CCGCTTCTCTAGAAACCAACCAAGTTCATCTCCTGGGGAACATGCCAAGCTCTGCT 12891
QY 1577 GCAGAGCTGACGTGAAGATGAGCGTGGGAGCTGGGCTTGGCTCCGACGAGGCC--- 1633
    |||||
Db 12892 GCAGAGCTGACGTGAAGATGAGCGTGGGAGCTGGGCTTGGCTCCGACGAGGCCAG 12951
QY 1634 ----- 1633
Db 12952 TGAGAGAGTGTGCGCCCTGCGAGGGCCCAAGGCCAGAGCTGAATGACATGAGGGCTCAGA 13011
QY 1634 ----- 1633
Db 13012 AAAGGGGACAGCAGAGCCCTGTGCTCCTGTCATGTCACGTGAGGACACAGCTGCT 13071
QY 1634 ----- 1633
Db 13072 TTTGCTCAGAGCTGAGTGGAGACAGSGTATCTCTGCTCTGCTCTCCTCTCTGTCAG 13131
QY 1634 ----- 1633
Db 13132 TTTGATATAACTTACGAGGTTCACTTCAAGCTTTTGATGACACGGGTTTTCAGAGGCC 13191
QY 1634 ----- 1633
Db 13192 GAGGCCAGACATGAAACAGAGAGGCTGGGCGCGCAGTGAGGCCGGGTTGCCGCAAT 13251
QY 1634 ----- 1633
Db 13252 GGGGGAAGTGTGGAAGCAGACAGACGCTGTGGGAGGTTGCCGAGGTACCTATAT 13311
QY 1634 ----- 1633
Db 13312 CCTCTCGCAATTTCAAGGGTGGAAATGAGAGTGGGAGAGAACCCCTCTCTGCGG 13371
QY 1634 ----- 1633
Db 13372 GGTGGAGATAGGGTTTTCAGGTGCAAGTGTGACCAATATGACAGGTTTGTGTTAA 13431
QY 1634 ----- 1633
Db 13432 GATTAATTTGTGTGACGCGCAGGTGGGGGTGTCACGCGTAAATCCAGCACTTGG 13491
QY 1634 ----- 1633
Db 13492 GGAAGCTAGAGCAGGTGATCACTGAGGTGACAGAGTTTGAGACACAGCTGACCAATG 13551
QY 1634 ----- 1633
Db 13552 GTGAAACCTTATCTGTACTAAATAATACAAAATTAAGTGGGCATGTGGTGTGCTGCT 13611

QY 1634 ----- 1633
Db 13612 AATCCACACTACTTGGAGGCTGAGGACAGAGAAATCACTTGAACCCAGGAGCGAGGCT 13671
QY 1634 ----- 1633
Db 13672 GCAGTACGTGAGATTGTGCCATTTGACTCCAGCCTGGGACAAAGAGTGAATCTGTG 13731
QY 1634 ----- 1633
Db 13732 TTTAAAAAAGTGTGTTGTTATGTGCCAGAGCAGGATGAGGGAGGAGATAAAG 13791
QY 1634 ----- 1633
Db 13792 CTGTCTCAGACACAGATCTGTCCTCATCTTTAGTATGAAAGAGGCCACATGGAGCA 13851
QY 1634 ----- 1633
Db 13852 GAGGACAGCAGATGGCTCCACTGCTAGAGAAAGGACAGTGTGTGGGTTCAGGGGA 13911
QY 1634 ----- 1633
Db 13912 TGTGCTGTGGGCTGCGCGTGTCCACCCCTGTGTTCTGTGATTTGATGTAGGAAC 13971
QY 1634 ----- 1633
Db 13972 CTGCGCTCAGCCCTCTTTGGCTCCAGTGTCCAGGCCCTACCGTGGCAGCTAGAG 14031
QY 1634 ----- 1633
Db 14032 AAGTCCGATTTACCCCTCCCAAAACTCCCAAGACATGTAAGACTTCGGCCATGC 14091
QY 1634 ----- 1633
Db 14092 AGACAAAGAGGAGTACCTCTTGGGGCTCTTTTCTTTTCTTTTATGATGTGCA 14151
QY 1634 ----- 1633
Db 14152 AAGTCAATATACATGAGATTTGGCACCTCTAACACCTTTCTGTGTACATGACAGATT 14211
QY 1634 ----- 1633
Db 14212 GCTTAATGGCGGTGTTTACAGCAGTTGCTTGAATGCTGCTCTGCTGACTGGAAG 14271
QY 1634 ----- 1633
Db 14272 TCCCTAACCATGAAAGGAGCTGCTCACAAGCTGTGGGCTCAGGTGACACAGCCGA 14331
QY 1634 ----- 1633
Db 14332 GTACATTAAGGCTATGCAACCAAGTTTGCTTTTGTGTGCTCAGCTTCTTGTGAGG 14391
QY 1634 ----- 1633
Db 14392 AGAGTTGATGTTCTGTATCAGAGCTGTGCTGTCAATGTCTGTCTGACTGATGA 14451
QY 1634 ----- 1633
Db 14452 GGTCAATCTGCCCTGGCTTATGACAGGAGTGAAGCGTGHCCCGGGTGTCTGTG 14511
QY 1634 ----- 1633
Db 14512 ACGTCAAGGTGAGTGAAGGCTTGGCCCCAGGTGTCCCTGTACAGTGAAGGTAGAG 14571
QY 1634 ----- 1633
Db 14572 GCGCGGCCCGGGTGTCCCTGTCCCGTGCAGCTGATTAAGTGTGGCCCCCGGGTGT 14631
QY 1634 ----- 1633
Db 14632 CCTGTACAGTGTAGGTTGAGTGAAGCGCCATCCCGGGTGTCTCTGTACAGTGAAGG 14691
QY 1634 ----- 1633
```

Db 14692 AGTGAAGGCTGTCCTCCGGGTGTCTCTCCGTGCAAGGTGAGTGAACACTGTCCCG 14751
QY 1634 ----- 1633
Db 14752 GGTGTCCCTGACAGTGCAGGGGTAGTGAAGCGCGGTCCCGGTGTCTCTCAGTGT 14811
QY 1634 ----- 1633
Db 14812 AGGTGAGTGAAGCGCGGCCCCAGGGGTGTCCCTGTCAAGTGTAGGGGTAGTGAAGCACG 14871
QY 1634 ----- 1633
Db 14872 TCCCTGGGTGTCCCTCCAGGTATAGGGTGAAGGACACTGTCCCGGTGTCTCTGTCTC 14931
QY 1634 ----- 1633
Db 14932 ACGTGCAGGGTGAAGTGAAGCGCGGCCCGGGGTGTCTCTCAGTGTGAGGGTGAAGTGA 14991
QY 1634 ----- 1633
Db 14992 GCGGTGTCCCTGGGTGTCCCTGTCTCTGTGAGGGTGAAGGCTGTCTCCCAAGTGTCTC 15051
QY 1634 ----- 1633
Db 15052 CTTGGCGTTTGTCTACTTGAAGCTTGTCTGTGAATGTTTGTCTTTCTATAGCACAGCTG 15111
QY 1634 ----- 1633
Db 15112 CGCGGGTGGCCCAATGCTGTGGGTGAAGTGTGAAGCGCAGTGTGTCCCAAGCTATTC 15171
QY 1634 ----- 1633
Db 15172 TTTTCTGATGTGCGGCTCTTGTGTACCTCTCCGTTCATTTTGTACGGGAGACAGG 15231
QY 1634 ----- 1633
Db 15232 GACTGAGAGCTGTGCGCTCCCGGTGCGAGCAGTGCACAGACTTCAGGTCCGCTTG 15291
QY 1634 ----- 1633
Db 15292 CCTGTGTGGGCTGTGGCTTGTCTACACAGCTGCCGCCACATGCTGTCCAAATACTCT 15351
QY 1634 ----- 1633
Db 15352 CTCCAGCTGTCTCATGCGCAGGCTGAGCTCTGGGCTGCTGTGTCTGTCCACAGTGT 15411
QY 1634 ----- 1633
Db 15412 TGTGAGACATCCAGAAAGGTTCTGTGTCCCTGAAGAAAGCAAGTCAACCCACGCC 15471
QY 1634 ----- 1633
Db 15472 CCCCTACTGTCTGTGTTTCTCCCAAGCTGCCCTGTGCTGGCCCCCTTGGGTGGGTGG 15531
QY 1634 ----- 1633
Db 15532 CAACGCTTGTACCTTATTTGAGGACCTGCGGCTCATTTGTTAGGCTGGGCTCTGCCTC 15591
QY 1634 ----- 1633
Db 15592 CAGTGGCCCCCTCAGATGATTGACGTCAAGCACAGGTTGAGTGTCTGTCTGTCTC 15651
QY 1634 ----- 1633
Db 15652 CTGCTGTGAGACCCAGCTGAGGGCGGTGTCTCCGCCAGCCTTCGTGACACTTCCCTCT 15711
QY 1634 ----- 1633
Db 15712 TGGGTCTAGTTTGAATTTCACTGATTTACCTCTGAAGTTTCTATCTCTCATTTGATG 15771
QY 1634 ----- 1633

Db 15772 CTTTTCCTGGTTATTTCTTTCATTTCTTTCTTCTAGCTTCTTAGTTAGTCAATGCTTTCC 15831
QY 1634 ----- 1633
Db 15832 CTCTAAGTGTGCTTACTTACTGACCCGTGTGTTGATGTGAATATCTCAACATCAGCC 15891
QY 1634 ----- 1633
Db 15892 ACTTCAAGTGTCTTAAATACTTCAAAAGTGAATTAATCTTTTAAATATCTTATTC 15951
QY 1634 ----- 1633
Db 15952 TGTGATTTTTCCTTGTGACGCTGTGTGTTGACGTGAATCAATTTGATATCAGTGAC 16011
QY 1634 ----- 1633
Db 16012 TTTTATGATTTCTTACTTATTTCTGTGATTTCTTTGACGAGTGAATTTGAAACACTG 16071
QY 1634 ----- 1633
Db 16072 TTTATGTTCAAGATATGTAGATATCAAGATACGTAGATATTTTAACTATCATTTTAT 16131
QY 1634 ----- 1633
Db 16132 TATGATTTCTAAGTCACTGTGTAGTGTGTGTATATACCAATTTATGAAGTTGCG 16191
QY 1634 ----- 1633
Db 16192 GAGCCTTGTCTTGTGATCTAGTGTGTGATGTGTTCCAGAACTGTCCATTTGAATTTGA 16251
QY 1634 ----- 1633
Db 16252 CATCTGTCAATAGTGGGATGATGTTCACTATATCCAGCTATTAAGTCCAGTGCA 16311
QY 1634 ----- 1633
Db 16312 AGCTTGTGTCTCTCTAGATGATGAATTCAGAAAGAGGCCAATGCTCCACTG 16371
QY 1634 ----- 1633
Db 16372 GGGATGGGTCTGTTCATTTCTCTCTGTTTGTGATGATTTATGTAGGATTTAGTGTG 16431
QY 1634 ----- 1633
Db 16432 CATGACGTGTAGAAATTTTATCTTCCTGATGATGAATCTTTGAGACTCTATGTC 16491
QY 1634 ----- 1633
Db 16492 TCTAGTATCTAGTAATTTCTTTTAAATGCTTTAGTACTGCACACTGGGCTTCTT 16551
QY 1634 ----- 1633
Db 16552 TTGATTAATTTTCTGCTGTGTGTGTTTCTGCTTTAATTTATATATATATAT 16611
QY 1634 ----- 1633
Db 16612 TTTTTTTTTTTGAAGACAGTGTGTGTGTGTGCCAGGAGTGAAGTCAAGTGTGAT 16671
QY 1634 ----- 1633
Db 16672 CACAGTCAAGTAACTTTTACTTGTGGCTGAGCGGTCTCTACCTCAGCCTCGA 16731
QY 1634 ----- 1633
Db 16732 GTAGCTGAAGTCAAGACACGACCGCTACACTGGCTAATTTTAAATTTTCTGAG 16791
QY 1634 ----- 1633
Db 16792 ACAGGCTTGTCTGTGTTGCCAGGCTGTCTCAAACTTTGACTCAAGGATCATCT 16851
QY 1634 ----- 1633
Db 16852 ACTCGGCTTCCAAAGTGTGAATTAACAGCATGAGCACCATGCTGTGGCTAATTTTC 16911

QY	1634	-----	1633
Db	16912	AACACTTTATATCTATAGTGTGGTATGTCTGTTAACACATGATGATTTCC	16971
QY	1634	-----	1633
Db	16972	AATCCAGTCGACAGTCGTGTTAACTGATTAACCTGATTTATTTTCATTTTTTGCA	17031
QY	1634	-----	1633
Db	17032	CTAGAGACCGCGCTGGTGCACCTCTGATTCCTGACCTGTCATGCTCGTTCCCT	17091
QY	1634	-----	1633
Db	17092	TGTTTTCTACACCTCTGGGTTGCCATGTCGTTCTGCGAGTGTGTGATCTC	17151
QY	1634	-----	1633
Db	17152	TGTTGCTCTGCTGCTACGTGGCATTTGCTTTATTTCTTGTAGTTACCCCT	17211
QY	1634	-----	1633
Db	17212	GATCTTTTATGTGTTGTTGTTGTTTATTTAGACAGTCTGATCTGCACCCAG	17271
QY	1634	-----	1633
Db	17272	GCTGAGTGTAAAGCACATCTCGGCTCAGTCGACACCTGCTGCTGTTCAAGCAG	17331
QY	1634	-----	1633
Db	17332	TTCCTATTCCTACACCTCATGATAGTGGGATTACAGGGCCACACAGCCTGCT	17391
QY	1634	-----	1633
Db	17392	AATTTTGTATTTTATAGTATAGATAGGCTTTACCATGTTGGCCAGCTGCTAACT	17451
QY	1634	-----	1633
Db	17452	CCTGACTCAAGTATCTGCCGCTTGCGCTCCACAGTCTGGGATTACAGTGCAG	17511
QY	1634	-----	1633
Db	17512	CCACGTCGCCGSCATACCTGATCTTTTAAATGAAGTCTGAACATTTGTAACCTGT	17571
QY	1634	-----	1633
Db	17572	CCTGAGCAATAAGACCTTAGTATTTATTTAGCTTGCCACCCCGAGCTGTGCTGT	17631
QY	1634	-----	1633
Db	17632	TTTCCCTGCTAGTATGTTCTATCTAGCATCTGAACCCCGACAGCTAAGCATAT	17691
QY	1634	-----	1633
Db	17692	TAAATATGTTTTCCGTTGAGTGTGTTCTGATGTTGCCCGCCGCTTTCTCTCT	17751
QY	1634	-----	1633
Db	17752	TGTTCCTCCGCTGTCTCTCTGTCAGGCCCGCTGCGGTTCCCTTCCTCTTT	17811
QY	1634	-----	1633
Db	17812	GCGTGTTCTTCTCTCTTTATTTGCTGTGAACCCAGCTTTACTGTGCTGCCA	17871
QY	1634	-----	1633
Db	17872	TGGCATGAGCAGCTCCGGGACCTCTGTTATGATGACAGATGAATGTGAGACT	17931
QY	1634	-----	1633
Db	17932	CACGAGAGGCGGTCATCTTGCCCGTGTGATGTCGAGACACAGTGCGCAGCTTC	17991

QY	1634	-----	1633
Db	17992	TTAGCAGTAGTACAGCAGACGTCCTCGCTGCGTTCAACCTGAAAAACCCAGGC	18051
QY	1634	-----	1633
Db	18052	ATGTGGGCTGTGTGTGCTCCGCGGTGTCGATTTGAATCGCGCAACTGCGGTGG	18111
QY	1634	-----	1633
Db	18112	CCCGAGCTCTAGCGTCTGCTGCGCGGAGTGTCTCTCTCTCTCTCTGGA	18171
QY	1634	-----	1633
Db	18172	ACCAGACAAGATGAGGCTCCGACCGTTGTGCCCAACAGAGCATGATGAGCA	18231
QY	1634	-----	1633
Db	18232	TGTGATTAATTTTAAATTTCTAGCTGGGCGGCTGCTACGCTGTATCCAGCAC	18291
QY	1634	-----	1633
Db	18292	TTTGGAGGCCAAGCGGCTGATCAGAGGTGAGAGTCTGAGACCATCTGGCAACA	18351
QY	1634	-----	1633
Db	18352	TGATGAACCCATCTGTACTAAAAACAAAAAATAGTGGCGTGTGGCGGTGCT	18411
QY	1634	-----	1633
Db	18412	GTAATCCAGCTACTCGGAGGCTGAGCAGAGATTTGCTGAACCTGGAGTTGMA	18471
QY	1634	-----	1633
Db	18472	TTGCAATGAGCCGATTTGACACACTGCACCTGCGCAACAGGAGACTGTCTC	18531
QY	1634	-----	1633
Db	18532	TCAAAAAAATAAAAAAAAAAAAAAAAAAATTTCTAGTACCATTTAAAAAGTAAAA	18591
QY	1634	-----	1633
Db	18592	AGAAAAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	18651
QY	1634	-----	1633
Db	18652	TCAATTTAGGCTGTTATTTGTTGAGCATCATCATGACATTTGATTTTGTAGCT	18711
QY	1634	-----	1633
Db	18712	TTGCTGGGATCCGTTGTAGTCCCGTGGCTGACATCTCGGCTGAGCTGTGG	18771
QY	1634	-----	1633
Db	18772	GCTTCCATGGCATGGCTGTGTGTACAGATGTGACAGTCCGGATGAGTCCGACAGC	18831
QY	1634	-----	1633
Db	18832	CCTCAGTAGCTGATGTGACAGTCTCCGATGTGACAGTCTGTGGATGAGTCCGACAGC	18891
QY	1634	-----	1633
Db	18892	CCTGCTGAGCTGATGT	18951
QY	1634	-----	1633
Db	18952	CCCTGCTGAGCTGAGTATGAGATGCGGATGATGACAGTCCGGGATGAGTCCGACAGC	19011
QY	1634	-----	1633
Db	19012	CCCTGCTGAGCTGATGT	19071
QY	1634	-----	1633

D 19072 GCCCTCGTAAGCTGAGGATGAGTCCGATGATCAGGTCGGGGTGAGTCCGAC 19131
Q 1634 ----- 1633
D 19132 GCCCTGCTGAGCTGATGTGTGTCTGATGTCAGGTCGGGGTGAACCA 19191
Q 1634 ----- 1633
D 19192 GGCCCTCGGAGAGCTGGGTGTGCGTGTCTGATGGTGCAGTCTGGAGTGAAGTGGC 19251
Q 1634 ----- 1633
D 19252 AGACGTCGACAGACCATGCGGTGAGTGAATATCCGGTTCGCGATGGTGCAGTCTGG 19311
Q 1634 ----- 1633
D 19312 GTGAGTTGCCAGGCCCTGCTGTGATTTGATGTGGGGTTCGCGATGTCAGGTCGG 19371
Q 1634 ----- 1633
D 19372 TGTGAGTCAACAGGCCCTGCTGTGAGCTGAGTGTGTGTCTGATGGTGCAGTCTG 19431
Q 1634 ----- 1633
D 19432 GGTGAAGTCCAGGCCCTGCTGTGAGCTGAGTGTGTGTCTGTGATGGTGCAGG 19491
Q 1634 ----- 1633
D 19492 TCTGAGTGAAGTCCAGGCCCTCGGTGAGCTGAGTGTGATGTCAGTGTCCAGTGTG 19551
Q 1634 ----- 1633
D 19552 TCCGGGGTGAAGTCCAGACCCCTGCGGTGAGTGTGATGTGCGGTGTCTGTGATGTG 19611
Q 1634 ----- 1633
D 19612 GTCTGAGTGAAGTCCAGGCCCTCGGTGAGCTGATGATGATGCCGATGCCGATGCCG 19671
Q 1634 ----- 1633
D 19672 GTCCGGGGTGAAGTCCAGACCCCTGCTGTGAGCTGATGTGCGGTCTGTGATGTACA 19731
Q 1634 ----- 1633
D 19732 GGTCTGAGTGAAGTCCAGACCCCTGCTGTGAGCTGATGATGCCGATGCCGATGCC 19791
Q 1634 ----- 1633
D 19792 AGTCAAGGGTGAAGTCTCAGGCCCTCGGTGAGCTGAGATGAGATGCCGATGATGC 19851
Q 1634 ----- 1633
D 19852 AGTCCGGGGTGAAGTCCAGGCCCTGCTGTGAACTGATGTGCGCGTCTGTGATGTG 19911
Q 1634 ----- 1633
D 19912 CAGGTCTGGGGTGTGTCCGACGCCCTCGGTGAGCTGAGATGAGATGCCGATGATG 19971
Q 1634 ----- 1633
D 19972 CAGGTCCGGGGTGAAGTCCAGGCCCTGCTGTGAGCTGATGTGCGCGCTGTGATGTG 20031
Q 1634 ----- 1633
D 20032 GCAGGTCTGGGGTGTGTCCGACGCCCTCGGTGAGCTGAGATGAGATGCCGATGAT 20091
Q 1634 ----- 1633
D 20092 GCAAGTCCGGGGTGAAGTCCAGGCCCTGCTGTGAGCTGATGTGTATCCGATGG 20151
Q 1634 ----- 1633

D 20152 TGCAGTCCGGGGTGAAGTCCGACGCCCTGCTGTGAGCTGATGTGCTATCCGATGC 20211
Q 1634 ----- 1633
D 20212 TGCAGTCTGGGGTGAAGTCAACAGGCCCTGCGGTGAGTGTGTGTGCGGGTGTG 20271
Q 1634 ----- 1633
D 20272 CTGCAAGTCCGGGGTGAAGTTCGACAGGCCCTCGGTGAGCTGATGTGCGGTGCCGTG 20331
Q 1634 ----- 1633
D 20332 TCCGATGTGACAGTCCAGGGTGAAGTCCCTAGGCCCTTGTGGGCTGATGTGCCGTG 20391
Q 1634 ----- 1633
D 20392 TCCGATGTGACAGTCTGGGGTGAAGTCCGACGCCCTTGTGAGCTGATGTGCCGTG 20451
Q 1634 ----- 1633
D 20452 TCTCATGTGACAGTCTGGGGTGAAGTCCGACGCCCTTGTGGGCTGATGTGTGTTG 20511
Q 1634 ----- 1633
D 20512 TCCGATGTGACAGTCCGGGGTGAAGTCCGACGCCCTGCTGTGAGCTGATGTGCCGT 20571
Q 1634 ----- 1633
D 20572 GTCTGATGTGACAGTCCGGGGTGAAGTACCAAGGCCCTTGTGATGTGATGTGGG 20631
Q 1634 ----- 1633
D 20632 TGTCCGATGTGACAGTCCGGGGTGAAGTCCGACGCCCTGCGTTAGCTGATATGC 20691
Q 1634 ----- 1633
D 20692 GTTCCGATGTGACAGTCCGGGGTGAAGTCAACAGGCCCTGCGTTAGCTGATATGC 20751
Q 1634 ----- 1633
D 20752 GGTCTGATGTGACAGTCCGGGGTGAAGTCCGACGCCCTGCTGTGATGTGATGTG 20811
Q 1634 ----- 1633
D 20812 CTGTATCCGATGTGACAGTCCGGGGTGAAGTCCGACGCCCTGCACTGATGATGT 20871
Q 1634 ----- 1633
D 20872 GCTGTATCCGATGTGACAGTCTGCGGTGAGTCCGACGCCCTGCGTTAGCTGATG 20931
Q 1634 ----- 1633
D 20932 TCCGATGTGACAGTCCGAGGTCCGGGGTGAAGTCAACAGGCCCTGCGTTAGCTGATG 20991
Q 1634 ----- 1633
D 20992 TCCGATGTGACAGTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGATGTGAT 21051
Q 1634 ----- 1633
D 21052 GTGCTTATCCGATGTGACAGTCCGGGGTGAAGTCCGACGCCCTGCGGTGATGTGA 21111
Q 1634 ----- 1633
D 21112 TGTCTTATCCGATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 21171
Q 1634 ----- 1633
D 21172 ATGTCAAGTGTACGATGTGACAGTCCGGGGTGAAGTCCGACGCCCTGCGGTGAGTGTG 21231
Q 1634 ----- 1633
D 21232 TATGTGTGTGTGTGATGTGACAGTCCGGGGTGAAGTTCGACAGGCCCTGCGGTGAGT 21291

Dh 23452 TGGGGTCTGCTGGGGCCAGCCCTTGGGCTACCCAGTGGCTTACCAAGAGGACAGGC 23511
Qy 1829 ----- 1828
Dh 23512 ATCTGTGTGAGGGGCATGGGTTACGTGGCCAGATGCAGCCTGGAGCCAGGCTCCC 23571
Qy 1829 ----- 1828
Dh 23572 TGGTCTGATGGTGGGACAGTCAACCCCTGGGGTTGACCCGGAGCTGGGCTCCCCAGG 23651
Qy 1829 ----- 1828
Dh 23652 TTGACTATAGGACAGAGTGTCCAGTGCCTGCAGTAGAGGGGCTCTAGAGCGCTGTG 23691
Qy 1829 ----- 1828
Dh 23692 GCTGGCATGGGTGACAGTGGCCCGGGGATGGCTTACAGCTGTGCTGCCGTGGTCCC 23751
Qy 1829 ----- 1828
Dh 23752 TGAGCCCTCAGTGAAGTGGTGGGGCTTGTGGCTTCCGCTAGCTTCCCTAGTCTGT 23811
Qy 1829 ----- CAGACAGCATTTGAAGAGGTGC 1851
Dh 23812 GTCTGGCTGAGCAAGCCTCTGAGGGGCTCTATTTGACAGACAGCATTTGAAGAGGTGC 23871
Qy 1852 AGCTGGGGAGCTGTGAGAGCAGAGTCAAGCAGCATCGGGAAGCCAGGCCGCTGC 1911
Dh 23872 AGCTGGGGAGCTGTGAGAGCAGAGTCAAGCAGCATCGGGAAGCCAGGCCGCTGC 23951
Qy 1912 TGAGCTCAGAGCTCGCTTCAATCCCAAGCTGACGGGCTCGGCCGATTTGAACATG 1971
Dh 23952 TGAGCTCAGAGCTCGCTTCAATCCCAAGCTGACGGGCTCGGCCGATTTGAACATG 23991
Qy 1972 ACTAGCTGTGGAGCCAGAGCTTCCGACAGAAAGAG----- 2011
Dh 23992 ACTAGCTGTGGAGCCAGAGAGCTTCCGACAGAAAGAGGGTGGCTGTGCTTGTGTTA 24051
Qy 2012 ----- 2011
Dh 24052 ACTTCCTTTTAAAGAGAGTGGCTTTGAGCCCACTTTGATACAGTTAGATGAGG 24111
Qy 2012 ----- 2011
Dh 24112 GCCCGAGAGGGGCCAGGGACACAGCCAGGCCANTGACAGGGCCCAACCATTTGTG 24171
Qy 2012 ----- 2011
Dh 24172 CGCAGAGTGAAGTGGCCGAGGTCCGGTCTCCAGAAAAGCAGCTGGGGGTAGGGG 24231
Qy 2012 ----- 2011
Dh 24232 GAGTCTCGGGGAGGAGCAGAGCTGTGAGACACAAGAAAGACAGCCGGGCGAGGCTGG 24291
Qy 2012 ----- 2011
Dh 24292 ATGAGACAGGCCCGAGAGTCTGTGATCCGTCTCTGTGTGTGTCAGACCTCCGTGGC 24351
Qy 2012 ----- 2011
Dh 24352 TTCCGCTTACGGGGCCGGGGAGCAGGACAGACTGCCAGGAGCCACCGGGCTCTGAGG 24411
Qy 2012 ----- 2011
Dh 24412 ATCTGAGACCTTGGCCACAGGCTCTGAGACCCACCCCTGTGGGTGGGTGGCTGGCTG 24471
Qy 2012 ----- 2011
Dh 24472 ACCCCGTCATCTGAGAGAGTGTGGGTGAGGTGAGAGAGAGTGTGCATGAGATCCCG 24531
Qy 2012 ----- 2011

Dh 24532 TGTGCACACACATGCGGCCAGGAACCCGTTTCAAAACAGGGTCTGAGGAAGCTGGGAGG 24591
Qy 2012 ----- 2011
Dh 24592 GTTCTAGTCCCGGGTCTGGGTGCTGGGACACTGGGGAGGGCTGCTTCTCCCTGGG 24651
Qy 2012 ----- 2011
Dh 24652 TCCCTATGGTGGGGGACTTGGCCGATCCACTTCTGACTGTCTCCATGCTGTG 24711
Qy 2012 -----GCCGAGCGTCTCACCTGAGGGTGAAAGCACTGTACGCTGCTCAACTACG 2064
Dh 24712 CCGGACAGCCGAGCGTCTCACCTGAGGGTGAAAGCACTGTACGCTGCTCAACTACG 24771
Qy 2065 AGCGGGCGGGGCGCCCGGCTCTGGGGGCTGTGCTGTGGGCTGGACATATCCACA 2124
Dh 24772 AGCGGGCGGGGCGCCCGGCTCTGGGGGCTGTGCTGTGGGCTGGACATATCCACA 24831
Qy 2125 GGGCTGGGACACCTTCTGCTGCTGTGCGGGCCAGAGACCCGCGCTGAGTGTG-- 2182
Dh 24832 GGGCTGGGACACCTTCTGCTGCTGTGCGGGCCAGAGACCCGCGCTGAGTGTGACT 24891
Qy 2183 ----- 2182
Dh 24892 TTGTCAAGTGGTGTCCGGGAGCCCGCTGAGACCCCTGTGACCTTGGGAGTGGCTG 24951
Qy 2183 ----- 2182
Dh 24952 CCTGATTTGGACCTTATGTTGGGTGAGAGAGTACTCTGGGTGGGCGGAGAGTGTCA 25011
Qy 2183 ----- 2182
Dh 25012 GGTGACCTGTACCTGTGAGAGACACACCTGGACCTAGGGTGAGGCTTACAGCTTTC 25071
Qy 2183 ----- 2182
Dh 25072 CTGCAGCAGATGGGGCGAGCTGTGCACCTGACTGCCCCGCTCTTATTTCCAAAGAGG 25131
Qy 2183 ----- 2182
Dh 25132 TCCCACTGATTCAGTTTCCGCTCAGAAAGAAACCGCACGGCTCAGCCACAGGCCCC 25191
Qy 2183 ----- 2182
Dh 25192 GGTGCTTGCACCCAGCTGAGGACAGGGGCTCTCTGTGAGGCTCAGAGAGGGAC 25251
Qy 2183 ----- 2182
Dh 25252 ACAGCCGCGCTTGGCTTGGGGTGTGAGTGGTGGGTGAGAGAGAGTGGGGACAC 25311
Qy 2183 ----- 2182
Dh 25312 CGCCAGGCGAGGCCCTGAGGGCAGAGTGTGAGTTCTGTGCGTGGCCACTGTGAGT 25371
Qy 2183 -----CATCCCCAGGA 2194
Dh 25372 CTCTCGCTCAGTCAACAGAGTGTGATGACGGGCGCTGACAGACACACATCCCCAGGA 25431
Qy 2195 CAGGCTCAGGAGGTCATCGCAGCATCATCAAAACCCAGAAACAGTACTCGGTCGTCG 2254
Dh 25432 CAGGCTCAGGAGGTCATCGCAGCATCATCAAAACCCAGAAACAGTACTCGGTCGTCG 25491
Qy 2255 GTATGCCGTGGTCCAGAAAGCCGCGCATGTGGCAGCTGCGCAAGGCTTTCAGAGACAC-- 2312
Dh 25492 GTATGCCGTGGTCCAGAAAGCCGCGCATGTGGCAGCTGCGCAAGGCTTTCAGAGACACGT 25551
Qy 2313 ----- 2312
Dh 25552 AAGGTCACGTGTGATGCTGTCTCAGAGATGTGTCTTGGGATATGATGTGTAG 25611
Qy 2313 ----- 2312
Dh 25612 AATGACGTGCTGTGTGATGCGTTTCTGTGTGAGAGTACTTCCATGATTTACACATCT 25671

Db 27832 CGGATTTCTGTGATGCTTTCCGCCGACCTCAGACCATGGGCTATTGTGGCGGTGTC 27891
QY 2313 ----- 2312
Db 27892 CTCTCTGGGTTGGAAAGGTCAGGCCCATGTACTTCTGTTACTGCTTCCAGGT 27951
QY 2313 ----- 2312
Db 27952 TGGTTTCAGAGTTGATCTACTCATGTGTGTTTAGCCACGCGCCCTGCGCAGCTC 28011
QY 2313 ----- 2312
Db 28012 CTGGGGCTGGGGAACATGCTGAAGCAGAGTCACCGTCGCGCTTTTGTATGCTCAC 28071
QY 2313 ----- 2312
Db 28072 AAGCTGAGGCCCTCTGTCTCCGTGTAGTGTGTACAGTGCCTGCTCACAATCCTGT 28131
QY 2313 ----- 2312
Db 28132 TGGGACGACAGGGGCTTAGCAGGTCCCGTAGTAATGACAAGCGTCTGGGGAGTCTGC 28191
QY 2313 ----- 2312
Db 28192 AGAATAGAGAGTGGGGGTCCGGTCTCTCTCCCGCTCTTCAGACTCTCTCTGCTGT 28251
QY 2313 ----- 2312
Db 28252 GCTGTGGCTGCACCTGCATCCCTGCAATCCCTCCAGACACTGGGCTGAGAGCCCGGAG 28311
QY 2313 ----- 2312
Db 28312 CTCGAGTGCACCTTGTCCACGTACTGTGATGAGCAGTGCAGCGGGGCTCATGTG 28371
QY 2313 ----- 2312
Db 28372 TGGTACTGTGATGCGCGTTGTCACAGGGTCTGATGTGTGTGACTGTGATGCGG 28431
QY 2313 ----- 2312
Db 28432 TCGTGGGGTCTGATGTGTGACTGTGATGCGCGTCTGCGGCTCATGTGTGTGACTG 28491
QY 2313 ----- 2312
Db 28492 TCGATGGCGGCTCGGGGCTGTGATGTGTGACTGTGATGCGCGTCTGCGGCTCATGT 28551
QY 2313 ----- 2312
Db 28552 GGTGACTGTGATGCGCGTCTGCGGCTGTGATGTGTGACTGTGATGCGAGTCTGCGG 28611
QY 2313 ----- 2312
Db 28612 TCTGATGTGTGACTGTGATGCGCGTCTGCGGCTGTGATGTGTGACTGTGATGCG 28671
QY 2313 ----- 2312
Db 28672 AGTCGTGGGCTGTGATGTGTGACTGTGATGCGCGTCTGCGGCTGTGATGTGTG 28731
QY 2313 ----- 2312
Db 28732 ACTGTGATGCGCGTCTGCGGCTGTGATGTGTGACTGTGATGCGCGTCTGCGGCTC 28791
QY 2313 ----- 2312
Db 28792 TGTATGTGTGACTGTGATGCGCGTCTGCGGCTGTGATGTGTGACTGTGATGCGG 28851
QY 2313 ----- 2312
Db 28852 TCGTGGGGTCTGATGTGTGACTGTGATGCGTCAAGGGTCTCATGTGTG 28911
QY 2313 ----- 2312

Db 28912 GTGACTGTGATGCGCGTCTGGGGTCTGATGTGTGTGACTGTGATGCGTCA 28971
QY 2313 ----- 2312
Db 28972 CAGGGCTCATGTGTGTGACTGTGATGCGCGTCTGGGGTCTGATGTGTGTGACTG 29031
QY 2313 ----- 2312
Db 29032 TGGATGCGGTTGTCCCGGGGCTGTGATGTGTGACTGTGATGCGATCGTCACA 29091
QY 2313 ----- 2312
Db 29092 GGGGCTCATGTGTGTGACTGTGATGCGCGTCTGCGGCTGTGATGTGTGACTGTG 29151
QY 2313 ----- 2312
Db 29152 GATGGCGGTGTGGGCTCATGTGTGTGACTGTGATGCGCGTCTGGGGTCTGATGT 29211
QY 2313 ----- 2312
Db 29212 GTGACTGTGATGCGCGTCTGGGGTCTGATGTGTGACTGTGATGCGCGTCTGCGG 29271
QY 2313 ----- 2312
Db 29272 TCTGATGTGTGTGACTGTGATGCGCGTGTGTCCGGGGTCTGATGTGTGACTGT 29331
QY 2313 ----- 2312
Db 29332 GGATGGCGGTCGTGGGGTCTGATGTGTGACTGTGATGCGACGTGCGGGGCTCATGTG 29391
QY 2313 ----- 2312
Db 29392 TGGTACTGTGATGCGCGTCTGGGGTCTGATGTGTGACTGTGATGCGCGTCTG 29451
QY 2313 ----- 2312
Db 29452 GGGTCTGATGTGTGTGACTGTGATGCGCGTGTGGGGTCTGATGTGTGTGACTGTG 29511
QY 2313 ----- 2312
Db 29512 ATGGCGGTCGTGGGGTCTGATGTGTGACTGTGATGCGCGTGTGGGGTCTCATGTGTG 29571
QY 2313 ----- 2312
Db 29572 GTGACTGTGATGCGTCTGCGTCAAGGGTCTGATGTGTGACTGTGATGCGGCTC 29631
QY 2313 ----- 2312
Db 29632 GTGGGCTGTGATGTGTGTGACTGTGATGCGCGTGTGGGGTCTGATGTGTGTGACTGTG 29691
QY 2313 ----- 2312
Db 29692 GATGGCGGTCGTGGGGTCTGATGTGTGACTGTGATGCGCGTGTGGGGTCTGATGT 29751
QY 2313 ----- 2312
Db 29752 GTGACTGTGATGCGTCTGCGTCAAGGGTCTGATGTGTGACTGTGATGCGG 29811
QY 2313 ----- 2312
Db 29812 GTCTGGGGTCTGATGTGTGTGACTGTGATGCGCGTCTGCGGCTGTGATGTGTGTA 29871
QY 2313 ----- 2312
Db 29872 CTGTGATGCGCGTCTGCGGCTGTGATGTGTGACTGTGATGCGCGTCTGCGGCTCT 29931
QY 2313 ----- 2312
Db 29932 GATGTGTGACTGTGATGCGTCAAGGGGCTCATGTGTGTGACTGTGATGCGAGTG 29991
QY 2313 ----- 2312
Db 29992 GAGTCCAGGTGTGTGTGTGACTTGTGCGTCTGCGGCCCGCCCGCCCGCTTCCAA 30051

Db	30052	ACGAAAGCTTCCACAGGGGCTCTCTGGGGCTTATCCCGCATCGGGCTTGCCGACGTCC	30111
Qy	2313	-----	2312
Db	30112	ACAGCTCTGATCGAAGAAACAAGTGCCAGCTGTGGCCGGGACGGCCACATTGTGG	30171
Qy	2313	-----GTCTACCTTACAGACCTTCACGGCGTACATGCG	2347
Db	30172	CTCATCCCTCTCTCTCTGCCCCGAGGTCTCTACCTTACAGACTTCACGGCGGTACATGCG	30231
Qy	2348	ACAGTTCGTGAGCTACATGTCAGAGACACAGGCCCGCTAGAGGATGCGCTGTCATCGA---	2404
Db	30232	ACAGTTCGTGAGCTACATGTCAGAGACACAGGCCCGCTAGAGGATGCGCTGTCATCGAGCA	30291
Qy	2405	-----	2404
Db	30292	GGTCTGGGAGCTGGCCCTGCAGGGTTGGGACGGACTCCACGAGTGGGTCTCCCTCGGG	30351
Qy	2405	-----	2404
Db	30352	CAATCACCTGGGCTATATACCGGACAGACTGTTGGCCCTGGGGGGCAGTGGGGGAATGAG	30411
Qy	2405	-----	2404
Db	30412	CTGTATGGGGGCAATGATGAGCTGTGTGCTTGGCAATCTGAGCTGGCCATGCCAGG	30471
Qy	2405	-----	2404
Db	30472	CTGCGACAGCTGTGCATTCAGGACACTGTACAGTTTGACTGGGGGCTCTCTCCAGT	30531
Qy	2405	-----	2404
Db	30532	TCCGAGTGCCTTTGTTTCATGATTTGTCTAAATGTCTTCTGCGCAGTTTGTATCTTAGG	30591
Qy	2405	-----	2404
Db	30592	CCAAAGAAAGGTGTCCCCCTCTCTTAGAGAGGACGCACTGTTGAGCGGTGTCCTGCC	30651
Qy	2405	-----	2404
Db	30652	CAGTGTGGCCCCCAGTGTCTGGGTCTGAGGCCAAGAAAGATGTCTCCCTCTTAGAGAG	30711
Qy	2405	-----	2404
Db	30712	ACGGGCGGTGTTTAGCGCACGCCCGGCTGAGGGGCTCTCAGTGTGGGTCTCTCAGC	30771
Qy	2405	-----	2404
Db	30772	TGGCCCTGTGGCCCTTGTGCAGATGTGTGTGTGCAGGTGGCCCTGTGGCTCTTGCAGAT	30831
Qy	2405	-----	2404
Db	30832	GGCTGTTAGCACTGTCTCGGCTCTTAGGGAGACATGTCTCACCGCATGAGGCTCAGAGA	30891
Qy	2405	-----	2404
Db	30892	CCCTGTGGGCAATTTCTTGGCTCCAGGGGTGGGGGTGAGAGTGGGCTGGGCTGTGCGGA	30951
Qy	2405	-----	2404
Db	30952	CCCAAGACCTGTGGCCGGCAGCTGGGCAAGCAATCTTGATTCATATGCCATCCGGGCC	31011
Qy	2405	-----	2404
Db	31012	ACGGTGGGCTGTGTGGGTGTGAGCCACAGCTGAGCCCAAGTGGGCCAGAGAGACGTTG	31071
Qy	2405	-----	2404
Db	31072	TGTGTCAACACTTGCTTAAGCCCATGTGTGTCTGCAGAGACTGGCCCGGCCAGCCCA	31131

2405	----	2404
Db	31132 CGATGGCCCTGATCTTACGAGCCAGCCCGGACCTTCATCATCAAAACACTGACCCCAAAAGG	31191
2405	----	2404
Db	31192 ACGGAGGCTTTGGCCACGTTGGCTTGGCTGTCTTCAGACACCCAGCCGCTCACTCCCATGT	31251
2405	-----GCAAGCTCTCTCCCTGAATGAGGCGACGATGGCCCTTCTGAC	2447
Db	31252 GTCTCCGCTGTGCTTTGGACAGACTCTCTCCCTGAATGAGGCGACGATGGCCCTTCTGAC	31311
2448	GTCTCTTACGCTTTCATATGTGCTCCACACGCGCTGGCATCAGGGGCA	2494
Db	31312 GTCTCTTACGCTTTCATATGTGCTCCACACGCGCTGGCATCAGGGGCAAGTGAATCAGGTGG	31371
2495	-----	2494
Db	31372 CCAGGTGCATTTGGCCCTGCGGCTGGGCTGGGCGGGCTGGCAGGGCTTCTGCTACCTCTCT	31431
2495	-----	2494
Db	31432 CTTGCCCTTCCCACTGACCTTCTGCTCCGGGGGACACAGAGTCTCTTTCTGAGCCCC	31491
2495	-----	2494
Db	31492 GCCCCCTCCGAGCTCTGTGGGCTGAGGCTCCGAGGCCCGGAACATGTCCTGGCTTGG	31551
2495	-----	2494
Db	31552 GCAGCCGAGCGAGACAGATGTCCACACGAGGCTTGAAATGGCAGCGGGGTGTGAGATT	31611
2495	-----	2494
Db	31612 GCTTCCTGGAGGAGCAGAGGGCGGGGGTGTCTTGGGTCAAGTGTGCGCCGACGCTT	31671
2495	-----	2494
Db	31672 TGAGCTGCAGCTGTGTAGCTCCAACTTACTATGACGTGACACCGGCTCTACACG	31731
2495	-----	2494
Db	31732 CTTGTATCTCTCTCCCGATACAAAAGATTATTCGATTCCTCTGCTCTGTC	31791
2495	-----	2494
Db	31792 GTGTGACCCCGCAGAGGCGCGGGCTTCTCTCTGTGACTAGATTTCATCCATCTGGAAG	31851
2495	-----	2494
Db	31852 TGGCGGTTGACCGTGTAGTTGTCTCTCGGGGGGCTGTGGCCATGGGGCAGGC	31911
2495	-----	2494
Db	31912 GGGCTGGGAGAGCTGGCGTCAACAGCCACTGGGTGAGCCACACTCAGGTGTGAGAGCC	31971
2495	-----	2494
Db	31972 ACGATCCGTTGGCCACATCACTCTCTGATTTTAAGTAAACACACACACTCCGGC	32031
2495	-----	2494
Db	32032 AGGCATCTCCCTGGGACCCCTGTGTGTGCTGGGGAGAGTGTAGCACGGAGAAATTCGT	32091
2495	-----	2494
Db	32092 GCACACTCAAGTCAATCAGCAAGGTCAATCCGAGTCAAGTGAACGTGGAGCCCTCTCTC	32151
2495	-----	2494
Db	32152 TGGGATCTCTCAGCGGATAAAGACTGTGCACAGCTTGGAAAGCTTTATTTAAAAAT	32211
2495	-----	2494

Dy	2608	-----	2607
Db	34432	CCTGCCAACCATAATGTGTTCAACACTCAGCTGGCTTTATTATGCAGCAGTACTTTTTTTT	34491
Oy	2608	-----	2607
Db	34492	TTTTTAATCCTTAAAGTTCTTAGGGTACATGTGCACGACGTGACAGTTAGTACATATATAT	34551
Oy	2608	-----	2607
Db	34552	ACATGTGCATGTTGTGTGTGTGCACCCATTAACTCATTCATTTAAATTAGGTATATCTCC	34611
Oy	2608	-----	2607
Db	34612	TAAATGATATCCCTCCCACACTCCCCCATCCCATGACAGGCCCTGTGTGTATGTCCCC	34671
Oy	2608	-----	2607
Db	34672	ACCGTGTCGAAGTGTTCATGTTCAGTTCCACCTGTGAGTAGAACATGTGTTGT	34731
Oy	2608	-----	2607
Db	34732	TTGGTTTCTTCTTGCCAAATAGTTTGCTCAGAGTATGTTTCCAGGTTGTGCATGTC	34791
Oy	2608	-----	2607
Db	34792	CCTAACAAGACATGACACTACCTTTTTTTATGACTCATAGATTTCCGTGTATATG	34851
Oy	2608	-----	2607
Db	34852	TGCAACATTTCTTAAATCCACAGTCTATCATGCATGGACATTTGGGTTGGTTCGAAGTCTT	34911
Oy	2608	-----	2607
Db	34912	GCTACTGCAATAGTGCCTGCATTAACATACGTGTGCATGTCTTTATAGACAGCATGAT	34971
Oy	2608	-----	2607
Db	34972	TTATATATCCTTTGGGTATATATCCACAGTAAATGGATGGCTGATCAATATTTCTAGT	35031
Oy	2608	-----	2607
Db	35032	TCTAAGTCTTTGAGGAATCACACACACTGCTCTTCCACAATGGTTGAACATGTTCACTCC	35091
Oy	2608	-----	2607
Db	35092	CACCAACAGTATAAAGTGTTCGTGCTGAGAGAGATGTGACAGCAGTATTTTTTTTA	35151
Oy	2608	-----	2607
Db	35152	TGAAAATAGTATCACTGAACCAACAGACAGTTAGTGAAGATGCTGCAGGAAGCTCGAG	35211
Oy	2608	-----	2607
Db	35212	GCACACAGCATTTCCTCTGGAAGACTCGGGTTTTTCCTGTGCATCTTTTGAACCTGA	35271
Oy	2608	-----	2607
Db	35272	GCTCCATTTATAGCATATACAGTGGATCAAGTCTCTTCAATTAAAGTTCAAGTTCTAG	35331
Oy	2608	-----	2607
Db	35332	AATTGAATATAGTTTATGTAAACAGAAACAAAAATTTCTTTGACACACACTGTCTGGGA	35391
Oy	2608	-----	2607
Db	35392	TTTGGAGAAAGTGTCTCGAGCTGTGGCGCACACTGTGCAGCCCTGTGGAGAGATACC	35451
Oy	2608	-----	2607
Db	35452	TCTGGCCATGTGCATGGGGCGCTGGGCTTGCGCTGAGGCTCACACAGTGCACCATGCC	35511

OY	2608	-----	2607
Db	35512	CACGCTCCTGTGGATAGGATCTGGCTCTGGATCATGCTGAGGACACACAGCTGCCATGCT	35571
OY	2608	-----	2607
Db	35572	GGTAAAGGACACACGTGGCTCAGAGGGGGGAGGTTCCAGCCCGCTTCTTAACCGT	35631
OY	2608	-----	2607
Db	35632	CTTCACTAATTTTTTCCTAAGAGCTCGAAGAGTGGGGCCGCGCTGATGGCCCTTTCGTTCG	35691
OY	2608	-----	2607
Db	35692	TCCTACGTGGCAGAGATTCACAAGCTGATGTAAACACTGATACTATTAATGAATG	35751
OY	2608	-----	2607
Db	35752	AGGAATTCGTGACAGTTAACTGTAGAGAGCTGCTGTTGGAAAGAAATTAAGTTT	35811
OY	2608	-----	2607
Db	35812	TCATTTAACCCTTTGGAGAATGTACTTATTTATATGCGTGTAAATGTTGACATTC	35871
OY	2608	-----	2607
Db	35872	AGTCCCTGTAAGACATCTACTAGTAAAGAATGAAGTTAACTTCGTGATATTTCC	35931
OY	2608	-----GGCTGCTGCTGCTTGGTGGAGATTTCTGTTGGAGACCTGACTCA	2658
Db	35932	CTTATTTTAAAGCTGCTGCTGCTTGGTGGAGATTTCTGTTGGAGACCTGACTCA	35991
OY	2659	CCACGCCGAAAACCTTCTCT- 	2678
Db	35992	CCACGCCGAAAACCTTCTCTCAGGTGAGGCCGCTGCTGTCTGTGGGACCTCCACAG	36051
OY	2679	-----	2678
Db	36052	CGTGTGGCTTTGCAGTGAGCCCGCGTCTGCCCCGTCGACCCGACAGCGTTGCTCT	36111
OY	2679	-----	2678
Db	36112	GCCAAGTCCTCTCTCTGTGCGGTCGCTGATCCGCAAGACAGAGCGCTTGGCCGTGCA	36171
OY	2679	-----	2678
Db	36172	CCCAGGCTGGGGGCGCAGGGGACCTTGGGAGGAGTGGTACCGTGCAGGCCCTGGT	36231
OY	2679	-----	2678
Db	36232	CCTGAGAGACGACACCGAGGTTACACACGTGATGACAGGCGGTGACGTGCTCTGC	36291
OY	2679	-----	2678
Db	36292	TGCTTTTGAAGAAGTCAAGAGTGGCGGCTCTGGGGGCCCCAGTAGAACCOCGAGAGCTG	36351
OY	2679	-----	2678
Db	36352	TGACACAGGCGCTCGAAGGGCCGAGCGCGACGCTCTCCACAGGTCACACTGACCGCTGG	36411
OY	2679	-----	2678
Db	36412	GAAAGCAGAGAGCTGCTAGTGAAGTGGCCACAGCGTTCCGCTCGGCTCACGTTCCCTGCT	36471
OY	2679	-----	2678
Db	36472	GGGGTTGTTGGAGTCGGTGGGAAATTTGGATTTGCTGATGCTGCTGTCTTAACACAC	36531
OY	2679	-----	2678
Db	36532	GGAGATGCGTAGAGTGGGTTTTCAGAGTTGATTTTTTGTGAATCAATAAATCAGGCAC	36591
OY	2679	-----	2678

Db 36592 AGGGACCTGGCTCAGCACAGGGGANTTCCAAATGTGTCCCTCAAGGGCGCCAC 36551
QY 2679 ----- 2678
Db 36652 AGAGCCGTGGCTTGTTTTAAAGTCGATTTGACAGAGGACGAAACCTTGAAGCTG 36711
QY 2679 ----- 2678
Db 36712 TAAAGGAACCTCAGAAAATGTGGCCGACAGGGGTGGTTTCAAGTGTCTTGTGGGCTG 36771
QY 2679 ----- 2678
Db 36772 TGTTTGTGAAAACCAATTTGAGCCGCCCTCCAAATCCACCTCCAGTCCACCTCCAG 36831
QY 2679 ----- 2678
Db 36832 GGGCGCCCTGGGCTGGGGGTTTGCCTGGCTTCTTGTGCGGACGCCGAGCACAGCAG 36891
QY 2679 ----- 2678
Db 36892 GCTGTGCATTTAATCCACTAAGATTCACTCGGGGGGAGCCGAGTCCCAAGCACTG 36951
QY 2679 ----- 2678
Db 36952 AGGGCTAGAGTCTCTGAGGCTCTGAGGGGACAGAGCAGAGGGGAACGCTGCTTCTGT 37011
QY 2679 ----- 2678
Db 37012 GTGCAAGTTCCTAGAGGTGCTGGCCAGGGAGTGCTCAAGATGTATGTTGGGGTCCA 37071
QY 2679 ----- 2678
Db 37072 CCGGGGACAGAACTGTGTCTGTATGATGTCGGACCATGTATACAGAAAGGGTGGCCAC 37131
QY 2679 ----- 2678
Db 37132 AGGGAGCTGGGAATGACACAGGGAGCTGCGACGTGGCCGAGGTCCAGGGCCAGGCCA 37191
QY 2679 ----- 2678
Db 37192 CAGGAAGGCGAGGGGGACGCCCGGCCACAGCAGAGCCCGCAGAAAGGAGGATGC 37251
QY 2679 ----- 2678
Db 37252 CCAGGCCAGAGCAGAGGCTACCGGGCAGAGGGGGCTCCGTGAGCTGGTGAGCGAGCT 37311
QY 2679 ----- 2678
Db 37312 CATGACTCGGGGAGGAACCTCTTGAAGTGAAGCTGACGACTGAGTGTGCCAGCTCAC 37371
QY 2679 ----- 2678
Db 37372 AGCCACAGAGTCCCGGCTGAGCAGAACTCAGAAACCTCCCTTGTCTAAAGCAC 37431
QY 2679 ----- 2678
Db 37432 AGCAGATGCTTTCAGGCACTAGAGAAAACAGCAAAAGTCTTGAAGAACTTTAAA 37491
QY 2679 ----- 2678
Db 37492 AGAAGTGGGATGTGCAATTTCTTGTCCAGATTTAGTGTGCCGCGACACAGATGA 37551
QY 2679 ----- 2678
Db 37552 GTCTAATACGGGATTTGTGTGTTCATGGGACACATGAGATGACATCACAGAGCC 37611
QY 2679 ----- 2678
Db 37612 ACTGGGCTGACCTCCATCTGAGTCTGTGCTGCCGGGTCCAGGCCAGTCTTCA 37671
QY 2679 ----- 2678

Db 37672 TGCTACCTACTGTCTGCTCCCGGAGACAGGAAAGCACCCGAAAGTCTGAGCAGGGC 37731
QY 2679 ----- 2678
Db 37732 TGGGTCCAGGCTCCCTCAGAGCTCCTGCCAGGCCACCTGTGCTCAATACACACTTC 37791
QY 2679 ----- 2678
Db 37792 TCTGGGGTTTTCCAAAGCATTTAACAAAGGTGTAGTTTACCTCTGTGGTGAGGCCCG 37851
QY 2679 ----- 2678
Db 37852 CATCTGGGGCTGACATTTGCCCTCTGCTTAAAGACCTGTGTCGAGGTGCTCCAGTA 37911
QY 2708 TGGCTGCGTGTGAACCTTCGGAAGACAGTGTGAACCTTCCCTGAGAAAGAGAGCCCT 2767
Db 37912 TGGCTGCGTGTGAACCTTCGGAAGACAGTGTGAACCTTCCCTGAGAAAGAGAGCCCT 37971
QY 2768 GGGTGGACAGGCTTTTGTTCAGATGCGCGCCACGAGCTATTTCCCTGTGCGGCTGCT 2827
Db 37972 GGGTGGACAGGCTTTTGTTCAGATGCGCGCCACGAGCTATTTCCCTGTGCGGCTGCT 38031
QY 2828 GCTGATACCGGACCTCGGAGGTGCAAGGACTACTC----- 2866
Db 38032 GCTGATACCGGACCTCGGAGGTGCAAGGACTACTCAGTGTAGCGCACTTGCCCG 38091
QY 2867 ----- 2866
Db 38092 AAGTGAACCTGTGCGCGCTGGGGCAGGTGCTGTGACAGGGCGGTTCCGTCACACTGTG 38151
QY 2867 ----- 2866
Db 38152 CTTCGTTGGGGAGCGGACCTGCCAATCCCAAGGGTACAGAGGCACAGGGTCCCTC 38211
QY 2867 ----- 2866
Db 38212 GTCCATCTGGGGCTGACGACAGAAATGCACTTTCTGTGGAGTGAGGCTGTCAACACGG 38271
QY 2867 ----- 2866
Db 38272 GAGCAGTTTCTGTGCTATTTTGGTAAAGGAATGTGTGCACACAGACTGGGTGCACCTGA 38331
QY 2867 ----- 2866
Db 38332 GGTCTTTCAGAAAGCTGTGATCCGAACCAAGACGCCCGGCTGTGGGCGTGA 38391
QY 2867 ----- 2866
Db 38392 GTCTCTCAAAACCGAACAAGGGGCGCTGTGGCATGATCCTCTGAACCCGAGACC 38451
QY 2867 ----- 2866
Db 38452 TGGGGCCCTGTGGGCGTGAATCTCTCCGAACCCAGAGACTTCAAGGCCCTTTGGGGGT 38511
QY 2867 ----- 2866
Db 38512 GAGTCTTCCGCTGTGAGCCCGACACTTCAAGGCTCATCAGACTACAGAGATGCCATG 38571
QY 2867 ----- 2866
Db 38572 AGTTCATGATCAGTGTGACCCATCAGGGGACAGGGCCATGTGTGGGGGGGTCTCAC 38631
QY 2867 ----- 2866
Db 38632 AAAATTCGGGGTCTTGTTTCCAGAGCCCGAGAGTCAAGGCCCGCTCAGAGCTCAG 38691
QY 2867 ----- 2866
Db 38692 ACACAAATGAATGAAGATGACACAGATGACAGAAATCTGTCTTTTATGATA 38751
QY 2867 ----- 2866
Db 38752 AAAAGTATCAACATTCAGGCGAGGCAAGGTGGCTCACACTATTAATCCAGCACTTTGG 38811

QY	2867	-----	2866
Db	38812	GAGCGGAGTGGGTGGATCATTTAGAGCCAGAGTTGAGGCCAATACCAACATAG	38871
QY	2867	-----	2866
Db	38872	TGAATTCATTTCTACTTAATAAAATACAAAAATAGCCTGGCTGGTGGACAGCCCTG	38931
QY	2867	-----	2866
Db	38932	TAGTCCCGCTATGCGGAGGCTGAGGAGAGAAATCATTTGAACCGAGGAGAGAGT	38991
QY	2867	-----	2866
Db	38992	TGCAGTGAAGCCAGATACACACACTGCACCTCCAGCTGGGCAACAGAGTGAAGTTCATC	39051
QY	2867	-----	2866
Db	39052	TTAAAAAATAAATAAAGTATCAGCATTCMAAACATAGTGAAGGTTTTTTAT	39111
QY	2867	-----	2866
Db	39112	TCTGTCCTTCATATAATTTACTGTGCTGTCTAGAGCCGGAACCTGGGCTCCCTTC	39171
QY	2867	-----	2866
Db	39172	TCTGAAGGACACCTTCATGGAGAGAAATAGTGTGAATGTTTAAACAGAGG	39231
QY	2867	-----	2866
Db	39232	TTTAAACGGGGTCTGTGCTGTCTGAGTTACAGTCAGATCTGACCTTGGCTTTTC	39291
QY	2867	-----	2866
Db	39292	AGATGCTCCTGGGTTTGTCTTCATGGGGAGAGCAGAGTGTGACACCTCTGATGG	39351
QY	2867	-----	2866
Db	39352	GAGAGAGAGGTGACAGACGCCCTCATGTAGTGGGAGTGGCAGGTGACACCTTGTG	39411
QY	2867	-----	2866
Db	39412	CATGTGCCCAGCATGTCCCTGTTGAGCTCCCTCCCAAGAGATGCCGGTCTCTGTG	39471
QY	2867	-----	2866
Db	39472	CTCCCAAGTCCCTGCTCTCTCTACAGCCTTACTGTCTGGCTCTCACCTGGCTTT	39531
QY	2867	-----	2866
Db	39532	GTCTGATGATTTCCACATTTCTGGGCTCCAGACACCTTCTGCTCTCCAGGACCT	39591
QY	2867	-----	2866
Db	39592	CTGCAGTGTGGCATACAGTAGCTGTGAATGTGCTACTGCTTATTTTGTCCCATG	39651
QY	2867	-----	2866
Db	39652	AAATGATTTTTTAGACAGGACACCCCTGTCTTCAGCCTTGACAGCATCATGTAATG	39711
QY	2867	-----	2866
Db	39712	TTATTGAAGACAAAGACAGACAAACAATCAGSAAATGGTCTCTTAACACAT	39771
QY	2867	-----	2866
Db	39772	GCAAGCCACAGAGCTAGTGCAGATGGGTGGGATCAGTCAATGATGGGTCAA	39831
QY	2867	-----	2866
Db	39832	TGCCAGATATTCTGTCTCCCAAGGCCACTTGTGTGAGAGTGTGTGAGAGGTGG	39891

QY	2867	-----	2866
Db	39892	CTCTAAAGCTCAGCAGTGGAGGAGGTGGTTCGCCATCTCAGGGTGAATCACATCTC	39951
QY	2867	-----	2866
Db	39952	TGTGTGTAAGTATACAGCAGAGCTTGAAGGCACTGGGAGAGMAAAGCAAAAT	40011
QY	2867	-----	2866
Db	40012	GATTAAGAAAGTGAATAAAGAAAAAGTGTGAATGGAAATTTCTTGTCCAGATTTAG	40071
QY	2867	-----	2866
Db	40072	TCTCCAAACACAGCTCAGATGTAGAAATGTGTGCAAGCTGATGACAGACATAGA	40131
QY	2867	-----	2866
Db	40132	ACAAACGGAAGCCCTATCTCTCAGAAAGTGTGTATGTGTATGTGGCAGAGTAT	40191
QY	2867	-----	2866
Db	40192	GAAAAAGAGTGTGTGTATTTTTTTTCTGAGAAACTGACTGAGCAATTAAT	40251
QY	2867	-----	2866
Db	40252	TGTGCTTTACAGCATATACAGAGCATTTCTAGTAGAAGAGAGACATGCAACA	40311
QY	2867	-----	2866
Db	40312	ACACCAACACAGAAATATAAACAAAGACTCAAGGAGAGGTGAACGTTCCGTG	40371
QY	2867	-----	2866
Db	40372	TTGTGTTGGGAGAGACACACAGAGGAGGATGAACAGTGAAGCAAGGCATTCG	40431
QY	2867	-----	2866
Db	40432	TTTCACTGAGAAACTACGTTGTGTGAGCCACAGTGAATATGSCCATTCCTGGAGC	40491
QY	2867	-----	2866
Db	40492	GTTTGTGACGTGATTTATTTAAGGCCCTGTGAGTCTGTGACATTTATCTCACT	40551
QY	2867	-----	2866
Db	40552	TTGTTCTCTAACCACTGAGAGTGAAGAGAAAGGCTCCAGGGGAGACGCCCTT	40611
QY	2867	-----	2866
Db	40612	GGTCAACGAGCTGGCAAGGCAATGATGATTCAGCCTGCTCTCGGGGCCCT	40671
QY	2867	-----	2866
Db	40672	TGCTTGCCGAGGAGCCCAACAAAGTCAGACCCATAGGCTCAGGGTGAAGGCCCA	40731
QY	2867	-----	2866
Db	40732	AGGTGCTTGGGATGCTGTGAAAGAAATGAGAGTGTGATGATCACTTGGGAAG	40791
QY	2867	-----	2866
Db	40792	TCTACACAGAGCTCAAGAAATGATGTGAATCAACGACGAGACCATCCCAAG	40851
QY	2867	-----	2866
Db	40852	AAACGACGTAAACTGATGCGAGACCTGTCCCATCCCTCATGTGGCTCTTTCTG	40911
QY	2867	-----	2866
Db	40912	GGCTTCCAGAGCCACATCAGTTGAGGCAAGCTGAAAGACTTTCTGTGAAAGAGC	40971
QY	2867	-----	2866

Db 40972 TTGTTGATGGAAGTCCCTCAAAATGTCCTGTCTCCAGTAATTCACATCTTGAAAT 41031
QY 2867 ----- 2866
Db 41032 GACCAGACATTATACAGGGGTCTTATTTACATTTCCAGTGTCCAGGAGGGACTTGC 41091
QY 2867 ----- 2866
Db 41092 CACAGACAGTCAAGAACCTGCCAAATACAGGGCTAAGAGATATTATGATCACAAC 41151
QY 2867 ----- 2866
Db 41132 TTGCTGTCCATTAAACATTTTTCAAAGATTTTGAAGATGTTTAATGGACAAACG 41211
QY 2867 ----- 2866
Db 41212 TTTATTTCAATGTAGACAGTGTTCAAAGCTGATGTAAGAACACACCCAGAGACCTTGC 41271
QY 2867 ----- 2866
Db 41272 CGTGATGTCAATGTGTCTTCAATCTTTGACATGACATACATGAGCAGTGTGTG 41331
QY 2867 ----- 2866
Db 41332 AGCCCTGAGAGACATCGGTGGATGCTCCATCCTGCCCTGTGAGACACATGTGTG 41391
QY 2867 ----- 2866
Db 41392 CCAGCTGACATCTGGAGCCCTGTTTACGTGTGCCACCTGGCTCTTCCATCCCTGAGA 41451
QY 2867 ----- 2866
Db 41452 TTCAACACAGTAGATATCCCAAGCCCACTCAGTGTCTCCCAACAAAACCTGAGTC 41511
QY 2867 ----- 2866
Db 41512 ACACCTGTCTACTCGAGGAGCCCGGAGCCAGGGCTCCACAGTTTATATGTCTT 41571
QY 2867 ----- 2866
Db 41572 TTGGCTGAGTTATGTGAGATCTCATCAGGCGAGATGATGATGCACAAACCGCCGTG 41631
QY 2867 ----- 2866
Db 41632 CGAGGTTGATACATCAATCATACTAGCAGGTCTGTGGAGTTTGGTCATGACAG 41691
QY 2867 ----- 2866
Db 41692 TCTGATGGCATGTAGCATTTGGAGTCATGAGTGAAGACCCACCCCTCGGGCTGCA 41751
QY 2867 ----- 2866
Db 41752 GCGCATGCCCAGGAGAGCAAGAGGAGGAGAGGAGGAGGCTTTTGGAGCAAGC 41811
QY 2867 ----- 2866
Db 41812 TTTGAGAGGAGGGGTGGGTGGGGCAGCACCTGTCTGTGACATTTCCCTGTGTCT 41871
QY 2867 ----- 2866
Db 41872 CAGCATGCCCGGAGCTCCATCAGAGCCAGTCTCACTTCAACCCGGCTTCAAGGCTGG 2926
Db 41872 CAGCATGCCCGGAGCTCCATCAGAGCCAGTCTCACTTCAACCCGGCTTCAAGGCTGG 41931
QY 2927 GAGGACATGCGTGCAGAACTCTTTGGGGTCTTGGGCTGGAAGTTCACAGGCTGTCT 2986
Db 41932 GAGGACATGCGTGCAGAACTCTTTGGGGTCTTGGGCTGGAAGTTCACAGGCTGTCT 41991
QY 2987 GGATTTGC----- 2994
Db 41992 GGATTTGAGGTGAGCAGGCTGATGCTCAGACACAGATTTCAAGAGTGTGTGC 42051
QY 2995 ----- 2994

Db 42052 GCAAGTATGTGTGTGTGTGTGTGCGCGGCTGCTGCAAGGCTGATGTGACTGCTGCAC 42111
QY 2995 ----- 2994
Db 42112 GTAAGATGCAATGTACCATATACAGTGAACATATGTGTGATGTGTACAT 42171
QY 2995 ----- 2994
Db 42172 GAAGCATGGCAGTGTGTGACAGAGTGTGCAAGGGCAACAAGTGTGTGACATGGGAATGC 42231
QY 2995 ----- 2994
Db 42232 ACACCTGACATGATGTGTGTGTGTGTGACAGTGTGTGGCATTCACGTGAGTGCATGC 42291
QY 2995 ----- 2994
Db 42292 GTGTGGTGTCAAGTGTGATGATGATGTGTGCACATATGATGAGGGGTCTGTGTG 42351
QY 2995 ----- 2994
Db 42352 TTCAACCCCGTAGTGTCTCAGACACAGTGCACATCTTACAGATGAGAGGGGTCCAG 42411
QY 2995 ----- 2994
Db 42412 GCTTGTGTGGCTGAGGCTCTGAAGCTGCACGCTGAGGGCATTTGCCATCTGGCATTC 42471
QY 2995 ----- 2994
Db 42472 CGGCTCCACTCTCTCTCTGTGGGCTTGTGTGCATCTCCCTCTGTGTGGCATTTA 42531
QY 2995 ----- 2994
Db 42532 CATCACTCACTCCCTCTCTCTGTGGGATCCGCGTCACTCCCTCTGTGTGGCA 42591
QY 2995 ----- 2994
Db 42592 TCTGCTGACCTCCCTCTCTGTGGGATTTGGTGCATCTCTCTGTGTCTTCC 42651
QY 2995 ----- 2994
Db 42652 TGTCTGGCCAGAGCTCGGGGGCAGGAGATGACACAGATCTTGTACGCGCCAGGGTGG 42711
QY 2995 ----- 2994
Db 42712 TTCCAGCTGCCGGGTGAGGGCCAGGCCGATTTCACTGGGAGAGGATGTTCTTGT 42771
QY 2995 ----- 2994
Db 42772 CAAATGTTCTCTTCTTGTTCATCTGAATGATGATTAAGCAAAAAGTAAAACTTA 42831
QY 2995 ----- 2994
Db 42832 AAATGCCAGAGGTTTCTACCGTTTCTCACTCTTCTTGTGCGACTGTAGGTGAACGCC 42891
QY 3007 TCCAGAGGTTGTGACCAACATCTAAGATCTCTCTGTGAGGCTA----- 3055
Db 42892 TCCAGAGGTTGTGACCAACATCTAAGATCTCTCTGTGAGGCTA----- 42951
QY 3056 ----- 3055
Db 42952 CCACCAAGGGTGCAGGCCACGCTCCAGGAGACCTCCGCTCTGCTCACCTGTGACCC 43011
QY 3056 ----- 3055
Db 43012 GGGGCTTACCTTGAATCTCTGGGTTTAAAGGCAAGAAATGTCTTACGTTTCAGTGG 43071
QY 3056 ----- 3055
Db 43072 TGTGTGTCTGTGTGACAGTCTGTGTGCGGTGTGTGCAAAAGACATGTCTCATTC 43131
QY 3056 ----- 3055
Db 43132 TCTGTGTGTGTGTGAGACCGGTGTGGCCAGGTGTGCCACATGTGTGTGTGACATGGC 43191


```
QY 3056 ----- 3055
Db 43192 CGTGGAGCTGATGAGGAGCCATCCAGGGCAGAGGGCATGGGGTAAGAGATGTTAT 43251
QY 3056 ----- 3055
Db 43252 GGGAGCTTTAGCAGAGAGGCTGGGAAGTGTCTGAACAGTAGATGGAGATCAGATGC 43311
QY 3056 ----- 3055
Db 43312 CCGAGAGATTTGGGCTCTCAGCAAAAGAGGCCAGGTGGGTGCAGGTGAGGGTCGTGC 43371
QY 3056 ----- 3055
Db 43372 CCCACCCCCGGGAAGGTGCAGCAGAGCTGTGTGCCACACAGCCCGCCAGCACCTGT 43431
QY 3056 ----- 3055
Db 43432 GCTCTGGGCATGCGTGTCTGTCTGAGACGTTCCCTGTCTGGCTGTGTCAGGGGGTGC 43491
QY 3056 ----- 3055
Db 43492 TGCCAAGATGACACTTATTCACAGAGGAGGCCAATCTGTGAGGCCACAGGGCC 43551
QY 3056 ----- 3055
Db 43552 AGCTTCTCGTAGTAGTAGGAGGAGGTGTGGCACAAGCTTCGGGGCTGTACCAAGGCA 43611
QY 3056 ----- 3055
Db 43612 GTGGGACACAGAGGCCGGGGCTCCACCTGACAGAGGCTCCGAGGCTGACGAGCTGA 43671
QY 3056 ----- 3055
Db 43672 ATGCCAGAGGCCGAGGCCCTGCCCCAGAGGCTGAGAGGCTGAGACATTTGTGT 43731
QY 3056 ----- 3055
Db 43732 TACCCAGGGCGAGGCGTGGCGAATTAACGTGACACTGATGTGAATGAGCTGTGTGT 43791
QY 3056 ----- 3055
Db 43792 CTATGCTGGAACCCAGCAAGGCTCAGGGAGAGTTTCCATTACAGGTGTATCCATG 43851
QY 3056 ----- 3055
Db 43852 AAAATGTTTTTAACCCAGAGTGTGTGCGCTTCACTGTGCAAGGAGGAGGCCAC 43911
QY 3056 ----- 3055
Db 43912 AGCTGCATGTTACCGCTTTGACACAGCTCAGAGGCTTGGACACAGGCTGTCTAGTTT 43971
QY 3056 ----- 3055
Db 43972 CAGGGTGGCTCCGGCTCAGACGCGCCCTCTCTGCTCTCTCTGCTCAAAATCTTC 44031
QY 3056 ----- 3055
Db 44032 CCTGTTTCATCTCCCTGACGGGTGCTGGGCCCTGTGCAAGCTGTTGACTCTTTC 44091
QY 3056 ----- 3055
Db 44092 CGGAACCCCTTGGGGTGTGTGTGATACAGGTGCACAGAGACTGAGAGTGTGTGACACT 44151
QY 3056 ----- 3055
Db 44152 GTGTGTGACCCAGAGGTCCAGCTGGCGTGTCTGGGGCTCTGTGGGCATGATGAGTCA 44211
QY 3056 ----- 3055
Db 44212 GAGGAGTTTTCCAGGTGAAGAACTCTGTGGAAGCTCCAGGGCATGTGACTGCCACT 44271

QY 3056 ----- 3055
Db 44272 GCTCCTCCCATATTCAGCTAGCTCTTGTCTCATTTCCACACAGGGTCTAGCTCGA 44331
QY 3056 ----- 3055
Db 44332 GAGGCTCCCTAGAGGCGCTGGGCTCAGGGCAGGGCGGCTGAGTTTCCACCCATGTGG 44391
QY 3056 ----- 3055
Db 44392 GAGCCCTGGGTAGTCGCTTGTATGTTAGCCCTGAGAGGCCGAGATGCATGGGCCAC 44451
QY 3056 ----- 3055
Db 44452 GGGCCGTTTCCAAACACAGAGTCAGGACAGTGTGAAGGCCAGGAAATCCCTTCCGAG 44511
QY 3056 ----- 3055
Db 44512 GCAGAGTGGGAGACGAGAGCTGGGCCCGGATTTACGGCACGCCAGGCTGCAGTGGC 44571
QY 3056 ----- 3055
Db 44572 GAGGCTGTGTGTCCACGTTGCGCTGGGGCGGGGTCTGATTCAAATCCGTGGGCTC 44631
QY 3056 ----- 3055
Db 44632 GGCCTTCTGGCCCGTGTGTGCGCGCCCTCCACAGGGCTTGGGGTGGACGCCCGACT 44691
QY 3056 ----- 3055
Db 44692 CTAGCAGTGGCTATTTCTCCCTTTGAAAGAGACCCCTACCATGCTAGGTGTTCC 44751
QY 3056 ----- 3055
Db 44752 TCTGTGGTCAGAGCGTGGCGGCTGTGGCAACCCCGGACCTTAGGCTATTATTGTTT 44811
QY 3056 ----- 3055
Db 44812 AAAAATCTTGGGCGCTGCGCTTCCGTTGTCTTAATGGGGAAGACATCCACCTCAG 44871
QY 3056 ----- 3055
Db 44872 CAGAGTCTAGAGGCTGAACCGGGGTGCTGAGCTTGATGTGATCTCAGGTATT 44931
QY 3056 ----- 3055
Db 44932 CCAGAGTGGCTCAGGAAGTCAGTGAACAGGATACATGGGGGCTCAGGCAGTGGTGA 44991
QY 3056 ----- 3055
Db 44992 GATGAGTACACGGGGGCTCAGGCAGTGGGTGAGGCCAGGTATCATGGGGGCTCAGGCA 45051
QY 3056 ----- 3055
Db 45052 CTGGGTAGATGATACACGGGGGCTCAGGCAAGAGGTCAAGACGATCAGGGGGC 45111
QY 3056 ----- 3055
Db 45112 TCTGATCACAGCAATATGACACATGTGCATGTGCTTTTATGATGATGACAGGTCT 45171
QY 3056 ----- 3055
Db 45172 GTGCACACTGCCCAAAAGTCCAGGAAGCTGAGAGGCCAAAGATGAGGCTGCAGGGC 45231
QY 3056 ----- 3055
Db 45232 TGGCGCGGTGGCTCACACCTGTAGTCCAGCACTTTGGAGGCCGAGGCGAGAGATCC 45291
QY 3056 ----- 3055
Db 45292 TTGAGCCAGGAGTTTAAGACAGGCTGAGCAACATAGTAGAACCCCATCTTATGAAA 45351
QY 3056 ----- 3055
```

Db 45352 ATAAAAAATTAAGTGAACATGGTGTGCGCCTGAGTTCATTAATCTGGAGG 45411
QY 3056 ----- 3055
Db 45412 CTGAATGGAGGATCACTTGAGCCCAAGAGGTGAAAGCTGCACTGAGATTGCAC 45471
QY 3056 ----- 3055
Db 45472 CACTGTAAGTGGCTGGGTGACAGAGTGAAGGCCATCTCAACACACAAAGAAAGACT 45531
QY 3056 ----- 3055
Db 45532 GACAAATGCACTTCTTGAAAGAAACATTTAGTAGAACTTAACCTACACAGAAAGCC 45591
QY 3056 ----- 3055
Db 45592 AAGTCGGTCTCCGGTGTCACTGAGATGATGGTCTCTACACCACACCCAGAC 45651
QY 3056 ----- 3055
Db 45652 CCAGGTTTATGACACACAGGGGGGGGTGCTCAGAAAGGATGGCAGAGCTTGATATA 45711
QY 3056 ----- 3055
Db 45712 CGATGACATCAAGGTGTGTGACGAGAGGCGAGATTATGATTAAGTACTGTGTACAC 45771
QY 3056 ----- 3055
Db 45772 AAGGAACAATGGAATTAACCTGGAACCTTAGAGCCTTCCCGGAACAGGGCTAATCAGAA 45831
QY 3056 ----- 3055
Db 45832 GCCAGATGGGGGGCTGGCATCCAGATGAGAGTGTTCACCTCCACATGCTGTTCAT 45891
QY 3056 ----- 3055
Db 45892 ACAGATGTTGACAGAAACGCAAGTGTACTGTGACACACAGACACGCACTACTGCGAC 45951
QY 3056 ----- 3055
Db 45952 ACACAGACACACACAGACATGATGATCCGTGTGTGACACTGTGCCCATGA 46011
QY 3056 ----- 3055
Db 46012 GGAACCCATGATGTGATTCATGCAAGCACACAGGACCGGTGGGCCATGGCCACAC 46071
QY 3056 ----- CAGGT 3060
Db 46072 CCACGAGACCGTGTGATTAGAGGCGCTTCTCTGACGCTGCCCATCCTCTCAGGT 46131
QY 3061 TTCACGATGTTGTGTCAGAGTCCCATTTCTATCAGCAAGTTTGAAGAACCCCATTTT 3120
Db 46132 TTCACGATGTTGTGTCAGAGTCCCATTTCTATCAGCAAGTTTGAAGAACCCCATTTT 46191
QY 3121 TCCTGCGCTATCTGTACACAGGCGCTCCCTGTCTACTCCATCTGAAGCCAAAGACG 3180
Db 46192 TCCTGCGCGTATCTGTACACAGGCGCTCCCTGTCTACTCCATCTGAAGCCAAAGACG 46251
QY 3181 ----- 3180
Db 46252 CAGGTATGTGACAGTGCCTGGCCCTCAGTGGCAGCAGTGCCTGCTGTGTAGTGTG 46311
QY 3181 ----- 3180
Db 46312 TCAGAGACTGAGTGAATCTGGGCTTAGGAATTTCTTACCCCTTTTGCATCAGAAAGTG 46371
QY 3181 ----- 3180
Db 46372 GTTTAACCAACACACTGTCAAGGCTGTGTGCCCCCTCTGTGTGGGTGAGACAGCAC 46431
QY 3181 ----- 3180

Db 46432 TGATGAAGGACAGAGACTGTCTGAGAGCTGCCATCTTCCACCTTGCTTGCGTGGG 46491
QY 3181 ----- 3180
Db 46492 GAAGCGCTGGGGGGCTGTGTCTCTCTGTTTGGCCCATGTGGGATTTGGGGGGCTTGGC 46551
QY 3181 ----- 3180
Db 46552 CTCTCTGTTTGGCCTGTGGTGGGATTTGGGCTGTCTCCGTCATGGCAGCTTAGGGCCT 46611
QY 3181 ----- 3180
Db 46612 TGTCAAAACCCAGGCCAAGGGCTTAGAGAGAGGCCAGGCCAGCTACCCACCCCTCTC 46671
QY 3181 ----- 3180
Db 46672 AGGACAGAGGGCCCGTATACACAGACAGAGCCCGCCGCTCTGCTTCCAGTCA 46731
QY 3181 ----- 3180
Db 46732 CCGTCTGTGCCCTTGACACTTTGTCCAGCATCAGGAGGTTTCTGATCCGTGAAT 46791
QY 3181 ----- 3180
Db 46792 TCAAGCCATGTGAACCTGCGGCTCTGAGCTTAACAGCTTCTACTTCTGTCTGTGT 46851
QY 3181 ----- 3180
Db 46852 GTTGTGAATTTTCACTGGAGAAAGCCGAGAAACATTTCTGTGTGACTCTGCGGTG 46911
QY 3181 ----- 3180
Db 46912 CTTGGGTGGGACACAGAGATGAGACCAACCCGACAGCGTGGGTGTGGGAGCTTT 46971
QY 3181 ----- 3180
Db 46972 CCGGTGTCTCTGGAGAGGAGCTGGGCTGGGCTGTGACTCTCAAGCTCTGTCTTTCC 47031
QY 3181 -CAGGATGTCGTGGGGGCCAAGGGCGCGCGGCGCTGTGCCCTCGAGAGCCGTGAG 3239
Db 47032 CCAGGGATGTGCTGGGGGCCAAGGGCGCGCGGCGCTGTGCCCTCGAGAGCCGTGAG 47091
QY 3240 TGGCTGTGCCAACAAGATTTCTGCTCAAGCTGTGACACCGTGTACCTTACGTGCCA 3299
Db 47092 TGGCTGTGCCAACAAGATTTCTGCTCAAGCTGTGACACCGTGTACCTTACGTGCCA 47151
QY 3300 CTCTGGGGTCACTCAGAA ----- 3318
Db 47152 CTCTGGGGTCACTCAGAGACAGGCAAGTGTGGGTGAGGCCAAGTGGGCCCACTGCC 47211
QY 3319 ----- 3318
Db 47212 CAGGGGTCACTCTTGAACGCCCTGTGTGGGGCCAGCAGCTCAGATGCTGTAAGTGA 47271
QY 3319 ----- 3318
Db 47272 GAGCCCCCGGGCTGACCTTGGGGGCTGTGAGCCAGCTGTGAGCTTATGATTAAA 47331
QY 3319 ----- 3318
Db 47332 CGCTGTGTCCCAAGGCCAGGAGCTGTGAGAGGTGCCCAACTTTTGAACCCCTGCTTC 47391
QY 3319 ----- 3318
Db 47392 CCATCTCAGGGGGCATGTGCTCCCAAGCTTGGGAGCCTTCTGACCCCTGACCTGTCTC 47451
QY 3319 ----- 3318
Db 47452 CTCAAGCTCTTCCCTGGGCTGTGCTGAGCTCTGAGGCTCTGAGCAAGTTCTCTCC 47511
QY 3319 ----- 3318
Db 47512 CCGCCCCCGCTCAGAGCTACTGGGCTGCTGTGTGCGCCCGGTGAGGGGTGTG 47571

OY	3319	-----	3318	OY	3987	-----	3986
Db	47572	TGTCCCTTCACTGAGTTCCTCCACCAGCGGCACAGAGTGCAGGCCCTGCTGCCGG	47631	Db	48652	AGCAGAGATGCTGGGGGCCACGCTTGGCGCGGGGATGATGAGGGCTTGCCAGAGGTG	48711
OY	3319	-----	3318	OY	3987	-----	3986
Db	47632	CCACCACACGTCTAGGAGGGTTGGAGGATCCACCTTGCCCTCTCTGSAAGGAGT	47691	Db	48712	GCAGGATGATGGGGGCCACGCTGGGTGGCAGGAGGTGATGGGGGGGGTGTCTGGGT	48771
OY	3319	-----	3318	OY	3987	-----	3986
Db	47692	CTGATTTTGGCCCCGACGCCAGACGACGTGATGCGGAATCTCCGGGGAGCAGCTGA	47751	Db	48772	GGGGGGAATGGGGAAGCTTGCTGGGCCCTCTCCCTGCTCCACCTGCAGGC	48831
OY	3364	CTGGCCCTGGAGGCGGAGCCACCCGGACCTCCCTGCAATTCAGACATCTGGACT	3423	OY	3987	-----	3986
Db	47752	CTGCCCTGGAGGCCGACCCACCCGGACCTCCCTGCAATTCAGACATCTGGACT	47811	Db	48832	GTCGATCCGGATGTGCTTCCCTGTGTGCACATCTCTGGGCATCAGCTTTCATGAGGTG	48891
OY	3424	GATGGCACACCGCCACACGACGAGCGAGACAGACACACACCTCTGTACGCCGGCC	3483	OY	3987	-----	3986
Db	47812	GATGGCACACCGCCACACGAGCGAGACAGACACACACCTCTGTACGCCGGCC	47871	Db	48892	GGGGCAGGGGCATGACACCATCTGTATAAATCCAGATTCCTCTCTGACGCCCC	48951
OY	3484	TCTACGCTCCAGGAGGAGGAGGGCGGCCACACCCAGCCGACCGCTGGAGTCTGAG	3543	OY	3987	-----	3986
Db	47872	TCTACGCTCCAGGAGGAGGAGGGCGGCCACACCCAGCCGACCGCTGGAGTCTGAG	47931	Db	48952	AACCTAGTTGAAGTCAATTCCTGCTCTGACATTCCTTAAGATGACAGAGATTTC	49011
OY	3544	GCCCTGAGTGTGTTTGGCCGAGGCTGCATGTCCGGCTGAAGGCTGAGTCCGGCTGA	3603	OY	3987	-----	3986
Db	47932	GCCCTGAGTGTGTTTGGCCGAGGCTGCATGTCCGGCTGAAGGCTGAGTCCGGCTGA	47991	Db	49012	TGATCTTGAAGGGTGGGTAGGGTGGGCGAGTGAAGGATGTGACACAGAGAGCTTCAGG	49071
OY	3604	GGCCTGAGCGAGTGTCCAGCCAAAGGGCTGAGTGTCCAGACACCTGCGCTTTCATTC	3663	OY	3987	-----	3986
Db	47992	GGCCTGAGCGAGTGTCCAGCCAAAGGGCTGAGTGTCCAGACACCTGCGCTTTCATTC	48051	Db	49072	GTCGGGCTGTGATGCTCTCTCATCTCTTATCATCTCCAGTCTCATCTCATCTCT	49131
OY	3664	CCACAGGCTGGGCGCTCGGCTCCACCCAGGGCCAGCTTTTCTCACCAGGAGCGGGCTT	3723	Db	49132	TATCATCTCCAGTCTCATCTCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTT	49191
Db	48052	CCACAGGCTGGGCGCTCGGCTCCACCCAGGGCCAGCTTTTCTCACCAGGAGCGGGCTT	48111	OY	3987	-----	3986
OY	3724	CCACTCCCCACATAGAGATGTCCATCCCATGATTCGCGATCTGTCCCGCTGCGCTGC	3783	Db	49192	ACCATCTCCAGTCTCATCTCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTT	49251
Db	48112	CCACTCCCCACATAGAGATGTCCATCCCATGATTCGCGATCTGTCCCGCTGCGCTGC	48171	OY	3987	-----	3986
OY	3784	CCCTCTTGGCCCTCCACCCACCATCCAGGTGAGAGACCTGAGAAAGACCTGGAGACT	3843	Db	49252	CAGGGCGGGTCCAGGCTCCGACGTGAGAGCTGACATACGTCCTTCTCAGGAGAAAGAA	49311
Db	48172	CCCTCTTGGCCCTCCACCCACCATCCAGGTGAGAGACCTGAGAAAGACCTGGAGACT	48231	OY	3987	-----	3986
OY	3844	CTGGGAATTTGGAGTGACCAAAGGTGCTGCTGTACACAGCGAGGACCTGCACCTGGA	3903	Db	49312	CTGGGAAGATTGCAGAGACAGAGAGGGCGGCTCAGAGGAGCGAGCTTGGGGTGAAGA	49371
Db	48232	CTGGGAATTTGGAGTGACCAAAGGTGCTGCTGTACACAGCGAGGACCTGCACCTGGA	48291	OY	3987	-----	3986
OY	3904	TGGGGTCTCTGTGGGTCAAAATTTGGGGAGGTGCTGTGGAGTAAATATATATAT	3963	Db	49372	AACAGCCCTCTCTCAGAAATTTGGCTTGGGCCACAGAAACCGAGGGCCCTGCGTAGTGG	49431
Db	48292	TGGGGTCTCTGTGGGTCAAAATTTGGGGAGGTGCTGTGGAGTAAATATATATAT	48351	OY	3987	-----	3986
OY	3964	GAGTTTTTCAGTTTTGAAAAA-----	3986	Db	49432	CTCCAGAGCTTCCAGCAGGTCCCTGTGGGGCTTATGTATGCGCGGGCTCTACTGAG	49491
Db	48352	GAGTTTTTCAGTTTTGAAAAAATCTCATGTTTGAATCTAATGTGCACTGATAGACAC	48411	OY	3987	-----	3986
OY	3987	-----	3986	Db	49492	TGCACCTTGACAGAGGCTCTGTGTTTGAATGACGCCGAGAGTGCCTGGGTGG	49551
Db	48412	CACTGTATGCAATTCAGAAAGCCGTGAGTGAACGGGGTGTGTCAGTCCGGGCCATG	48471	OY	3987	-----	3986
OY	3987	-----	3986	Db	49552	GGGCTTATGGCCACTGATATATGCGTCATTATTTGCTGTGCTTACAGAAATGCTGAGT	49611
Db	48472	GCTGTGCTGCAATTTACGGAAGTATAGTGAATGGGTTGTGTCAGTGGGGCCCA	48531	OY	3987	-----	3986
OY	3987	-----	3986	Db	49612	GACCGAGCTTATGTGTATGTGTGGGCCAAGTCCACAGACTGTGTGTAATGCACTGTG	49671
Db	48532	TGGCCTGGCTGGGCTCGGAGAGTTTCTGATGCTGTGAGCAGAGGAGGAGAGGGTAGG	48591	OY	3987	-----	3986
OY	3987	-----	3986	Db	49672	GTCCTTGAGCCCCGTATATGAGCTGTGAGGAGAGAGGGCTCTTGGCAGCGGGCTGG	49731
Db	48592	GGATAGACAGTGGAGCCCCCACCCTGGAAGACATACATGTAAGTCCAGGCCGGAAGGC	48651	OY	3987	-----	3986

[illegible]

Db 2513 GGGAGAGTCTACAGTTCAGTGGCAGGGGATCCGCGAGGCTCATCTCTCCACGCTGCT 2572
 Qy 2549 CTGACAGCCTGTGCTACAGGGGACATGGAGAAAGCTGTTTGGGGGATTTGGGGGAGG 2608
 Db 2573 CTGACAGCCTGTGCTACAGGGGACATGGAGAAAGCTGTTTGGGGGATTTGGGGGAGG 2632
 Qy 2609 GCTGCTCCTGCTGTTGGTGGATGATTTCTTGTGGTACACCTCACTCCACGACGAA 2668
 Db 2633 GCTGCTCCTGCTGTTGGTGGATGATTTCTTGTGGTACACCTCACTCCACGACGAA 2692
 Qy 2669 AACCTTCTCAGAGACCTGCTGCGAGGTCCCTGAGTATGCTGCTGCTGTAACCTGCG 2728
 Db 2693 AACCTTCTCAGAGACCTGCTGCGAGGTCCCTGAGTATGCTGCTGCTGTAACCTGCG 2752
 Qy 2729 GAAGACAGTGTGAACCTTCTGTGAAGACAGAGGCTGGGTGGAGGCTTTTGTCA 2788
 Db 2753 GAAGACAGTGTGAACCTTCTGTGAAGACAGAGGCTGGGTGGAGGCTTTTGTCA 2812
 Qy 2789 GATGCGGCGCCAGGCGTATTCCTGCTGCGGCTGCTGCTGATATCCGAGACCTGGA 2848
 Db 2813 GATGCGGCGCCAGGCGTATTCCTGCTGCGGCTGCTGCTGATATCCGAGACCTGGA 2872
 Qy 2849 GGTGCAAGAGGCTACTGCTGAGTATGCCGAGCTTCATCAGAGCAGTCTACCTTCAA 2908
 Db 2873 GGTGCAAGAGGCTACTGCTGAGTATGCCGAGCTTCATCAGAGCAGTCTACCTTCAA 2932
 Qy 2909 CCGCGGCTTCAAGGCTGGGAGGACATGCGTGCAGAACTCTTGGGGCTTTCGCGTGA 2968
 Db 2933 CCGCGGCTTCAAGGCTGGGAGGACATGCGTGCAGAACTCTTGGGGCTTTCGCGTGA 2992
 Qy 2969 GTGTACAGACCTGTGTTGAGATTTGCAAGTGAACAGCTTCACAGCGTGTGACCAACAT 3028
 Db 2993 GTGTACAGACCTGTGTTGAGATTTGCAAGTGAACAGCTTCACAGCGTGTGACCAACAT 3052
 Qy 3029 CTACAAGATCCCTGCTGCGAGGCTTTCAGAGTTCACCATGTGCTGCTGCTGCTGCT 3088
 Db 3053 CTACAAGATCCCTGCTGCGAGGCTTTCAGAGTTCACCATGTGCTGCTGCTGCTGCT 3112
 Qy 3089 TCATCAGCAAGTTTGGAGAACCCACATTTTCTGCGCGCTCATCTGACAGCGCTC 3148
 Db 3113 TCATCAGCAAGTTTGGAGAACCCACATTTTCTGCGCGCTCATCTGACAGCGCTC 3172
 Qy 3149 CCTGTGCTACTCATCTGTAAGAACCCAGAACGCGAGGATGCTGCGGGGCCAAGGGCGC 3208
 Db 3173 CCTGTGCTACTCATCTGTAAGAACCCAGAACGCGAGGATGCTGCGGGGCCAAGGGCGC 3232
 Qy 3209 CGCGGCGCTTGGCTCGAGAGGCGGTGAGTGGCTGGCCACGACGATTCCTCTCA 3268
 Db 3233 CGCGGCGCTTGGCTCGAGAGGCGGTGAGTGGCTGGCCACGACGATTCCTCTCA 3292
 Qy 3269 GCTGACTGACACCGTGTACCTACCTAGTGCACCTCTGGGGTCACTCAGAGACGCCAGAC 3328
 Db 3293 GCTGACTGACACCGTGTACCTACCTAGTGCACCTCTGGGGTCACTCAGAGACGCCAGAC 3352
 Qy 3329 GCAGTGAAGTGGAGAGCTCCGGGACGACGCTGACTGCTCGAGGCGCAGGCCAACCC 3388
 Db 3353 GCAGTGAAGTGGAGAGCTCCGGGACGACGCTGACTGCTCGAGGCGCAGGCCAACCC 3412
 Qy 3389 GGCATGCGCTTCAGACTTCAGACCATCTGTGATGATGGCCACCGCCCAAGCGAGCG 3448
 Db 3413 GGCATGCGCTTCAGACTTCAGACCATCTGTGATGATGGCCACCGCCCAAGCGAGCG 3472
 Qy 3449 CGAGAGCAGACACGACGAGCCCTGTACGCGCGGCTTACGTCACGAGGAGGAGGAGGCG 3508
 Db 3473 CGAGAGCAGACACGACGAGCCCTGTACGCGCGGCTTACGTCACGAGGAGGAGGAGGCG 3532
 Qy 3509 GCGCCACACGAGGCGCGACCGCTGGAGTCTGAGGCTGAGTGTGTTGGCGAGGC 3568
 Db 3533 GCGCCACACGAGGCGCGACCGCTGGAGTCTGAGGCTGAGTGTGTTGGCGAGGC 3592
 Qy 3569 CTGCACTGCGCGGTGAAGGCTGAGTGTGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 3628
 Db 3593 CTGCACTGCGCGGTGAAGGCTGAGTGTGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 3652

Qy 3629 GCTGAGTGTCCAGACACCTGCGCTTCTACTTCCACAGGCTGCGCTGCGCTCAC 3688
 Db 3653 GCTGAGTGTCCAGACACCTGCGCTTCTACTTCCACAGGCTGCGCTGCGCTCAC 3712
 Qy 3689 CCAGGCGCAGCTTTTCTTCCACAGGAGCCGCGCTTCCATCCCAATAGAAATAGTCA 3748
 Db 3713 CCAGGCGCAGCTTTTCTTCCACAGGAGCCGCGCTTCCATCCCAATAGAAATAGTCA 3772
 Qy 3749 TCCCCAGATTGCGCATTTGTACACCCCTGCGCTGCGCTTCTTGTGCTTCCACCCACCA 3808
 Db 3773 TCCCCAGATTGCGCATTTGTACACCCCTGCGCTGCGCTTCTTGTGCTTCCACCCACCA 3832
 Qy 3809 TCCAGGTGAGACCCCTGAGAAAGACCCCTGAGACTCTGGGAATTTGAGTGTACCAAGGT 3868
 Db 3833 TCCAGGTGAGACCCCTGAGAAAGACCCCTGAGACTCTGGGAATTTGAGTGTACCAAGGT 3892
 Qy 3869 GTGCCCTGTACAGAGCGAGACCCCTGACACTGATGAGGCGTCCCTGCGGTCAATTTGG 3928
 Db 3893 GTGCCCTGTACAGAGCGAGACCCCTGACACTGATGAGGCGTCCCTGCGGTCAATTTGG 3952
 Qy 3929 GGGGAGTGTCTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAAGAAAAA 3988
 Db 3953 GGGGAGTGTCTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAAGAAAAA 4012
 Qy 3989 AAAAAAAAAAAAAA 4005
 Db 4013 AAAAAAAAAAAAAA 4029

RESULT 12 US-09-438-486-173

Sequence 173, Application US/09438486
 Publication No. US20030009019A1

GENERAL INFORMATION:

APPLICANT: Cec'h, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: No. US20030009019A1el Telomerase
 NUMBER OF SEQUENCES: 223
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111-3834

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/438.486
 FILING DATE: 12-NOV-1999

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

CLASSIFICATION: 536

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

CLASSIFICATION: 536

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

CLASSIFICATION: 536

APPLICATION DATA:

```
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01 OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY:
LOCATION: 1..4029
OTHER INFORMATION:
OTHER INFORMATION: human TRP cDNA insert of
OTHER INFORMATION: plasmid pGRN121
US-09-436-486-173

Query Match          95.7%; Score 3832.6; DB 9; Length 4029;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 3951; Conservative 0; Mismatches 39; Indels 47; Gaps 11;

QY 8 GCAGCGCTGCTCTGCTGCGACAGTGGGAAACCCCTGAGCCCGGACACCCCGCGATGCC 67
DB 1 GCAGCGCTGCTCTGCTGCGACAGTGGGAAACCCCTGAGCCCGGACACCCCGCGATGCC 60
QY 68 GCGCGCTCCCGCTGCGAGCCGCTGCGCTCCCTGCTGCGAGCAGCAGTACCGGAGAGTCT 127
DB 61 GCGCGCTCCCGCTGCGAGCCGCTGCGCTCCCTGCTGCGAGCAGCAGTACCGGAGAGTCT 120
QY 128 GCGCGTGGCCAGTTCGTTGCGGAGCCTGGGAGCCGAGAGGCTGGGCTGTGTACAGCGGG 187
DB 121 GCGCGTGGCCAGTTCGTTGCGGAGCCTGGGAGCCGAGAGGCTGGGCTGTGTACAGCGGG 180
QY 188 GGAACCGGCGGCTTCCGCGCGCTGGTGGCCAGTGGTGTGTGCTGCTCGGAGAGC 247
DB 181 GGAACCGGCGGCTTCCGCGCGCTGGTGGCCAGTGGTGTGTGCTGCTCGGAGAGC 240
QY 248 ACGGCGGCGCGCGCGCGCGCGCTCTCTCCGCCAGTGTCTGCTTAAGAGAGTGGTGGC 307
DB 241 AAGGCGGCGCGCGCGCGCGCGCTCTCTCCGCCAGTGTCTGCTTAAGAGAGTGGTGGC 300
QY 308 CCGAGTGTGAGAGAGCTGTGCGAGCGCGCGCGAGAGAGTGTGTGGCTTGGCTTGC 367
DB 301 CCGAGTGTGAGAGAGCTGTGCGAGCGCGCGCGAGAGAGTGTGTGGCTTGGCTTGC 360
QY 368 GCTGTGAGACGGGCGCGCGGGGGGCGCGCGAGGCTTTCACACAGAGAGTGCAGAGTA 427
DB 361 GCTGTGAGACGGGCGCGCGGGGGGCGCGCGAGGCTTTCACACAGAGAGTGCAGAGTA 420
QY 428 CTGGCCCAACAGGCTGACGACGACTGCGGGGAGCGGGGCGTGGGGCTCTCTCTCG 487
DB 421 CTGGCCCAACAGGCTGACGACGACTGCGGGGAGCGGGGCGTGGGGCTCTCTCTCG 480
QY 488 CGCGGGGAGAGAGCTGTGTGTACCTGTGAGAGCTGTGGCGCTTTTGTGTGGTGGT 547
DB 481 CGCGGGGAGAGAGCTGTGTGTACCTGTGAGAGCTGTGGCGCTTTTGTGTGGTGGT 540
QY 548 GGTCTCCAGCTGGGCTTACAGAGTGTGGGGGCGCGCGTGTACCAAGCTGGCGCTGCAC 607
DB 541 GGTCTCCAGCTGGGCTTACAGAGTGTGGGGGCGCGCGTGTACCAAGCTGGCGCTGCAC 600
QY 608 TCAGGCGGCGCGCGCGCGCGCGAGCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667
DB 601 TCAGGCGGCGCGCGCGCGCGCGAGCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 658
```

```
QY 668 CTGGAACCATATGCTCAGGAGAGCGGGGCTCCCTTGAGCTTGCACAGCCCGGGTGGAG 727
DB 659 CTGGAACCATATGCTCAGGAGAGCGGGGCTCCCTTGAGCTTGCACAGCCCGGGTGGAG 717
QY 728 GAGGCGCGGGGGGAGTGTCCAGCCGAAGTCTGCGCTTGCCTCCAGAGAGCCAGGCTGGCG 787
DB 718 GAGGCGCGGGGGGAGTGTCCAGCCGAAGTCTGCGCTTGCCTCCAGAGAGCCAGGCTGGCG 777
QY 788 TGCCTTGAAGCGGAGCGAGCGCGCTTGGGAGAGGCTCTGGGCGCCACCGGAGAGAG 847
DB 778 TGCCTTGAAGCGGAGCGAGCGCGCTTGGGAGAGGCTCTGGGCGCCACCGGAGAGAG 837
QY 848 GGTGAGACGAGTACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
DB 838 GGTGAGACGAGTACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 897
QY 908 CACCTCTTGGAGAGGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 967
DB 898 CACCTCTTGGAGAGGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 957
QY 968 GCACCAAGCGGGGCGCGCGCGCGCGATCCATCGAGGCGCACAGCTCTGGGACAGCTGTCC 1027
DB 958 GCACCAAGCGGGGCGCGCGCGCGCGATCCATCGAGGCGCACAGT-CCTGGGACAGCTGTCC 1016
QY 1028 CCCGCTGAGCGCGAGACCAAGCACTTCTCTACTCTCTCAAGGAGACAGAGACCTGCG 1087
DB 1017 CCCGCTGAGCGCGAGACCAAGCACTTCTCTACTCTCTCAAGGAGACAGAGACCTGCG 1074
QY 1088 GCCCTCTCTCTACTCTC-AGCTCTGTGAGGCGCGAGCTGAGTGGCGCTC-GGAGGCTGTG 1145
DB 1075 GCCCTCTCTCTACTCTCAATATATCTGAGGCGCGAGCTGAGTGGCGCTGCGGAGGTGTG 1134
QY 1146 GAGACCATCTTCTTGGGTTTCAGGCGCGCTGAGAGGAGTCCCGGAGGTTGGCGCGC 1205
DB 1135 GAGACCATCTTCTT-GGTTTCAGGCGCGCTGAGAGGCA-GAATTCGCGGAGGTTGGCGCGC 1192
QY 1206 CTGGCCCAAGCGCTCTGCGCAAGTGGGCGCGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1265
DB 1193 CTGGCCCAAGCGCTCTGCGCAAGTGGGCGCGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1252
QY 1266 CAGTGCCTCTAGGGGCTGTCTCTCAAGAGCACTGCGCGCTGCGAGCTGTGGTCAACCCA 1325
DB 1253 CAGTGCCTCTAGGGGCTGTCTCTCAAGAGCACTGCGCGCTGCGAGCTGTGGTCAACCCA 1312
QY 1326 GCAGCGGCTGTGTGTGCGCGGAGAAAGCCCGAGGAGCTGTGTGGCGCGCGCGAGAGAG 1385
DB 1313 GCAGCGGCTGTGTGTGCGCGGAGAAAGCCCGAGGAGCTGTGTGGCGCGCGCGAGAGAG 1372
QY 1386 G-ACAGAGACCCCGCTGCTGCTGAGTGTCTCGCAGACAGAGAGAGAGAGAGT 1444
DB 1373 GAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1432
QY 1445 GTACGAGCTTGTGCGGGGCTGCGCTGCGCGGAGTGTGTGCGCGCTGTGGGGCTCAG 1504
DB 1433 GTACGAGCTTGTGCGGGGCTGCGCTGCGCGGAGTGTGTGCGCGCTGTGGGGCTCAG 1492
QY 1505 GCACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1564
DB 1493 GCACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1552
QY 1565 CAAAGCTCTGTGTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1624
DB 1553 CAAAGCTCTGTGTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1612
QY 1625 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1684
DB 1613 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1672
QY 1685 GGCAGAGTCTCTGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1744
DB 1673 GGCAGAGTCTCTGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1732
QY 1745 TTATGTCAAGGAGACAGAGTTCATAAAGAGAGAGCTTTTCTTACCGAAGAGTGTCTG 1804
```

Db	1733	TTATGTCA	CGSAGAC	CCAGTTTCA	AAAAAGAA	CAGGCTCTTTTCT	CA	CGGAAG	GTCTG	1792
Qy	1805	GAGCAAGT	TGCAAG	CAATTG	GAATCAG	ACAGCACTTGA	AGAGGT	CA	GTGCGGAGCT	1864
Db	1793	GAGCAAGT	TGCAAG	CAATTG	GAATCAG	ACAGCACTTGA	AGAGGT	CA	GTGCGGAGCT	1852
Qy	1865	GTGGAAG	CAGAGT	TCAGG	AGCATG	GGGAAGCCAG	GGCCGCGCTG	CA	GTGAGTCCAGCT	1924
Db	1853	GTGGAAG	CAGAGT	TCAGG	AGCATG	GGGAAGCCAG	GGCCGCGCTG	CA	GTGAGTCCAGCT	1912
Qy	1935	CCGCTTC	ATCCCC	AAAGCCTC	AGCGGCTG	CGGCGATTTG	GAACATG	CACTAC	GTGTGGG	1984
Db	1913	CCGCTTC	ATCCCC	AAAGCCTC	AGCGGCTG	CGGCGATTTG	GAACATG	CACTAC	GTGTGGG	1972
Qy	1985	AGCCGA	AACTTCCG	CAGAGAA	AAAAAGAGG	CCAGGCTCTC	ACCTG	GAGGTGA	AGGCACT	2044
Db	1973	AGCCGA	AACTTCCG	CAGAGAA	AAAAAGAGG	CCAGGCTCTC	ACCTG	GAGGTGA	AGGCACT	2032
Qy	2045	GTTCAG	CGTGTCTCA	ACACAG	AGGCGGCGGCGCCCGG	CGCTCTG	AGGCGCGCTG	GTGTCT		2104
Db	2033	GTTCAG	CGTGTCTCA	ACACAG	AGGCGGCGGCGCCCGG	CGCTCTG	AGGCGCGCTG	GTGTCT		2092
Qy	2105	GAGCGT	GAGAGAT	ATCCAC	AGAGGCTG	GGCGACCTTCTG	GTGCTGTG	CGGGGCC	AGGA	2164
Db	2093	GAGCGT	GAGAGAT	ATCCAC	AGAGGCTG	GGCGACCTTCTG	GTGCTGTG	CGGGGCC	AGGA	2152
Qy	2165	CCCGCG	CGCTAG	GTGA-----					CATCC	2188
Db	2153	CCCGCG	CGCTAG	GTGA-----						2212
Qy	2189	CCAGCA	AGGCTCA	CGAGAGT	CACTCG	CAACATCA	AAACCC	CAGAAC	CGTACTG	2248
Db	2213	CCAGCA	AGGCTCA	CGAGAGT	CACTCG	CAACATCA	AAACCC	CAGAAC	CGTACTG	2272
Qy	2249	GCGTGG	ATCCGTTGG	TCCAGAA	AGGCGCGCA	TGGGCAAGT	CCGCAAG	GGCCTCA	AG	2308
Db	2273	GCGTGG	ATCCGTTGG	TCCAGAA	AGGCGCGCA	TGGGCAAGT	CCGCAAG	GGCCTCA	AG	2332
Qy	2309	CCACGT	CTCTAC	CTTGGAC	AGACTTCC	AGCCGTA	CAATG	CAACAG	ATTG	2368
Db	2333	CCACGT	CTCTAC	CTTGGAC	AGACTTCC	AGCCGTA	CAATG	CAACAG	ATTG	2392
Qy	2369	GGAAG	CAAGCCCG	GTGAGG	ATCCGTC	GTCAATG	CAAGCA	AGACTTCC	CTCTG	2428
Db	2393	GGAAG	CAAGCCCG	GTGAGG	ATCCGTC	GTCAATG	CAAGCA	AGACTTCC	CTCTG	2452
Qy	2429	CAGCA	GTGGCTCTT	TCCACAG	CTTCTCC	ACAGCTTCA	GTCCAC	AGCGCTG	CGCATAG	2488
Db	2453	CAGCA	GTGGCTCTT	TCCACAG	CTTCTCC	ACAGCTTCA	GTCCAC	AGCGCTG	CGCATAG	2512
Qy	2489	GGGCA	AGTCTT	CAAGTCC	AGTCCAG	GGGATCC	CGAGGG	CTCATCTC	TCTCC	2548
Db	2513	GGGCA	AGTCTT	CAAGTCC	AGTCCAG	GGGATCC	CGAGGG	CTCATCTC	TCTCC	2572
Qy	2549	CTGCA	GCCTTGT	CTACAG	CGCATG	GAAGAA	CAAGTCTT	TGGGG	GAATTC	2608
Db	2573	CTGCA	GCCTTGT	CTACAG	CGCATG	GAAGAA	CAAGTCTT	TGGGG	GAATTC	2632
Qy	2609	GCTGCT	CTGCTT	TGATGAT	ATTTCTT	TGTGTG	ACACTT	CACTCAC	CGCGAA	2668
Db	2633	GCTGCT	CTGCTT	TGATGAT	ATTTCTT	TGTGTG	ACACTT	CACTCAC	CGCGAA	2692
Qy	2669	AACCTT	CTCTAG	AAACCTT	GTGCGAG	GTGCTCTG	CTGATG	AGTCTG	GTGA	2728
Db	2693	AACCTT	CTCTAG	AAACCTT	GTGCGAG	GTGCTCTG	CTGATG	AGTCTG	GTGA	2752
Qy	2729	GAAGCA	AGTGTGA	ACTTCCCT	GTAGA	AAAGCA	AGGCGCTG	GGTG	CACAGGCTT	2788
Db	2753	GAAGCA	AGTGTGA	ACTTCCCT	GTAGA	AAAGCA	AGGCGCTG	GGTG	CACAGGCTT	2812
Qy	2789	GATGCG	CGGCCA	CGGCTAT	TCCCTG	TGTG	CGGCTG	CTGTG	ATACCG	2848

Dd	2813	GAAGCGCGCCACAGGGCCTATTTCCTCCCGTGGTGGCGGCTGCGTGTGGATACCCGGACCTTGA	2872
Qy	2849	GGTGACAGAGCAGCTACTCTACAGCTATATGCCCCGGAGCTCTCATACAGCCAGCTTACTCTTCA	2908
Dd	2873	GGTGAGAGGCGACATCTACCTACAGCTATATGCCGGAGCTTCCATACAGGCGAGCTTACTCTTCA	2932
Qy	2909	CCGGGGCTTCAAGGCTGGAGGAAACATGCGTCCCAACTCTTTGGGGTCTTGGCGGCTGAA	2968
Dd	2933	CCGGGGCTTCAAGGCTGGAGGAAACATGCGTCCCAACTCTTTGGGGTCTTTGGGGCTTGA	2992
Qy	2969	GTGTACAGCCTGTTTCTGGAATTTGCAGGTGAACAGCCTCCACAGCGGTGTGCACCAACAT	3028
Dd	2993	GTGTACAGCCTGTTTCTGGAATTTGCAGGTGAACAGCCTCCACAGCGGTGTGCACCAACAT	3052
Qy	3029	CTCAAGAATCCTCCTGTGTGAAGGCGTAAAGGTTTACAGCATGTGCTGCGACGCTCCCTT	3088
Dd	3053	CTCAAGAATCCTCCTGTGTGAAGGCGTAAAGGTTTACAGCATGTGCTGCGACGCTCCCTT	3112
Qy	3089	TCATACAGCAATTTGGAAAGAACCCCAATTTTTCGCGCGCTCATCTCTGACAGGGCTC	3148
Dd	3113	TCATACAGCAATTTGGAAAGAACCCCAATTTTTCGCGCGCTCATCTCTGACAGGGCTC	3172
Qy	3149	CCTCTGCTACTCTCATCTCTGAAAGCCAAAGAACGAGGATGTGGCTGGGGGCCAAGGGCG	3208
Dd	3173	CCTCTGCTACTCTCATCTCTGAAAGCCAAAGAACGAGGATGTGGCTGGGGGCCAAGGGCG	3232
Qy	3209	CGCGGGCCTTGTGGCCTCCAGAGGCCGCTGAGTGGCTGTCCACACAAAGATTCTCTTCA	3268
Dd	3233	CGCGGGCCTTGTGGCCTCCAGAGGCCGCTGAGTGGCTGTCCACACAAAGATTCTCTTCA	3292
Qy	3269	GCTGACTGTAGACACCGGTGTACACTTACGTGCACTCTCTGGGGTCACTCAGSAGACGCCAGAC	3328
Dd	3293	GCTGACTGTAGACACCGGTGTACACTTACGTGCACTCTCTGGGGTCACTCAGSAGACGCCAGAC	3352
Qy	3329	GCAGGTGATGTGGAAAGCTCCCGGGGAGAGAGCGTGCATGTGCCCTGAGAGCGCGAGCCACCC	3388
Dd	3353	GCAGGTGATGTGGAAAGCTCCCGGGGAGAGAGCGTGCATGTGCCCTGAGAGCGCGAGCCACCC	3412
Qy	3389	GGCACTGCGCTCAGACTTCAAGACCATCTGTGACTGATGTGGCCACCGGCCACAGCCAGGC	3448
Dd	3413	GGCACTGCGCTCAGACTTCAAGACCATCTGTGACTGATGTGGCCACCGGCCACAGCCAGGC	3472
Qy	3449	CGAGAGCGAGAACAGAGAGGCCGTGTACGCGCGGGGTCTACGTGCCAGGGAGGAGGGGCG	3508
Dd	3473	CGAGAGCGAGAACAGAGAGGCCGTGTGTACGCGCGGGGTCTACGTGCCAGGGAGGAGGGGCG	3532
Qy	3509	GCCCAACCCACAGGCCCGCACCGCTGGGAGTCTGAGGCGCTGAGTGAATGTTGGCGGAGGC	3568
Dd	3533	GCCCAACCCACAGGCCCGCACCGCTGGGAGTCTGAGGCGCTGAGTGAATGTTGGCGGAGGC	3592
Qy	3569	CTGCAATGTCCGGGCTGAAGGCTGAATGTCCGGGCTGAGAGCCTGAGGCCAGTGTCCAGCCAGG	3628
Dd	3593	CTGCAATGTCCGGGCTGAAGGCTGAATGTCCGGGCTGAGAGCCTGAGGCCAGTGTCCAGCCAGG	3652
Qy	3629	GCTGAGTGTCCAGACACACTGCGGCTTTCACCTTCCCAAGGCTGAGCGCTCGGCTCCACC	3688
Dd	3653	GCTGAGTGTCCAGACACACTGCGGCTTTCACCTTCCCAAGGCTGAGCGCGTGGGCTCCACC	3712
Qy	3689	CCAGGGCCAGCTTTCCTCACACAGAGACCCGGCTTCCACTCCCCACATATGGAATAGTCCA	3748
Dd	3713	CCAGGGCCAGCTTTCCTCACACAGAGACCCGGCTTTCACATCCCCACATAGGAATAGTCCA	3772
Qy	3749	TGCCCAAGTTTGGCAATTTGACCCCGTCCGCGCGCTCTCTTGGCTTCCACCCCCACCA	3808
Dd	3773	TGCCCAAGTTTGGCAATTTGACCCCGTCCGCGCGCTCTCTTGGCTTCCACCCCCACCA	3832
Qy	3809	TCCAGGTGAGACCCCTAGAGAGACCCCTGGAGCTCTGGGAATTTGAGTGAACCAAAGT	3868
Dd	3833	TCCAGGTGAGACCCCTAGAGAGACCCCTGGAGCTCTGGGAATTTGAGTGAACCAAAGT	3892
Qy	3869	GTGCCCTTGTACACAGGCGGAGAGACCTGTACACTTGGATGGGGGTCCCTGTGGGTCAAAATGG	3928
Dd	3893	GTGCCCTTGTACACAGGCGGAGAGACCTGTACACTTGGATGGGGGTCCCTGTGGGTCAAAATGG	3952

QY 3929 GGGGAGTGTCTGTGGAGTAAATATATGAGTTTTCAGTTTGAAGAAAAA 3988
Db 3953 GGGGAGTGTCTGTGGAGTAAATATATGAGTTTTCAGTTTGAAGAAAAA 4012
QY 3989 AAAAAAAAAAAAAA 4005
Db 4013 AAAAAAAAAAAAAA 4029

RESULT 13

US-10-053-758-173
Sequence 173, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: LOCATION: 1..4029
OTHER INFORMATION: /note= "preliminary sequence for
human TRT cDNA insert of
plasmid pGRN121"
SEQUENCE DESCRIPTION: SEQ ID NO: 173:
US-10-053-758-173

Query Match 95.7%; Score 3832.6; DB 9; Length 4029;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 3951; Conservative 0; Mismatches 39; Indels 47; Gaps 11;
QY 8 GCAGCGCTGGCTCTGCTGCGAGTGGGAAAGCCCTGAGCCCGGGCCACCCCGGAGTCCC 67
Db 1 GCAGCGCTGGCTCTGCTGCGAGTGGGAAAGCCCTGAGCCCGGGCCACCCCGGAGTCCC 60
QY 68 GCGGCTTCCCGCTGCGAGCCGTGCTCTGCTGCGAGCCACTACCCGAGTGTCT 127
Db 61 GCGGCTTCCCGCTGCGAGCCGTGCTCTGCGAGCCACTACCCGAGTGTCT 120
QY 128 GCGGCTGCGACGTTGCTGCGGCGCTGCGGCGCCCAAGGCTGCGGCTGCGAGCCCG 187
Db 121 GCGGCTGCGACGTTGCTGCGGCGCTGCGGCGCCCAAGGCTGCGGCTGCGAGCCCG 180
QY 188 GGAACCCGCGCTTTCCGCGCTGTGTGGCCAGTGTGTGTGTGTGTGTGTGTGTGTGT 247
Db 181 GGAACCCGCGCTTTCCGCGCTGTGTGGCCAGTGTGTGTGTGTGTGTGTGTGTGTGT 240
QY 248 AGGCGCGCGCCCGCGCCCGCTCTCTGCGAGTGTGTGTGTGTGTGTGTGTGTGTGT 307
Db 241 AGGCGCGCGCCCGCGCCCGCTCTCTGCGAGTGTGTGTGTGTGTGTGTGTGTGTGT 300
QY 308 CCGAGTGTGTGAGGCTGT 367
Db 301 CCGAGTGTGTGAGGCTGT 360
QY 368 GCTGTGTGAGCGGGGCGCGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 427
Db 361 GCTGTGTGAGCGGGGCGCGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 428 CCGGCGCAACGAGT 487
Db 421 CCGGCGCAACGAGT 480
QY 488 CCGGCTGGCGGAGCAGT 547
Db 481 CCGGCTGGCGGAGCAGT 540
QY 548 GCGCTCCAGCTGCGCTTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 607
Db 541 GCGCTCCAGCTGCGCTTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
QY 608 TCAGGCG 667
Db 601 TCAGGCG 658
QY 668 CTGGAGCAATGAGGT 727
Db 659 CTGGAGCAATGAGGT 717
QY 728 GAGGCG 787
Db 718 GAGGCG 777
QY 788 TCAGGCG 847
Db 778 TCAGGCG 837
QY 848 GCGTGTGAGCGAGT 907
Db 838 GCGTGTGAGCGAGT 897
QY 908 CACGCTTTGAGGAGT 967
Db 898 CACGCTTTGAGGAGT 957
QY 968 GCAGCAGCG 1027
Db 958 GCAGCAGCG 1016

QY	1208	CCGCGGTACGCGGAGGACCAAGACACTCCTCTACACCTCAGGCGCAAGAGGACGCTGC	11111	1087
Db	1017	CCGCGGTACGCGGAGGACCAAGACTCTCTACTCTCTAGGCGACAAGNA--CACTGC	11111	1074
QY	1088	GGCCTCCCTTCTACTCT-AGCTCTCTAGAGCCCAAGCCTGACTCTGGGCGCTC	1145	
QY	1146	GAGACCATCTTTCTGGGTTCCAGGCGCTTGATGCCAGGGACTCCCCGAGTTGCCCC	1205	
Db	1135	GAGACCATCTTTCT-GGTTCCAGGCGCTTGATGCCA-GGATTCCCCGAGGTTCCCCG	1192	
QY	1206	CTGCGCCAGGCGCTACTGGGCAAAATGGGCGCCGTTTCTGGAGACTCTTGGGAACACAGCG	1265	
Db	1193	CTGCGCCAGGCGGACTACTGGCAAAATGGGCGCCGTTTCTGGAGACTCTTGGGAACACAGCG	1252	
QY	1266	CAGTGCCTCTACGGGGGTGCTCCCTCAAGAGCAGCATGCCGCTGCGAGCTCGGTCACCCA	1325	
Db	1253	CAGTGCCTCTACGGGGGTGCTCCCTCAAGAGCAGCATGCCGCTGCGAGCTCGGTCACCCA	1312	
QY	1326	GCACCGCGTCTGTGCGCGGGAAGAGCCCAAGGCTCTGTGTGGGCGCCCCGAGAGAG	1385	
Db	1313	GCACCGCGTCTGTGCGCGGGAAGAGCCCAAGGCTCTGTGTGGGCGCCCCGAGAGAG	1372	
QY	1386	G-ACACAGACCCCGGTGCGCTGTGTGACGTGCTCCGCGACAGACAGCCCTGGAGGT	1444	
Db	1373	GAAACACAGACCCCGGTGCGCTGTGTGACGTGCTCCGCGACAGACAGCCCTGGAGGT	1422	
QY	1445	GTACGGCTTGTGTGCGGCGCTGCTGCGCGGCTGCTGTGCCCCAGGCGCTGTGGGCTCAG	1504	
Db	1433	GTACGGCTTGTGTGCGGCGCTGCTGCGCGGCTGCTGTGCCCCAGGCGCTGTGGGCTCAG	1492	
QY	1505	GCACAAAGAAAGCGCGCTTCTCTACAGGAACACAAAGATTCACTCTCCCTGGGGAAGCATGC	1554	
Db	1493	GCACAAAGAAAGCGCGCTTCTCTACAGGAACACAAAGATTCACTCTCCCTGGGGAAGCATGC	1552	
QY	1565	CAACCTCTGCGTGCAGAGATGACGCTGAGGAAGATGACCGTGGGGAAGCTGGGCTGGCG	1624	
Db	1553	CAACCTCTGCGTGCAGAGATGACGCTGAGGAAGATGACCGTGGGGAAGCTGGGCTGGCG	1612	
QY	1625	CAGAGGCCACAGGGGTGTGGCTGTGTTCCGGCGCGAGAGCACCGCTGCGCTGAGAGATCT	1684	
Db	1613	CAGAGGCCACAGGGGTGTGGCTGTGTTCCGGCGCGAGAGCACCGCTGCGCTGAGAGATCT	1672	
QY	1685	GGCCAACTCTGCTGACACTGCGTGAATGATGTGTAAGTCTGCGAGCTGCTCAGGCTTTCTT	1744	
Db	1673	GGCCAACTCTGCTGACACTGCGTGAATGATGTGTAAGTCTGCGAGCTGCTCAGGCTTTCTT	1732	
QY	1745	TTATGTACGAGAGACCAAGTTTCAAAAAGAAAGGCTTTTCTACCGGAAGAGTGTG	1804	
Db	1733	TTATGTACGAGAGACCAAGTTTCAAAAAGAAAGGCTTTTCTACCGGAAGAGTGTG	1792	
QY	1805	GAGCAAGTTGCAAAAGCTTGTGAATCAGACAGCACTTGAAGAGGTGACAGCTCGGGAAGT	1864	
Db	1793	GAGCAAGTTGCAAAAGCTTGTGAATCAGACAGCACTTGAAGAGGTGACAGCTCGGGAAGT	1852	
QY	1865	GTGCGAAGCAGAGGTACGAGCATCGGGAAGCAGAGCCCGCTGCTGACGTCCAGCT	1924	
Db	1853	GTGCGAAGCAGAGGTACGAGCATCGGGAAGCAGAGCCCGCTGCTGACGTCCAGCT	1912	
QY	1925	CCGCTTATCCCAAGCTTACAGGCGCTGGGCGCGATTGTGAACATGTGACTAGTGTGTGG	1984	
Db	1913	CCGCTTATCCCAAGCTTACAGGCGCTGGGCGCGATTGTGAACATGTGACTAGTGTGTGG	1972	
QY	1985	AGCCAGAAGCTTCCGCGAGAAAAAGAGGCGCGAGCTCCACTGTGAGGTGAAGGCACT	2044	
Db	1973	AGCCAGAAGCTTCCGCGAGAAAAAGAGGCGCGAGCTCCACTGTGAGGTGAAGGCACT	2032	
QY	2045	GTTCAGGCTGTCAACTACAGAGGCGCGCGCGCCCGGCTCTGTGGAGGCTCTGTGCT	2104	
Db	2033	GTTCAGGCTGTCAACTACAGAGGCGCGCGCGCGCCCGGCTCTGTGGAGGCTCTGTGCT	2092	
QY	2105	GGGCGCTGACGATATTCACAGAGGCGCTGCGCACCTTGTGCTGCTGCGGCGCCACGA	2164	

D	2093	GGGGCTGGAGATATCCACAGGGCCGGGCGACCTTCGTGGGTGGGGGCCAGGA	2152
Q	2165	CCGCGCCCTGAGCTGA-----CATCCC	2188
D	2153	CCCCGCCCTGAGACTGTACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACATCCC	2212
Q	2189	CCAGNACAGGCTCACGGAGGTCTATGGCCAGATTCATCAACCCCAAGAACATGTACTCGT	2248
D	2213	CCAGAGACAGGCTCACGGAGGTCTATGGCCAGCATTCATCAACCCCAAGAACATGTACTCGT	2272
Q	2249	GCGTGGGTATGACCGTGGGTCTCCAGAAAGGCCCCCATGGGACGTCCGCAAGGCGTTCAAGAG	2308
D	2273	GCGTGGGTATGACCGTGGGTCTCCAGAAAGGCCCGCATGGGACGTCCGCAAGGCGTTCAAGAG	2332
Q	2309	CCACGTCTTACCTTGACAGACCTCCAGCCGTACATGGGACAGTTCTGTGGCTCACCTGCA	2368
D	2333	CCACGTCTTACCTTGACAGACCTCCAGCCGTACATGGGACAGTTCTGTGGCTCACCTGCA	2392
Q	2369	GGAGACACAGCCCGCTGGGGATCCGTCGTTCATTCGACGAGACCTCTCCCTGATGAGAGC	2428
D	2393	GGAGAACAGCCCGCTGGGGATCCGTCGTTCATTCGACGAGACCTCTCCCTGATGAGAGC	2452
Q	2429	CAGCAGTGGCCTCTTGACAGCTCTTCTTACGCTTCATGTGCCACAGCCGCTGGCCATCAG	2488
D	2453	CAGCAGTGGCCTCTTGACAGCTCTTCTTACGCTTCATGTGCCACAGCCGCTGGCCATCAG	2512
Q	2489	GGGCAAGTCTTACGTCCAGTGGCCAGGGGATCCCCAGAGGCTCTCATCTCTCCAGCGTCT	2548
D	2513	GGGCAAGTCTTACGTCCAGTGGCCAGGGGATCCCCAGAGGCTCTCATCTCTCCAGCGTCT	2572
Q	2549	CTTGAGGCTTGAGTACGAGCCACATATGAGAAACAAGCTGTTGGGGGGATTCGGCGGGAGG	2608
D	2573	CTTGAGGCTTGAGTACGAGCCACATATGAGAAACAAGCTGTTGGGGGGATTCGGCGGGAGG	2632
Q	2609	GCTGCTCTGCGTTTGGTGGATGATTTCTTGTGTGACACCTCACCTCACCCAGCGAA	2668
D	2633	GCTGCTCTGCGTTTGGTGGATGATTTCTTGTGTGGAGACACTCACCTCACCCAGCGAA	2692
Q	2669	AACCTTCTCAGGACCTGTGTCGAGGCTGTCCTGAGTATGGCTTCGTGGTGAACCTTGGC	2728
D	2693	AACCTTCTCAGGACCTGTGTCGAGGCTGTCCTGAGTATGGCTTCGTGGTGAACCTTGGC	2752
Q	2729	GAACACAGTGGTGAACCTTCCCTTAAGAACAGAGGCCCTGGGTGGACAGGCGTTTGTGTCA	2788
D	2753	GAACACAGTGGTGAACCTTCCCTTAAGAACAGAGGCCCTGGGTGGACAGGCGTTTGTGTCA	2812
Q	2789	GATCGCGGCCACAGGCTTATTTCCCTGTGTGGGCGCTGCTGTGATACCCGAGACCTTGGGA	2848
D	2813	GATCGCGGCCACAGGCTTATTTCCCTGTGTGGGCGCTGCTGTGATACCCGAGACCTTGGGA	2872
Q	2849	GGTGCAGAGGACTACTTCCAGCTATGCCCCGGACCTTCATCAGAGCCAGTCTTACCTTCAA	2908
D	2873	GGTGCAGAGGACTACTTCCAGCTATGCCCCGGACCTTCATCAGAGCCAGTCTTACCTTCAA	2932
Q	2909	CCGCGGCTTCAAGGCTGGGAGGAACATGGGTGSCAAACCTTTTGGGGCTTGGCGGCTGAA	2968
D	2933	CCGCGGCTTCAAGGCTGGGAGGAACATGGGTGSCAAACCTTTTGGGGCTTGGCGGCTGAA	2992
Q	2969	GTTGTACAGCCTGTTTTTGATTTTGGAGGTGAACACCTCCAGAGAGGTGGCACCAACAT	3028
D	2993	GTTGTACAGCCTGTTTTTGATTTTGGAGGTGAACACCTCCAGAGAGGTGGCACCAACAT	3052
Q	3029	CTACAAAGTCCCTCTGCTGAGGCGTACAGAGTTTCAAGCATGTGTCTGACAGCTCCCAT	3088
D	3053	CTACAAAGTCCCTCTGCTGAGGCGTACAGAGTTTCAAGCATGTGTCTGACAGCTCCCAT	3112
Q	3089	TCTATCAGCAAGTTTGAAGAAACCCACATTTTCTGTCCGCTCATCTCTGACAGGCGTC	3148
D	3113	TCTATCAGCAAGTTTGAAGAAACCCACATTTTCTGTCCGCTCATCTCTGACAGGCGCTC	3172
Q	3149	CCTGTGCTACTCATCTGTGAAGCAACGAAGGATGTGGGTGGGGGCCAAGGGCGC	3208

Thu Apr 17 08:21:56 2003

us-09-424-686b-1del.rnpb

Page 47

Db	3173	CCCTGCTATCTCCATCTCGAAGAAGCAAGAACCCAGGATGTGTCGTGGGGCAAGAGGCC	3232
QY	3209	GGCGGGGCGCTGGCCCTCCGAGGCCGTGACAGGTGTGTGCACACAAAGATTCCGTGTCAA	3269
Db	3233	GGCGGGGCGCTGTGCCCTCCGAGAGCGCTGACAGGTGTGTGCACCAAGATTCTCGTGTCAA	3292
QY	3269	GCTGACGTACACACGTGTACACATACGTGTGCACACTCGTGGGTGTACACAGACGCCAGAC	3328
Db	3293	GCTGACGTACACACGTGTGTACATCTGTGCACACTCGTGGGTGTACACAGACGCCAGAC	3355
QY	3329	GCAGCTAGTGGGAAGCTCCGGGGAGCAGCGTACTGCTCCCTTGAGGCCGCGACACCC	3388
Db	3355	GCAGCTAGTGGGAAGCTCCGGGGAGCAGCGTACTGCTCCCTTGAGGGCGCGAGCAACC	3412
QY	3389	GGCACTGCTCCTGAGCTTCAAGACCATCTGTGACTGATGGCCACCGGCCACAGCCAGGC	3448
Db	3413	GGCACTGCTCCTGAGCTTCAAGACCATCTGTGACTGATGGCCACCGGCCACAGCCAGGC	3472
QY	3449	CGAAGAGAGACACACAGCGCCCTGTATCCCGCGCTGTACGTGCCAGGAGAGAGAGGCGG	3508
Db	3473	CGAGAGCAGACACACAGCGCCCTGTATCCCGCGCTGTACGTGCCAGGAGAGAGAGGCGG	3532
QY	3509	GGCCACACCCAGGGCCGACCGCGTGGGAGTGTGAGGGCTGATGAGTGTGGTGGCGAGGC	3568
Db	3533	GGCCACACCCAGGGCCGACCGCGTGGGAGTGTGAGGGCTGATGAGTGTGGTGGCGAGGC	3592
QY	3569	CTGCATGTCCGGGTGAAAGCTGATGTCCGGCTGAGGCCCTGAGACGATGTCCAGCCAAAG	3628
Db	3593	CTGCATGTCCGGGTGAAAGCTGATGTCCGGGTGAGGCCCTGAGACGATGTCCAGCCAAAG	3655
QY	3629	GCTGAGTGTCCACACACCTTCGCTTCACTTCCACAGGCTGGCGCTGGCTCCACC	3688
Db	3653	GCTGAGTGTCCACACACCTTCGCTTCACTTCCACAGGCTGGCGCTGGCTCCACC	3712
QY	3689	CCAGGGCCAGCTTTCCTACACAGAGAGCCGGCTTTCACATCCCAATAGGAATATGTCAA	3748
Db	3713	CCAGGGCCAGCTTTCCTACACAGAGAGCCGGCTTTCACATCCCAATAGGAATATGTCAA	3772
QY	3749	TCCCAATATTCGCAATTTTACCCCTTCGCCCTGCTCCTTTCGCTTCCACCCCAACA	3808
Db	3773	TCCCAATATTCGCAATTTTACCCCTTCGCCCTGCTCCTTTCGCTTCCACCCCAACA	3832
QY	3809	TCCAGGTGTGAGACCTCGAGAGAGACCTCTGGAGCTGTGGGAATTTGAGATACCAAAAGT	3868
Db	3833	TCCAGGTGTGAGACCTCGAGAGAGACCTCTGGAGCTGTGGGAATTTGAGATACCAAAAGT	3892
QY	3869	GTGCGCTGTACAGAGCCAGGACCCCTGACACCTGATGGGGGTCCCGTAGGGGTCAAAATGG	3928
Db	3893	GTGCGCTGTACAGAGCCAGGACCCCTGACACCTGATGGGGGTCCCGTAGGGGTCAAAATGG	3955
QY	3929	GGGAGGTGTGTGGGAGTAAATATACGAAATATATGAGTTTTCAGTTTGAATAAAAAAAA	3988
Db	3953	GGGAGGTGTGTGGGAGTAAATATACGAAATATATGAGTTTTCAGTTTGAATAAAAAAAA	4012
QY	3989	AAAAAATAAAAAAATA 4005	
Db	4013	AAAAAATAAAAAAATA 4029	

US-RESULT 14
US-10-054-295-173
: Sequence 173, Application US/10054295
: Publication No. US20030044953A1
: GENERAL INFORMATION:
: APPLICANT: Cech, Thomas R.
: Lingner, Joachim
: Nakamura, Toru
: Nakamura, Karen B.
: Chapman, Greg B.
: Morin, Gregg B.
: Harley, Calvin
: Andrews, William H.
: TITLE OF INVENTION: NO. US20030044953A1el Telomerase
: NUMBER OF SEQUENCES: 225

```

CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: 
```

|||||
Db 301 CGAGTGTGCGANAMGCTGTGCGANCGCGCGCGAANAACGTGTGCGCTTGCGC 360
Qy 368 GCTGTGACGAGGGGCCCCGAGGCGCTTACACACAGCGTCCGAGCTA 427
Db 361 GGTGTGAGAGGGGGCCCCCGAGGCGCTTACACACAGCGTCCGAGCTA 420
Qy 428 CCTGCGCAACAGGTGACCGGACGCACTGCGGGGAGCGGGGGCTGTCTGTG 487
Db 421 CCTGCGCAACAGGTGACCGGACGCACTGCGGGGAGCGGGGGCTGTCTGTG 480
Qy 488 CCGGTGGGCGAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 547
Db 481 CCGGTGGGCGAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Qy 548 GCGTCCAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 607
Db 541 GGNATCCAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Qy 608 TCAGGCGCGGCGCGCGCACAGCTAGTGACCGCGAAGCGCTGCGAAGCGGC 667
Db 601 TCAGGCGCGGCGCGCGCACAGCTAGTGACCGCGAAGCGCTGCGAAGCGGC 658
Qy 668 CTGGAACCATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 727
Db 659 CTGGAACCATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
Qy 728 GAGGCGCGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 787
Db 718 GAGGCGCGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 777
Qy 788 TGCCCTGAGCGCGGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 847
Db 778 TGCCCTGAGCGCGGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 837
Qy 848 GCGTGGACCGAGTGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 907
Db 838 GCGTGGACCGAGTGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
Qy 908 CACCTCTTGGAGGGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 967
Db 898 CACCTCTTGGAGGGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 957
Qy 968 GCACGACGCGGGCGCGCGCATCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 1027
Db 958 GCACGACGCGGGCGCGCGCATCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 1016
Qy 1028 CCGGTGTGACGCGGAGACGACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1087
Db 1017 CCGGTGTGACGCGGAGACGACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1074
Qy 1088 GCGCTCTTCTCTACTC-AGCTCTGAGGCGCGCGCGCGCGCGCGCGCGCGCTG 1145
Db 1075 NCCCTCTTCTCTACTCATAATATCTGAGGCGCGCGCGCGCGCGCGCGCGCTG 1134
Qy 1146 GAGACCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1205
Db 1135 GAGACCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1192
Qy 1206 CTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1265
Db 1193 CTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1252
Qy 1266 CAGTGTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1325
Db 1253 CAGTGTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1312
Qy 1386 GCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1385
Db 1313 GCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1372
Qy 1386 G-ACACAAACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1444

Db 1373 GACACAGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1432
Qy 1445 GTACGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1504
Db 1433 GTACGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1492
Qy 1505 GCACAAACGAGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1564
Db 1493 GCACAAACGAGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1552
Qy 1565 CAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1624
Db 1553 CAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1612
Qy 1625 CAGAGCCCGAGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1684
Db 1613 CAGAGCCCGAGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1672
Qy 1685 GCGCAAGTTCCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1744
Db 1673 GCGCAAGTTCCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1732
Qy 1745 TTATGTACGAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1804
Db 1733 TTATGTACGAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1792
Qy 1805 GAGCAAGTTCCTGCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1864
Db 1793 GAGCAAGTTCCTGCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1852
Qy 1865 GTGGAAGCAGAGGTGAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1924
Db 1853 GTGGAAGCAGAGGTGAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1912
Qy 1925 CCGCTTCAATCCCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1984
Db 1913 CCGCTTCAATCCCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1972
Qy 1985 AGCCAGAAAGTTCCTGCAAGAAAGGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2044
Db 1973 AGCCAGAAAGTTCCTGCAAGAAAGGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2032
Qy 2045 GTTACGCTGCTCAACTACGAGCGGCGCGCGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTG 2104
Db 2033 GTTACGCTGCTCAACTACGAGCGGCGCGCGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTG 2092
Qy 2105 GGGCTGGAACGATATCCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2164
Db 2093 GGGCTGGAACGATATCCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2152
Qy 2165 CCGCGCGCTGAGCTGTA-----CATCC 2188
Db 2153 CCGCGCGCTGAGCTGTA-----CATCC 2212
Qy 2188 CCAGGACAGGCTCAGCGAGGCTATGCGACGATCATTAACCCAGAACAGCTAGCTGCT 2248
Db 2213 CCAGGACAGGCTCAGCGAGGCTATGCGACGATCATTAACCCAGAACAGCTAGCTGCT 2272
Qy 2249 GCGTGGTATGCGCGTGCAGAAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2308
Db 2273 GCGTGGTATGCGCGTGCAGAAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2332
Qy 2309 CCACGCTCTTACTTGTAGACAGCTCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2368
Db 2333 CCACGCTCTTACTTGTAGACAGCTCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2392
Qy 2369 GAGAGCAGCCCGCTGAGGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2428
Db 2393 GAGAGCAGCCCGCTGAGGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2452
Qy 2429 CAGCAGTGGCGCTTCTGAGAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2488
Db 2453 CAGCAGTGGCGCTTCTGAGAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2512

OY 2489 GGGCAAGTCTTACGTCAGTCCAGGAGATCCCGAGGGCTCATCTCTCCACGCTGT 2548
 DB 2513 GGGCAAGTCTTACGTCAGTCCAGGAGATCCCGAGGGCTCATCTCTCCACGCTGT 2572
 OY 2549 CTGCAAGTCTTACGTCAGTCCAGGAGATCCCGAGGGCTCATCTCTCCACGCTGT 2608
 DB 2573 CTGCAAGTCTTACGTCAGTCCAGGAGATCCCGAGGGCTCATCTCTCCACGCTGT 2632
 OY 2609 GCTGCTCTGCTTGGTGGATGATTTCTTTGGTGGTACCTCACCACCGGAA 2668
 DB 2633 GCTGCTCTGCTTGGTGGATGATTTCTTTGGTGGTACCTCACCACCGGAA 2692
 OY 2669 AACCTTCTCAGAGACCTGTGCGAGGTGCTCAGATGATGCTGCTGCTGAACTTGG 2728
 DB 2693 AACCTTCTCAGAGACCTGTGCGAGGTGCTCAGATGATGCTGCTGCTGAACTTGG 2752
 OY 2729 GAAAGACAGTGTGAACTTCCCTGTAGAACAGAGCCCTGGGTGGCAGGCTTTTGTCA 2788
 DB 2753 GAAAGACAGTGTGAACTTCCCTGTAGAACAGAGCCCTGGGTGGCAGGCTTTTGTCA 2812
 OY 2789 GATGCGGCGCCAGGCGCTATTCCTGTGTGCGGCTGCTGCTGATACCGGACCTGGA 2848
 DB 2813 GATGCGGCGCCAGGCGCTATTCCTGTGTGCGGCTGCTGCTGATACCGGACCTGGA 2872
 OY 2849 GGTGCAAGACGCTACTCTGAGTATGCGCGGACCTCCTCAGAGCTCAGTCTCACTTCA 2908
 DB 2873 GGTGCAAGACGCTACTCTGAGTATGCGCGGACCTCCTCAGAGCTCAGTCTCACTTCA 2932
 OY 2909 CGCGGGCTTCAAGGCTGCGGAGGAAACATGCGTGAACCTTTTGGGTGCTTGGGCTGGA 2968
 DB 2933 CGCGGGCTTCAAGGCTGCGGAGGAAACATGCGTGAACCTTTTGGGTGCTTGGGCTGGA 2992
 OY 2969 GTGTCAAGACGCTTGTGATTTGAGATTTGAGAGTCCAGAGCTTGTGCAACAT 3028
 DB 2993 GTGTCAAGACGCTTGTGATTTGAGATTTGAGAGTCCAGAGCTTGTGCAACAT 3052
 OY 3029 CTGCAAGTCTTCTGCTGCTGAGGCTGACAGTGTTCACGATGTGCTGCACTTCCAT 3088
 DB 3053 CTGCAAGTCTTCTGCTGCTGAGGCTGACAGTGTTCACGATGTGCTGCACTTCCAT 3112
 OY 3089 TCATCAGCAAGTTTGAAGAAACCCACATTTTCTGCGGCTCATCTGACAGGCTCT 3148
 DB 3113 TCATCAGCAAGTTTGAAGAAACCCACATTTTCTGCGGCTCATCTGACAGGCTCT 3172
 OY 3149 CCTCTGCTACTCTGATCTGAAAGCAAGAACAGAGGATGTGCTGGGGCCCAAGGGCTC 3208
 DB 3173 CCTCTGCTACTCTGATCTGAAAGCAAGAACAGAGGATGTGCTGGGGCCCAAGGGCTC 3232
 OY 3209 CGCGGGCTTGTGCGGCTGCGAGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3268
 DB 3233 CGCGGGCTTGTGCGGCTGCGAGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3292
 OY 3269 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3328
 DB 3293 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3352
 OY 3329 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3388
 DB 3353 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3412
 OY 3389 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3448
 DB 3413 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3472
 OY 3449 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3508
 DB 3473 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3532
 OY 3509 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3568
 DB 3533 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3592

OY 3569 CTGATGTCGGGCTGAAGGCTGAGTGTCCGCTGAGGCTGAGGAGTGTCCAGCAAG 3628
 DB 3593 CTGATGTCGGGCTGAAGGCTGAGTGTCCGCTGAGGCTGAGGAGTGTCCAGCAAG 3652
 OY 3629 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3688
 DB 3653 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3712
 OY 3689 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3748
 DB 3713 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3772
 OY 3749 TCCGAGATGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3808
 DB 3773 TCCGAGATGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3832
 OY 3809 TCCGAGATGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3868
 DB 3833 TCCGAGATGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3892
 OY 3869 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3928
 DB 3893 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3952
 OY 3929 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 3988
 DB 3953 GGTGACGTCAGACGCTGTCACATGAGTGGCTGAGTGGCTGAGCCACCAATTTCTGCTCA 4012
 OY 3989 AAAAAAAAAAAAAA 4005
 DB 4013 AAAAAAAAAAAAAA 4029

RESULT 15
 US-10-054-611-173
 ; Sequence 173, Application US/10054611
 ; Publication No. US2003005978/A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; Linsner, Joachim
 ; Nakamura, Toru
 ; Chapman, Karen B.
 ; Morin, Gregg B.
 ; Harley, Calvin
 ; Andrews, William H.
 ; TITLE OF INVENTION: NO. US2003005978/A1el Telomerase
 ; NUMBER OF SEQUENCES: 225
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 94111
 ; COMPUTER, READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/054,611
 ; FILING DATE: 18-Jan-2002
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/854,050
 ; FILING DATE: <unknown>
 ; APPLICATION NUMBER: US 08/846,017
 ; FILING DATE: 25-Apr-1997
 ; APPLICATION NUMBER: US 08/844,419
 ; FILING DATE: 18-Apr-1997
 ; APPLICATION NUMBER: US 08/724,643
 ; FILING DATE: 01-Oct-1996
 ; ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY:
LOCATION: 1..4029
OTHER INFORMATION: /note= "preliminary sequence for
human TRT cDNA insert of
plasmid pGRN121"
SEQUENCE DESCRIPTION: SEQ ID NO: 173:
US-10-054-611-173

Query Match 95.7%; Score 3832.6; DB 9; Length 4029;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 3951; Conservative 0; Mismatches 39; Indels 47; Gaps 11;

8 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
1 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
68 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
61 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
128 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
121 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
188 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
181 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
248 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
241 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
308 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
301 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
368 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
361 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
428 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
421 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
488 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
481 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
548 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
541 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
608 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
601 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
668 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC
659 GCAGCGCTGCTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCGACCCCGCGATGCC

728 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
718 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
788 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
778 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
848 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
838 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
908 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
898 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
958 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1028 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1017 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1088 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1075 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1146 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1135 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1206 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1193 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1266 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1253 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1326 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1313 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1386 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1373 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1445 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1433 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1505 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1493 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1565 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1553 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1625 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1613 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1685 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1673 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1745 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG
1733 GAGCGCGCGGCGAGCTGCGCAGCGAGAGAGCTGCGCGTGGCCCAAGAGAGCGCGAGCGCG

us-09-424-686b-1del.rnpb

Page 52

Search completed: April 17, 2003, 05:39:43
Job time : 1537 secs


```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5529840"
/clone_1db="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."
BASE COUNT      172 a      290 c      276 g      187 t
ORIGIN

```

```

Query Match      19.1% Score 765.2; DB 13; Length 925;
Best Local Similarity 76.9%; Pred. No. 3.3e-59;
Matches 821; Conservative 0; Mismatches 30; Indels 216; Gaps 4;

```

```

QY 2156 GGGCCAGAGACCCGCGCTGAGCTGTA----- 2182
DB 2 GGGCCAGAGACCCGCGCTGAGCTGTAAGTGTGACGGGCGGTACGA 61
QY 2183 ---CATCCCCAGAGACAGCTCAGAGAGTATGCGCCAGATCAAAACCCAGAAAC 2239
DB 62 CACCATTCGCCAGAGACAGCTCAGAGAGTATGCGCCAGATCAAAACCCAGAAAC 121
QY 2240 GTACTGCGTGGTGGTATGCGGTGTCAGAGAGCCGCCATGGGACGTCGCCAAGG 2299
DB 122 GTACTGCGTGGTGGTATGCGGTGTCAGAGAGCCGCCATGGGACGTCGCCAAGG 181
QY 2300 CTTAAGAGCAGAGCTCTACTTACCTGACAGCTCCAGCCGATGACAGAGTTCGTGGC 2359
DB 182 CTTAAGAGCAGAGCTCTACTTACCTGACAGCTCCAGCCGATGACAGAGTTCGTGGC 241
QY 2360 TCACCTGAGAGAGACAGCCGCTGAGAGATGCGTCTCATGACAGAGCTCTCCCT 2419
DB 242 TCACCTGAGAGAGACAGCCGCTGAGAGATGCGTCTCATGACAGAGCTCTCCCT 301
QY 2420 GAATGAGAGCAGAGAGTGGCTTTCGAGAGTCTTCTGACGTTTCTGACAGAGCCGT 2479
DB 302 GAATGAGAGCAGAGAGTGGCTTTCGAGAGTCTTCTGACGTTTCTGACAGAGCCGT 361
QY 2480 GCGCATCAGAGAGAGTCTGACAGTCCAGAGAGTCCGAGAGGCTCCATCTCTC 2539
DB 362 GCGCATCAGAGAGAGTCTGACAGTCCAGAGAGTCCGAGAGGCTCCATCTCTC 421
QY 2540 CAGCCTGCTGACAGCTGCTGCTACAGGAGATGAGAAACAGCTGTTGGGGATTG 2599
DB 422 CAGCCTGCTGACAGCTGCTGCTACAGGAGATGAGAAACAGCTGTTGGGGATTG 481
QY 2600 GCGGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2659
DB 482 GCGGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
QY 2660 CCAGGCGAAACCTTCTCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2719
DB 542 CCAGGCGAAACCTTCTCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
QY 2720 GAACCTGCGAAGACAGTGTGAATTCCTGTAAGAACAGAGAGCTGCTGCTGCT 2779
DB 602 GAACCTGCGAAGACAGTGTGAATTCCTGTAAGAACAGAGAGCTGCTGCTGCT 661
QY 2780 TTTTGTTCAGATGCGGCGCCAGAGCTATTCCTGCTGCTGCTGCTGCTGCTGCT 2839
DB 662 TTTTGTTCAGATGCGGCGCCAGAGCTATTCCTGCTGCTGCTGCTGCTGCTGCT 721
QY 2840 GACCTTGAAGTGAAGAGCGTCTCAGTATGCGGAGAGCTCCATCAAGAGAGCT 2899
DB 722 GACCTTGAAGTGAAGAGCGTCTCAGTATGCGGAGAGCTCCATCAAGAGAGCT 781
QY 2900 CACCTTCAACCGGCTTCAA--GGCTGGAGAAACATGCTCGAAA----- 2945
DB 782 CACCTTCAACCGGCTTCAAAGGCTGGAGAAACATGCTCGAAAACCTTTTGGG 841
QY 2946 CTCTTTGGGGCTTTGGGCTGAAGTGTACAGCTGTTTCTGATTTGAGTGAAGC 3005

```

```

DB 842 GTCTTGGGCGCTTG----- 856
QY 3006 CTCAGAGAGTGTGACACCAACATCTACAAGATCTCTGCTGACAGGCTTACAGTTTAC 3065
DB 857 ----- 856
QY 3066 GCATGTGTCTGACAGTCCATTCATCAGCAAGTTTGAGAAACCCACATTTTCTCTG 3125
DB 857 ----- 856
QY 3126 CGCGTATCTGTACAGGCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3172
DB 857 -AAGTGTCAACAGCGCTTGTCCCTGGGATTTGCAAGGTGGAACC 902

```

RESULT 2

```

AM270031/c 468 bp mRNA linear EST 03-JAN-2000
LOCUS      xv57e03.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2817244 3'
DEFINITION mRNA sequence.
ACCESSION AM270031
VERSION   AM270031.1 GI:6657061
KEYWORDS  EST.
SOURCE     human.
ORGANISM  Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

REFERENCE 1 (bases 1 to 468)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgaps-remail.nih.gov
            Tissue Procurement: Chris Moskalko, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
            Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium DNA Sequencing by: Washington University
            Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            www-bio.llnl.gov/bdrip/image/image.html
            Seq primer: -400p from G1bco
            High quality sequence stop: 416.
            Location/Qualifiers
            1..468
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:2817244"
            /clone_1db="NCI_CGAP_Lu28"
            /tissue_type="two pooled squamous cell carcinomas"
            /lab_host="DH10B"
            /Note="Organ: Lung; Vector: pCMV-SPORT6; Site_1: SalI;
            Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
            Library constructed by Life Technologies."

```

```

BASE COUNT      100 a      137 c      144 g      86 t      1 others
ORIGIN

```

```

Query Match      11.6% Score 465.4; DB 10; Length 468;
Best Local Similarity 99.6%; Pred. No. 1.5e-32;
Matches 466; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 3514 CACCAGGCGCGACCGCTGGAGCTGAGAGCTGAGTGTGTCGAGGCTTCA 3573
DB 468 CACCAGGCGCGACCGCTGGAGCTGAGAGCTGAGTGTGTCGAGGCTTCA 409
QY 3574 TGTCCGCTGAAGCTGAGTCCGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 3633
DB 408 TGTCCGCTGAAGCTGAGTCCGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 349
QY 3634 GTGTCCAGACACCTGCGCTTCACTTCCACAGAGCTGCGCTGCGCTCACCCAGG 3693

```

Db 348 GATGTCACGACACCTGGCGGCTCTCACTTCGTCACAGAGCTGGAGCTGGCTGGCTGCTACACCCAG 289

Qy 3694 GCGACGTTTTCTCTACACGAGGCGCGCTTCACATCTCCGACATAGGAATAGTCCATCCG 3753

Db 288 GCGACGTTTTCTCTACACGAGGCGCGCTTCACATCTCCGACATAGGAATAGTCCATCCG 229

Qy 3754 AGATTTCGCGATCTGTTTCACCCCTGGGCGGCTCTCTTGGCTTCACACCCGACATCAG 3813

Db 228 AGATTTCGCGATCTGTTTCACCCCTGGGCGGCTCTCTTGGCTTCACACCCGACATCAG 169

Qy 3814 GTGGAGACCCGTGAAGAAGACCCGGGAGCTGTGGGAATTTGAGGTGACCAAGGTGGCC 3873

Db 168 GTGGAGACCCGTGAAGAAGACCCGGGAGCTGTGGGAATTTGAGGTGACCAAGGTGGCC 109

Qy 3874 GTGTACAGGCGAGGACCTGTGACCTGGATGGGGGTCTGTGGGTCAATTTGGGGGA 3933

Db 108 GTGTACAGGCGAGGACCTGTGACCTGGATGGGGGTCTGTGGGTCAATTTGGGGGA 49

Qy 3934 GGTGCTGTGGAGTAAATATCTGAATATATATAGTATTTTCAGTTTGA 3981

Db 48 GGTGCTGTGGAGTAAATATCTGAATATATATAGTATTTTCAGTTTGA 1

RESULT		3	
BM824748			
LOCUS			
DEFINITION	BM824748	492 bp	mRNA linear EST 06-MAR-2007
ACCESSION	FJ575963.35	SZSNU01n1 Homo sapiens CDNA clone SZSNU01n1-95-E07	
VERSION	BM824748		
KEYWORDS	BM824748.1 GI:19181161		
SOURCE	human.		

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 492)
Kim,N.S., Bahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS

TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel.: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsungemail.kr@ibb.re.kr
Plate: 99 row: E column: 07
High quality sequence stop: 492.
Location/Qualifiers
FEATURES
source 1.492

```

FEATURES
Source
location/Qualifiers
1. 492
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S22SNU16n1-99-E07"
/clone_11b="S22SNU16n1"
/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/cell_line="SNU-16"
/lab_host="DH10B"
/note="Organ: Stomach; Vector: pT7T3-Pac; Site:1: EcorI;
Site: 2: NotI; The S22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Ronaldso, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."
96 a 152 c 131 g 113 t
BASE COUNT
ORIGIN

```

Query Match	11.18;	Score 445;	DB 14;	Length 492;
Best Local Similarity	-100.08;	Pred. No. 9.4e-31;		
Matches 445;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	2739	GTGACATTCCTCCGTAGAAAGACGAGGCGCCCTGGGTGGCAAGCGCTTTTGTTCAGATGCGGGCC	2798
Db	1	GTGACATTCCTCCGTAGAAAGACGAGGCGCCCTGGGTGGCAAGCGCTTTTGTTCAGATGCGGGCC	60
OY	2799	CACGGCCTATTCCCTTGTCGGCCCTGCTGCTGGATACCCGAGACCTGGAGGTGTGACAGC	2858
Db	61	CACGGCCTATTCCCTTGTCGGCCCTGCTGCTGGATACCCGAGACCTGGAGGTGTGACAGC	120
OY	2859	GACTACTCCAGCTATGCGCCGAGACCTTCATCAGAGCCAGTCTCAGCTTTCAACCGCGCGCTTC	2918
Db	121	GACTACTCCAGCTATGCGCCGAGACCTTCATCAGAGCCAGTCTCAGCTTTCAACCGCGCGCTTC	180
OY	2919	AAGCGCGGAGGAACATGCGTCCCAACCTCTTGGGGGCTTGGGGGCTGGAAGTGTACAGC	2978
Db	181	AAGCGCGGAGGAACATGCGTCCCAACCTCTTGGGGGCTTGGGGGCTGGAAGTGTACAGC	240
OY	2979	CTGTTTCTGAGATTTCGACAGGTGAACAGCCTCCACAGAGCGTGTGACCAACATCTACAAAGTC	3038
Db	241	CTGTTTCTGAGATTTCGACAGGTGAACAGCCTCCACAGAGCGTGTGACCAACATCTACAAAGTC	300
OY	3039	CTCTGCTGCGAGGGGTACAGGTTTCACGCATGTGTGTCGACGCTCCCATTTTCATCAGCAA	3098
Db	301	CTCTGCTGCGAGGGGTACAGGTTTCACGCATGTGTGTCGACGCTCCCATTTTCATCAGCAA	360
OY	3099	GTTTGGAGAAACCCCAATTTTTCCTGGCGCGTCACTGTGACAGCGCCCTCCCTGTGCAC	3158
Db	361	GTTTGGAGAAACCCCAATTTTTCCTGGCGCGTCACTGTGACAGCGCCCTCCCTGTGCAC	420
OY	3159	TGCATCTCGAAAGCGAAGACGACGAG	3183
Db	421	TGCATCTCGAAAGCGAAGACGACGAG	445

LOCUS	851 bp	mRNA	linear	EST 05-JUN-2000
DEFINITION	602820803DF1 NCL_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4949887 5'			
ACCESSION	mRNA sequence.			
VERSION	BC917907			
FEATURES	BC917907.1	GI:14298383		
EXPORT	FAST			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	1 (bases 1 to 851)	Nih-MGC http://mgc.nci.nih.gov/ .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.			

Issue Procurement: delivery green n.d.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM10903 row: k column: 08
 High quality sequence stop: 753.
 Location/Qualifiers

```
/organism="Mus musculus"  
/strain="FVB/N"  
/db_xref="taxon:10090"  
/clone="IMAGE:4949887"  
/clone_lib="NCI_CGAP_Mam6"  
/sex="female, Virgin"  
/tissue_type="Infiltrating ductal carcinoma"
```

```

/dev_stage="5 months"
/lab_host="DH10B"
/Note="Organ: mammary; Vector: PCMV-SPOPT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies, Investigator
providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT      184 a      238 c      214 g      215 t
ORIGIN

```

```

Query Match      10.8%; Score 430.8; DB 13; Length 851;
Best Local Similarity 20.1%; Pred. No. 1.7e-29;
Matches 597; Conservative 0; Mismatches 227; Indels 2145; Gaps 3;

```

```

OY 458 GGGAGCGGGGGCTGGGGCTGCTGCGCGCGCTGGGCGACGACGTGCTTACCT 517
    ||| ||| ||| ||| ||| |||
DB 8 GTGGGTGCGAGCGGATGGTGTCTTTACG----- 37
OY 518 GGTGACCGCTCGGCTTTGTGTGTGTGCTCCACGCTGCGCTTACAGGTGCGG 577
    38 ----- 37
OY 578 GCCCGCGTACACAGTCGCGCTGCCACTCAGGCGCGCGCGCGCACAGCTAGTG 637
    38 ----- 37
OY 638 ACCCGAAGCGCTGCGATGCGAAGGGCGCTGAACCATAGCTCAGGAGGCGGGGT 697
    38 ----- 37
OY 698 CCCCCGGGCTGCCAGCCCCGGGTGCCAGAGCGCGGGGCGAGTCCAGCGGAAGTCT 757
    38 ----- 37
OY 758 GCCGTGCCAAGAGGCCCGAGCGTGGCGCTGCCCTGAGCGGAGCGGACCGCGTTGG 817
    38 ----- 37
OY 818 GCAGGGTCTGGGCCACCGCGGAGAGCGCGTGGACCGAGTGAACGTTCTGTGT 877
    38 ----- 37
OY 878 GGTGCACCTGCGAAGCCCGCGAAGAACCCACTTTTGGAGGTGCGCTCTGGCAC 937
    38 ----- 37
OY 938 GCGCCACTCCACCATCGTGGCGCGCACACACAGCGGGGCGCCCATCCACATCGCG 997
    38 ----- 37
OY 998 GCCACACGTCCTGGGACAGCGCTTGTCCCGGTGTACGCCGAGACCAACACTTCT 1057
    38 ----- 37
OY 1058 CTACTCTCAGCGACAGAGAGACACTGCGGCTCTTCTTACTTACGCTTCTGAGGCC 1117
    38 ----- 37
OY 1118 CAGCTGACTGGCGCTCGAGGCTGAGAGACATCTTTGGGTTCCAGGCCCTGAT 1177
    38 ----- 37
OY 1178 GCCAAGACTCCCGCAGGTGGCCCGCTGCCAGCGCTACTGCAATGCGGCCCT 1237
    38 ----- 37
OY 1238 GTTTCGAGCTGCTTGGGAACACGCGAGTGGCCCTTACGGGGGTGCTCTTAAGACGA 1297
    38 ----- 37
OY 1298 CTGCGCGTGGAGGTGGGTACCCCAAGACCGGCTGTGTGCGCGGGAAGACCCCA 1357
    38 ----- 37

```

```

OY 1358 GGGCTCTGTGGGCGCCCGCGAGAGAGACACAGACCCCGCTGCTGTGACCTGCT 1417
    38 ----- 37
OY 1418 CCGCCAGACACAGACAGCCCTGGCAGAGTGTACGGCTTCGTGGGGGCTGCTGCGCGGT 1477
    38 ----- 37
OY 1478 GGTGCCCCAGGCTCTGGGGCTCCAGGACACAAGAACGCCCTTCTCAGAGAACCA 1537
    38 ----- 37
OY 1538 GAAGTTCACTCTCGTGGGAACCATGCCAAGCTTCTGCTGACGAGACTGACGTGAAGAT 1597
    38 ----- 37
OY 1598 GAGCGTGGCGGACTGCGCTTGGCTGCGCAGAGGCCAGGGGTGGCTGTGTTCCGGCGCG 1657
    38 ----- 37
OY 1658 AGAGACCGTCTGCGTGAAGAGATCCGTGCCAAGTTCTGCACTGGCTGATGATGTGA 1717
    38 ----- 37
OY 1718 CGTCTGAGCTGCTCAGGTCTTCTTTATGTACAGGAGACCGATTTCAAAAGACAG 1777
    38 ----- 37
OY 1778 GCTCTTTTCTACCGGAGAGTGTGTGAGCAAGTTGCAACATTTGGAATCAGACAGA 1837
    38 ----- 37
OY 1838 CTTGAAGAGGTGACAGCTCGGAGCTGCGAAGCAGAGAGTACAGACATCGGGAAGC 1897
    38 ----- 37
OY 1898 CAGGCGCGCTGCTGAGCTCCAGACTCGCTTCATCCCAAGCTGACGGGCTCGGCC 1957
    38 ----- 37
OY 1958 GATTGTGAACATGACTACGTGTGGGAGCCAGAAAGTTCCGACAGAAAAAGAGGCCGA 2017
    38 ----- 37
OY 2018 GCGTCTCACCTGAGAGGTGAAGCACTGTTACGCTGCTCAACTACAGCGGGCGCGG 2077
    38 ----- 37
OY 2078 CCGCGGCTCTGCGGCGCTCTGTGCTGGGCTTGACGATATCACAGGGCTTGGCGAC 2137
    38 ----- 37
OY 2138 CTTGCTGCTGCTGTGGGGCCAGGACCGCGGCTGAGCTGTATATCCCCAGAGACAG 2197
    38 ----- 37
OY 2198 GCTACGAGGTATCGCCAGCATATCAAAACCCAGAACGTAAGTGGTGTGCGGA 2257
    38 ----- 37
OY 2258 TGCGGTGTCCAGAGGCCGCCCATGAGGACGTCCGCAAGGCTTCAAGAGCCAGCTTC 2317
    38 ----- 37
OY 2318 TACCTTGACAGACTCCAGCGCTACATGCGAGATTGCTGCTCACCTTCAGAGAACAG 2377
    38 ----- 37
OY 2378 CCGCGTGAAGGATGCGCTGCTATGAGAGAGCTCTCCGTAATGAGGCGCAGAGTGG 2437
    38 ----- 37
OY 2438 CCTTTCGACGCTCTTACAGCTTATGTGCCACACGCGGCTGCGCATCAGGGGCAAGTC 2497
    38 ----- 37

```

```

Db 38 ----- 37
Oy 2498 CTACGTCCAGTGCAGGAGGATCCGAGAGGCTTCATCTCTCCAGCGTGTCTGCAGCCT 2557
Db 38 ----- 37
Oy 2558 GTCTACGGCGACATGAGAAACAAAGCTGTTTGGGGGATTTGGGGGAGACGGGTGCTCCT 2617
Db 38 ----- 37
Oy 2618 GCCTTTGGTGGATGATTTCTTTGTTGGTACACCTCACTCAACCCAGCGAAACCTTCTCT 2677
Db 38 ----- 37
Oy 2678 CAGGACCCCTGTGTCGAGGTGCTCCCTAGTATGGCTGCTGTTGAATCTTGGGAAAGCACT 2737
Db 94 CAGACCCCTGTGTCAGGCGCTTCTAGTATGGTGCATGATTAACCTTGGCAGAAAGCACT 153
Oy 2738 GGTGAACCTTCCCTGTAGAAAGCAGGCGCTGGGTGTCAGCGCTTTGTTGATGATGCGGCG 2797
Db 154 GGTGAACCTTCCCTGTAGAGCGCTGGGTGTCAGCGCTTTGTTGATGATGCGGCGCT 213
Oy 2798 CCAAGGCGCTATTCCTGTAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2857
Db 214 TCACCTGCTGTTCCCTGTGTTGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 273
Oy 2858 CGACTCTCTCACTATTCCTGTAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2917
Db 274 TGACTCTCTCACTATTCCTGTAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 333
Oy 2918 CAGAGCTGTGAGAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2977
Db 334 CAAAGCTGTGAGAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 393
Oy 2978 CCGTTTTCGATTTTGCAGGTGAGAGAGCTTCCAGAGAGCTGCTGCTGCTGCTGCTGCTGCT 3037
Db 394 TCTATTCTCTGAGAGCTGAGAGAGAGCTTCCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 453
Oy 3038 CTTCTGCTGAGAGCTGAGAGAGAGCTTCCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 3097
Db 454 CTTCTGCTGAGAGCTGAGAGAGAGCTTCCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 513
Oy 3098 AGTTTGAAGAAACCCAGATTTTCCCTGCGCGCTCATCTGACAGAGAGCTTCCCTGCTGCT 3157
Db 514 TGTTAGGAAGAAACCTCAATCTTCTGCGGCAATCTGCAAGAGAGCTTCCCTGCTGCTGCT 573
Oy 3158 CTCATCTCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3217
Db 574 TGTATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 624
Oy 3218 TCTGCGCTCCGAGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3276
Db 625 -CTTCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 683
Oy 3277 GAGAGCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3336
Db 684 CTATCTCTCTGATCTACAAATGCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743
Oy 3337 GTTGGGAAGCTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3396
Db 744 GCGGGAAGCTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 803
Oy 3397 CTTGAGACTTCAAGACCATCTGAGCTGA 3425
Db 804 GGACAGACTTTCAGGACCATCTGAGCTAA 832

```

```

RESULT 5
AM276315/c 416 bp mRNA linear EST 03-JAN-2000
LOCUS x10b12.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2759711 3',
DEFINITION mRNA sequence.

```

```

ACCESSION AM276315
VERSION AM276315.1 GI:6663345
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap/
AUTHORS 1 (bases 1 to 416)
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Chris Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 413.
Location/Qualifiers
1. 416
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2759711"
/location="NCI-CGAP_Lu28"
/tissue_type="two pooled squamous cell carcinomas"
/lab_host="DH10B"
/notes="Organ: Lung; Vector: PCMV-SPORT6; Site: 1; Salt:
Site: 2; NCI: Cloned unidirectionally. Primer: Oligo dm.
Library constructed by Life Technologies."
BASE COUNT 90 a 118 c 130 g 78 t
ORIGIN
Query Match 10.4%; Score 416; DB 10; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.6e-28;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 3665 AGGCTGATGTCGCGGCTGAAGAGCTGATGTCGCGCTGAGGCTGAGAGAGAGAGAGAGAG 3624
Db 416 AGGCTGATGTCGCGGCTGAAGAGCTGATGTCGCGCTGAGGCTGAGAGAGAGAGAGAGAG 357
Oy 3625 AAGGCTGATGTCGAGACACCTGCGCTTCACTTCCACAGAGAGAGAGAGAGAGAGAGAGAG 3684
Db 356 AAGGCTGATGTCGAGACACCTGCGCTTCACTTCCACAGAGAGAGAGAGAGAGAGAGAGAG 297
Oy 3685 CACCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3744
Db 296 CACCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 237
Oy 3745 TGCATCCGAGATTCGAGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3804
Db 236 TGCATCCGAGATTCGAGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 177
Oy 3805 ACATTCAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3864
Db 176 ACATTCAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 117
Oy 3865 AGGTGTCCTGTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3924
Db 116 AGGTGTCCTGTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 57
Oy 3925 TTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3980
Db 56 TTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1

```

```

RESULT 6
AA281296

```

LOCUS	AA281296	389 bp	mRNA	linear	EST 14-MUG-1997
DEFINITION	z108902.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712562 5', mRNA sequence.				
ACCESSION	AA281296				
VERSION	AA281296.1 GI:1924194				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1 (bases 1 to 389) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (infoimage.llnl.gov) for further information. Insert Length: 2187 Std Error: 0.00 Seq primer: -28m13 rev2 E7 from Amersham High quality sequence stop: 385.				
FEATURES	Location/Qualifiers				
SOURCE	1..389 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:712562" /clone_11b="NCI_CGAP_GCB1" /tissue_type="germinal center B cell" /lab_host="DH10B" /note="vector: pT733-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Straudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-GTTACCAATCTGAAGTGGAGGGGGCCCTCAATTTTCTTTTCTTTT-3' 1. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT733 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."				
BASE COUNT	87 a 102 c 123 g 77 t				
ORIGIN					
Query Match	9.6%: Score 385.8; DB 9; Length 389; Best Local Similarity 99.5%: Pred. No. 1.7e-25;				
Matches 387; Conservative	0; Mismatches 2; Indels 0; Gaps 0;				
QY 1686	GCCAAAGTTCGCACTGGCTGATGAGTGTGACGTGTCGAGCTGTCAGGCTCTTTCTTT	1745			
Db 1	GCCAAAGTTCGCACTGGCTGATGAGTGTGACGTGTCGAGCTGTCAGGCTCTTTCTTT	60			
QY 1746	TATGTCACGGAGACCAAGCTTTCAAAAGCAAGGCTCTTTTCTTACCGAAGAGTGTCTGG	1805			
Db 61	TATGTCACGGAGACCAAGCTTTCAAAAGCAAGGCTCTTTTCTTACCGAAGAGTGTCTGG	120			
QY 1806	AGCAAGTTGCAAGCATTTGGAGATCGAGACGACTTGAAGAGGAGGCTCCGAGAGCTG	1865			
Db 121	AGCAAGTTGCAAGCATTTGGAGATCGAGACGACTTGAAGAGGAGGCTCCGAGAGCTG	180			
QY 1866	TGCGAAGCAGAGGTCAGGACAGCATTCGGGAGCAAGGCGCCGCTGCTACGTCAGATC	1925			
Db 181	TGCGAAGCAGAGGTCAGGACAGCATTCGGGAGCAAGGCGCCGCTGCTACGTCAGATC	240			
QY 1926	CGCTTCATCCCAAGGCTGACGGGCTGGCGGCGATTTGGAACATGAGACTACGTCGTGGGA	1985			
Db 241	CGCTTCATCCCAAGGCTGACGGGCTGGCGGCGATTTGGAACATGAGACTACGTCGTGGGA	300			
QY 1986	GCCAGAAAGCTTCCGAGAGAAAAGAGGGCCGAGGCTCTACCTCGAAGGCTGAAGCACTG	2045			
Db 301	GCCAGAAAGCTTCCGAGAGAAAAGAGGGCCGAGGCTCTACCTCGAAGGCTGAAGCACTG	360			

QY	2046	TTACAGCTGCTCACTACGACGGCGCCG	2074
Db	361	TTACAGCTGCTCACTACGACGGCGCGC	389
 RESULT 7 BQ258274 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT			
<p>BQ258274 664 bp mRNA linear * EST 06-MAY-2002</p> <p>NISC_Rp11g04.q3 Baker mouse embryo e7.5 Mus musculus cDNA clone IMAGE:5409222, mRNA sequence.</p> <p>BQ258274</p> <p>BQ258274.1 GI:20459030</p> <p>EST.</p> <p>house mouse.</p> <p>Mus musculus</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.</p> <p>1 (bases 1 to 664)</p> <p>NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.</p> <p>National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index</p> <p>Unpublished (1997)</p> <p>Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov</p> <p>cDNA Library Preparation: J. Baker (Stanford University) cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC) Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: info@image.lnl.gov MGI:1845958 Plate: LILAM2043 row: N column: 7</p>			
Seq primer: Sp6 primer.			
Location/Qualifiers			
1..664			
/organism="Mus musculus"			
/strain="CD-1"			
/db_xref="taxon:10090"			
/clone="IMAGE:5409222"			
/clone_1lb="Baker mouse embryo e7.5"			
/tissue_type="embryo, late gastrula"			
/dev_stage="embryo, 7.5 dpc"			
/lab_host="XLI-Blue"			
/note="Vector: pCS105; Site.1: NotI; Site.2: SalI; cDNA made by oligo-dT priming. Directionally cloned into SalI/NotI sites using the following 5' adaptor:			
5'-TCGACCCAGCGGCCG-3'. Size-selected for average insert size 1.8-1.9 kb. Library constructed by J. Baker (Stanford University)."			
BASE COUNT 155 a 177 c 183 g 149 t			
ORIGIN			
Query Match 9.1%; Score 362.8; DB 14; Length 664;			
Best Local Similarity 68.3%; Pred. No. 1.9e-23;			
Matches 479; Conservative 0; Mismatches 177; Indels 45; Gaps 1;			
QY	1115	GCCAGCGCTGACTGGCGCTGGAGGCTGTGTGGAGACATCTTTTGCGGTTCAGGCCTG	1174
Db	9	GCTTAACCTTGACTGGCGCAGAGAGCTGTGTGAGATCATCTTTTGTGGCTCAAGGCCATG	68
QY	1175	GATGCACAGGAGCTCCCCCGAGGTTGCCCGCGCTGCCAGCGCTACTGCGAAATGCGGCC	1234
Db	69	CACATCACGAGACCCTCTCTCAGAGACACACACCGCTCTATCCGCTGATATCTGCGAGATGCGGCC	128
QY	1235	CCTGTTTCTGGAGCTGTTTGGGAACACAGCCAGTGCCTTCAGGGGTGCTCTCAAGAC	1294
Db	129	CCTGTTTCCAACAGCGTGTGTGTAACCAATGAGAGTGGCCAAATATGTACAGATCTCTCAGGTC	188
QY	1295	GCACTGCCCCGCTGCGAGCTGGCGGTTCACCCACAGACCGCGTCTGTGTCCCGGGAGAAGCC	1354
Db	189	ACATTGACAGGTTTGCAMCAGCAAACCAACAGTAGTACAGANTCCCT-----	233

Qy	1355	CCAGGGCTGTGTGGCGGCCCCGAGAGAGAGACAGACGACCCCGGCTGAGTGCAGCT	1414
Dy	233	-----TCAACACAGCCACCGCACACCTCATGATTT	263
Qy	1415	GCTCGGCAGACAGCAGCCCGCTGGCAGAGTGTACGGCTTCGTGGGGGCTGCCTGGCCG	1474
Dy	264	GCTCGGCTGTGACAGCAGCTCCCTGGAGAGTATATGGTTCTTCTGGGCTGCTCTTCGAA	323
Qy	1475	GCTGTGTCGCCCAAGCCCTCTGGGGCTCCAGGACACAGAACGCCGCTTCTTCAGAGAAC	1534
Dy	324	GGTGTGTCTCTAGTCTCTCTGGGCTACCGAGCACAATGACGCCGCTCTTTAAGAACTT	383
Qy	1535	CAGAAGTTCATCTCCCTGGGGAGCATGCCAACCTCTGCTCAGAGAGCTGACGTGAA	1594
Dy	384	AAAGAAGTTCATCTCTGGGGAAATACGGCAACCTTATCTGACAGAACTGATGTGAA	443
Qy	1595	GATGAGCTGGGGAGCTGGCTTGGCTGCGAGAGAGCCAGAGGCTTGGCTGTGTCGGC	1654
Dy	444	GATGAAATGAGAGATTGCACTGGCTGCGAGAGGCCACAGGGAAGACGCTGTCCCGC	503
Qy	1655	CGCAGACACCGTGTGGCTGAGAGAAATCTTGCCCAAACTTCTCAGCTGAGTATGAT	1714
Dy	504	TGCAAGACACCGTGTGAGGAGAGATCTTGCTACCTCTCTGCTGAGTAGAGACAC	563
Qy	1715	GATGCTCTGAGAGCTGATGAGTCTTTTATGTACAGGAGACAGTTCAAAAGAA	1774
Dy	564	ATACGTGTACAGCTGCTTATGGTCATCTTTTATCATCAGAGAGACATTTCAGAAAGAA	623
Qy	1775	CAGGCTCTTTTATCAGCGAAGAGTCTGGAGCAATTCG	1835
Dy	624	CAGGCTCTTCTTACGCTGTAAGAGTGTGGAGGAGCAACTGC	664

RESULT	B
LOCUS	BB618671
DEFINITION	BB618671 RIKEN full-length enriched, 8 days embryo Mus musculus
ACCESSION	CDDA clone 5730412M20 5', mRNA sequence.
VERSION	BB618671
KEYWORDS	BB618671.1 GI:16458173
SOURCE	EST. house mouse. Mus musculus.
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 599)
AUTHORS	Arakawa,T., Carhuich,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hizemoto,K., Hoti,F., Ishii,I., Ito,M., Kawai,Y., Konno,H., Kouda, M., Koye,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,S., Okido,T., Saito,R., Sakai,C., Sakurai,K., Sano,H., Sasaki, T.d., Shibata,K., Shinagawa,A., Shiraki,A., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeeda,Y., Tanaka,T., Toyota,T., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001) Unpublished (2001) Contact: yoshihide hayashizaki
TITLE	
JOURNAL	
COMMENT	

The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel.: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp/
URL: genome-gsc.riken.go.jp/
Carnichl, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashiki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. *Genome Res.* 10 (10), 1617-1630 (2000)
Wagii, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneba, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura
, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and

Hayashizaki, Y.
RIKEN Integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. *Genome Res.*
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara,
Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamamaki, I., Alzawa,
K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. *Hum. Genome* 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

```

FEATURES
Source
Location/Qualifiers
1. 599
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="5730412M20"
/clone_11b="RIKEN full-length enriched, 8 days embryo"
/sex="mixed"
/dev_stage="8 days embryo"
/lab_host="DH10B"
/note="Site_1: Sali; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genetic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGACGAGAGATCCACAGACTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rat = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAAGAGAGATTCCTCGACTTAATAAATTAATGCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified plasmidic KS(+) after bulk excision from Lambda FdL-1. Cloning sites, 5' end: Sali; 3' end: BamHI."
91 a      185 c      181 g      142 t

```

Query Match	8.0%;	Score 322;	DB 10;	Length 599;
Best Local Similarity	74.9%;	Pred. No. 7.9e-20;		
Matches 403;	Conservative	0;	Mismatches 135;	Indels 0;
			Gaps	0;
QY	9	CAGGCGTCGCTGCTGCGCGACAGTGGGAAACCCCTGGCCCCCGGACACCCCGGAGATCCG	68	
Db	61	CACCTTTCACATTTGGTTCCCGCAGCTGGAGAGGCCATCCCGGCTTGTAGCACAATATAC	120	
QY	69	CGCGCTCCCCGCTGCGAGACGCTGGCTCCTGCTGCGACAGCCATACCGGAGAGTCTG	128	
Db	121	CCGCGCTCTGTTTCCCGCGGGTGGCGCTCTGTTGTGGACAGCCGATCCGGGAAGTCTGG	180	
QY	129	CGCGTGGCCACGTTCTGTGTGGGGGCGCTGGAGGGCCACAGGCGTGGCGGCTGTGTACAGCGCG	188	
Db	181	CCGCTGGGCACATTTGTGTGGGCGCCTCGGGGGCCACAGGCGAGGGGCTTTGTCAACCCGGG	240	
QY	189	GACCCGGGGGCTTTCGCGGGCGCTGGGCGCCACAGTGCCTGTGTGTCGCTGCCCTGGAGACGA	248	
Db	241	GACCCGGAAGATCTACGCGCACTTTGGTTGCCCAATGCCCTATGTGTCATCACTGGGGGTCA	300	
QY	249	CGGCGGCCCCCGCGCGCCCTCTTTCGCGGACAGGTGCTGTGAAGACATGGTGGCC	308	
Db	301	CAGCTTCACATGCGCACTTTCCTTCTTCCACCAAGTGTATCCTGTAAAGAGTGTGTGCC	360	
QY	309	CGAGTGTCTCAGAGAGCTGTGCGAGCGCGCGCGAAGACGTGTGACCTTCGGCTTGGCG	368	

Dd	361	AGGGTTGTGCAGACACTCTGCGAGCGCAACAGAGAAMAAGTGTGGCTTTTGCCCTTTGAG	420
Oy	369	CTGCTGGAAGAGGGGGCCCCGGGGGGCCCCCCCCCAGAGCGCTTCACCACCAAGCTGCGACGCTAC	428
Dd	421	CTGCTTAACGAGAGCGAGAGGGGGGGGCGCTCCCATATGSGCTTCACTAGTAGGCTGGCTAGCTAC	480
Oy	429	CTGCCCAACACAGCGTGAACCGACACTGTGGGGGGAGCGGGGGCGTGGGGGCGCTGTGCTGAGC	488
Dd	481	TTCGCCAACACGTATTATTTAGACACCTCGGTGTGTCATGTGTCATGTGATGCTACTGTTGAGC	540
Oy	489	CGCGTGGCGGACGACGCTGCTGCTTAACTGCTGTGCGACCGCTGCGCGCTCTTTGTGCTGG	546
Dd	541	CGAGTGGCGGACGACGCTCTGTGTACCTGTGTCGACACTGTGCTCTTATCTTCTGG	598
RESULT 9			
AAB11084/c			
LOCUS	AAB11084	340 bp	mRNA EST: 19-FEB-1998
DEFINITION	oa55c05.s1 NCI-CGAP_GCB1 Homo sapiens CDNA clone IMAGE:1319048 3'		
ACCESSION	AAB11084		
VERSION	AAB11084.1	GI:2880695	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 340) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)		
AUTHORS	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LTML at: www-bio.llnl.gov/dbrr/image/image.html Insert length: 2249 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 331.		
JOURNAL			
COMMENT			
FEATURES			
source	Location/Qualifiers		
	1..340		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone_image="1319048"		
	/clone_lib="NCI-CGAP_GCB1"		
	/tissue_type="germinal center B cell"		
	/lab_host="DH10B"		
	/note="Vector: pUT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD+), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was initiated with a Not I - oligo(dT) primer [5'-TGTACCAATCTGAAGTGGAGGCGCGCTCATTTTTTTTTTTT-3'] }. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pUT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."		
BASE COUNT	73 a 86 c 100 g 81 t		
ORIGIN			
Query Match	7.9%	Score 318.4;	DB 9; Length 340;
Best Local Similarity	99.1%	Pred. No. 1.7e-19;	
Matches 339; Conservative	0;	Mismatches 1;	Indels 2; Gaps 2;

OY	3656	TGCTTCCCAAGCGTCGGCGTGCGTTCCACACCAGGCGCAGCTTTCTTCACACGAG	3715
Db	340	TCACTTCCCACAGG-TGGCGGTGGCTTCACCCAGGCCACGCTTTCTTCACACGAG	282
OY	3716	CCGGCTTCCACATCCCCACATAGGAATAGTCATCCCGAATTGCCTTTTCACCCCT	3775
Db	281	CCGGCTTCCACATCCCCACATAGGAATAGTCATCCCGAATTGCCTTTTCACCCCT	222
OY	3776	CGCCCTGCCCTCTTCTTGGCTTCCACCCCCACCATTCAGTGGAGAACCCTGAAAGAACCC	3835
Db	221	CGCCCTGCCCTCTTCTTGGCTTCCACCCCCACCATTCAGTGGAGAACCCTGAAAGAACCC	162
OY	3836	TGGAGCTCTGGGAATTTGGAGTGCACCAAAGGTGCGCCCTTACACAGCGCAGCACCCTG	3895
Db	161	TGGAGCTCTGGGAATTTGGAGTGCACCAAAGGTGCGCCCTTACACAGCGCAGCACCCTG	102
OY	3896	CACCTGGATGGGGGGTCCCTGTGGGTCAAAATTTGGGGGAGTGTGTGGAGTAATAACT	3955
Db	101	CACCTGGATGGGGGGT-CCTGTGGGTCAAAATTTGGGGGAGTGTGTGGAGTAATAACT	43
OY	3956	GAAATATGAGTTTTTTCAGTTTTGAAAAAAAAAAAAAAA 3997	
Db	42	GAAATATGAGTTTTTTCAGTTTTGAAAAAAAAAAAAAAA 1	
RESULT 10			
B651920			
LOCUS			
DEFINITION	B651920 RIKEN full-length enriched, ES cells Mus musculus cDNA	614 bp mRNA linear EST 26-OCT-2001	
ACCESSION	B651920		
VERSION	B651920		
KEYWORDS	B651920.1 GI:16486058		
SOURCE	EST.		
ORGANISM	house mouse.		
	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 614)		
AUTHORS	Arakawa,T., Carninci,P., Fukuda,Y., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takehashi,F., Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,M. and Hayashizaki,Y.		
	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)		
TITLE	Unpublished (2001)		
JOURNAL	Contact: Yoshihide Hayashizaki		
COMMENT	Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsr.riken.go.jp/ URL:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matabiki,M., Yoneda,Y., Ishikawa,T., Osawa,K., Tanaka,T., Matsunaga,S., Kawai,U., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y. Sequencing integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a		

QY	3794	CTTC - ACCCCACCATCCAGTGGAGACCCTGGAAGAGAGCTTGGGAAT	3852
Db	194	GGGCCGGGGCCACCATCCAGTGGAGACCCTGGAAGAGAGCTTGGGAAT	135
QY	3853	TGAGTGCACCAAGGTGTGCTGTACACAGCGAGACCCTGCACCTGGATGGGGTTC	3912
Db	134	TGAGTGCACCAAGGTGTGCTGTACACAGCGAGACCCTGCACCTGGATGGGGTTC	75
QY	3913	CTGTGGGTCAATATGGGGGGAGGTCTGTGGAGATTAATATGAATATATGTTTC	3972
Db	74	CTGTGGGTCAATATGGGGGGAGGTCTGTGGAGATTAATATGAATATATGTTTC	15
QY	3973	AGTTTGAACAAA 3986	
Db	14	AGTTTGAACAAA 1	
RESULT 12			
LOCUS	BE371943	866 bp	linear
DEFINITION	601217728p1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3586614 5',		
ACCESSION	BE371943		
VERSION	BE371943.1	GI:9317215	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 866)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cga@bbs.frelai.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Lu29 at: http://image.llnl.gov Plate: LHM8748 row: h column: 07 High quality sequence stop: 639. Location/Qualifiers		
FEATURES			
source	1. 866		
	/organism="Mus musculus"		
	/strain="CECH 11"		
	/db_xref="taxon:10090"		
	/clone="IMAGE:3586614"		
	/clone_1ib="NCI_CGAP_Lu29"		
	/tissue.type="Spontaneous tumor, metastatic to mammary. Stem cell origin."		
	/lab_host="DH10B"		
	/note="Organ: Lung; Vector: pCKV-SPORT6, Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"		
BASE COUNT	157 a 231 c 253 g 225 t		
ORIGIN			
Query Match	6.9%; Score 276.2; DB 10; Length 866;		
Best Local Similarity	30.7%; Pred. No. 9.1e-16;		
Matches 474; Conservative 0; Mismatches 263; Indels 809; Gaps 4;			
QY	2437	GCCTTTGAGCTCTTCTACGCTTCATATGTCACACAGCCGTGGCATCAGGGCACT	2496
Db	2	GCCTTTGAGCTCTTCTACGCTTCATATGTCACACAGCCGTGGCATCAGGGCACT	61
QY	2497	CCTAGCTCAGAGCCAGGGAGATCCGGAGGGGTCTATCTCTCCACAGCTCTTCAGCC	2556
Db	62	GCTATACGAGAGCCAGGGAGATCCCGAAGGCTTCAGGCTATTCACCCCTGCTCAGATC	121

OY	2557	TGTCCTACGGCGACATGAGAAACAACCTGTTTGCGGGGATTGCGGGGACGGGCTGC	2616
Db	122	TGTTTCTTCGGAGACATGAGAAACAACCTGTTTGCTGAGTGCAGCAGGATGGTTGCTT	181
OY	2617	TGCGTTTGATGATATTTCTTGTTGGTACACCTCACCTCACCGACGCAAAACCTTCC	2676
Db	182	TACGTTTGTGTGATGACCTTCTGTTGGTAGCCGCTACCTTGGACCAACCAAAACCTTCC	241
OY	2677	TCAGAGACCCCTGCTCCGAGGTGCTCCCTGACATATGCGCTGGGTGAACCTGGGAAGAC	2736
Db	242	TCACACACCCGTGCTCAATGAGGCTTCGAGATGAGATGATGATTAACCTTGCAAGAACAG	301
OY	2737	TGGGAACTTCCCTGTGAGAAAGAGAGGCCCTGGGTGGACGGGCTTTTGTAGATGCGGG	2796
Db	302	TGGTGAACCTTCCCTGTGAGAACCTGTGTCCTGGGTGCTGACACTGCATACCAAGCTGCTG	361
OY	2797	CCCAAGGCGCTATTTCCCTGTGTGGCGGCTGCTGCTGATACCGGACCTGTGAGGTGACGA	2856
Db	362	CTACACTGCTGTTTCCCTGTGTGGGTGTGTTGCTGCTGTGACACTGACACTTGGAGGCTTCT	421
OY	2857	GCGACTACTCCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCT	2916
Db	422	GTCGACTACTCAGGTA-----	437
OY	2917	TCAAGCTGGGAGAGAACATGCTGCGCAAACTCTTTGGGGTCTTGGCGCTGAAGTGTACA	2976
Db	438	-----	437
OY	2977	GCGCTGTTCTGATTTGTGCAGGTGACAGCGCTCCGACAGGCTGTGCACCAACATCTACAGA	3036
Db	438	-----	437
OY	3037	TCTCTCTGCTGACGGCCTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTTCATCAGC	3096
Db	438	-----	437
OY	3097	AAGTTTGGAAAGAACCCCAATTTTCTCGGGGTCATCTGTACAAGGCTCCTCTGCT	3156
Db	438	-----	437
OY	3157	ACTCATCTCGAAAGCCAMAGACGACAGGGATGTGCTGGGGGCCAAGGCGCGCGCGCC	3216
Db	438	-----	437
OY	3217	C-----	3217
Db	478	CTTGGTACTACATTTCTGTTTCTTCTACTTCTAGACACAMGTGACCGCTGAGGCTGAAGTGA	537
OY	3218	-----	3263
Db	538	TAGAGGCGAAAGGTGTTCCTCTTTCTTCATGAGATGAGGACGACACTATGAGAGCATC	597
OY	3264	CTCAGGTGACTGCACACCTGTACACTTACGTGCCACTCTGGGTTCACTCAGACACACC	3323
Db	598	CTCAGCCTTGGTCA-----	612
OY	3324	CAGACGACGTGATGTGGAAGCTCCCGGGGACGACGCTGACCTGGAGGCGCACACC	3383
Db	613	-----	612
OY	3384	AACCGGACATGCCCTCAGCTTCAAGACATCTGTGACTGATGGCCACCGGCCACAGC	3443
Db	613	-----	612
OY	3444	CAGGCGAGAGACAGACACGACGACGCCCTGTACAGCGCGGCTACTAGTCCAGGAGGAG	3503
Db	613	-----	634
OY	3504	GGGCGGCCACACACGAGCGCCGACGCTGGGAGTGTGAGCGCTGATGAGTGTTTGGCC	3563
Db	635	CGAAGGCCCTCCTCTGTGTATGAGACTGGAGCGGATGGGGGCTTGGTCTCTTACTTACC	694

Query Match	Score	DB	Length
Best Local Similarity	22.08	Fed. No. 1.ee-15	Indels 1399; Gaps 8;
Matches 432; Conservative	0;	Mismatches 131;	

[illegible]

```

QY 1079 GCAGCTGGGGCCCTCTCTCTACTACAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGAG 1138
Db 318 ----- 317
QY 1139 GCTCGTGAGACATCTTTCTGTTCCAGGCCCTGATGCCAGGAGCTCCCCGAGGTT 1198
Db 318 ----- 317
QY 1139 GCCCGCTGCCCGCAGCCCTACTGCAAAATGCGGCCCTGTTCTGAGAGCTTGGGAA 1258
Db 318 ----- 317
QY 1259 CCACGGCAGTGCCTCTACAGGGGCTCTCTCAAGACGACTCCCGCTGCGAGCTGGGT 1318
Db 318 ----- 317
QY 1319 CACCCACAGCCGCTGTGTGCCCCGGAGAACCCCGAGGCTGTGCGGGCCCCCGA 1378
Db 316 ----- 317
QY 1379 GGAGGAGACACAGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1438
Db 318 ----- 317
QY 1439 GCAGGTGTACGGCTTCGTGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1498
Db 318 ----- 342
QY 1499 CTCACGACACAGACAGCCGCTTCCTCAGAACACACAAAGATTCATCTCCCTGGGAA 1558
Db 343 ATCTGATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 371
QY 1559 GCATGCCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1618
Db 372 ----- 371
QY 1619 GCTGGCAGAGACCCAGGGGTTGGCTGTGTTCCGGCCCGCAGACACCTGCTGCTGAGA 1678
Db 372 ----- 416
QY 1679 GATCTGGCAGATTCCTGCACTGCTGATGATGATGATGATGATGATGATGATGATGATG 1738
Db 417 GATCTGGCAGATTCCTGCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 476
QY 1739 TTTCTTT-TATGTCAAGAGACACAGTTTCAAAAGACAGGCTTTTCTTACCGAAGA 1797
Db 477 TTTCTTTATATGTCAAGAGACACAGTTTCAAAAGACAGGCTTTTCTTACCGAAGA 536
QY 1798 GTGTCTGAGCAATGTCGAAAGCATGATGATGATGATGATGATGATGATGATGATGATG 1857
Db 537 GTGTCTGAGCAATGTCGAAAGCATGATGATGATGATGATGATGATGATGATGATGATG 596
QY 1858 GAGAGCT-GTCGGAAGCAGAGGTCAGGAGATCGGG--AAGCCAGGGCCCGCCCTGCGA 1914
Db 597 GGGAGCTGTGTGAGAGCAGAGGTCAGGAGATCGGGGAAAGGCCCTGCTGCTG 656
QY 1915 CGTCAGACTCGCTTCATCCCAAGCCTGACGGGCTCGCG 1956
Db 657 CGTCCA--ACTCGTTCATCCCAAGGCTGAAGGGCTCGCG 695

```

```

RESULT 14
BE396606 679 bp mRNA linear EST 21-JUL-2000
LOCUS 601289077F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619674 5',
DEFINITION mRNA sequence.
ACCESSION BE396606
VERSION BE396606.1 GI:9341882
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

REFERENCE 1 (bases 1 to 679)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
        Email: cgapbs-remail.nih.gov
        Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
        cDNA Library Preparation: Ling Hong/Rubin Laboratory
        cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
        DNA Sequencing by: Incyte Genomics, Inc.
        Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
        Plate: LCM290 row: 1 column: 19
        High quality sequence start: 2
        High quality sequence stop: 656.

FEATURES
    source
        1..679
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_image="3619674"
        /clone_id="NIH_MGC_8"
        /tissue_type="Burkitt lymphoma"
        /lab_host="DH10B (phage-resistant)"
        /note="Organ: Lymph. Vector: pORF7. Site: 1: XhoI; Site: 2:
        EcoRI; cDNA made by oligo-dT priming. Directionally
        cloned into EcoRI/XhoI sites using the following 5'
        adaptor: GGCACAGG(G). Size-selected >500bp for average
        insert size 1.8kb. Library constructed by Ling Hong in
        the laboratory of Gerald M. Rubin (University of
        California, Berkeley) using ZAP-cDNA synthesis kit
        (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 104 a 157 c 256 g 162 t
ORIGIN
    Query Match 6.8%; Score 270.6; DB 10; Length 679;
    Best Local Similarity 24.3%; Pred. No. 2.9e-15;
    Matches 445; Conservative 0; Mismatches 174; Indels 1213; Gaps 7;

QY 119 CGAGGTGCTGCCGCTGCGCAGCTTCGTGCGCGCTGCGGCCCGCAGGCTGCGGCTGCT 178
Db 1 CGGGGTGAGTGTCCGACAGGCCCTGCGGCTGCGGTATGTGTGTCTGTGATGTGTCAGGT 60
QY 179 GCAGCGCGGAGACCCGCGGCTTTCGCGCGCTGTGCGCCAGTCCGTGCTGCTGCGCC 238
Db 61 CCGGGGTGAGTGTCCGACAGGCCCTGCGGCTGAGCTGATGTGTGTCTGCG----- 110
QY 239 CTGGAGCAGAGCGCCCGCCCGCCCGCCCTCTCTCCGCCAGGTGCTGCTGAGGA 298
Db 111 ----- 110
QY 299 GCTGTGCGCCGAGTGTGACAGAGCTGTGCGAGCGCGCGCGCAAGACGTGTGCTT 358
Db 111 ----- 135
QY 359 CGGCTTCCGCTGCTGAGAGGGGCCCGCGGGGCCCGCCCGAGGCTTTCACACAGGCT 418
Db 136 ----- 135
QY 419 GCGCAGTACTGCGCCACAGGTGACCGAGCAGCTGCGGGGAGCGGGGCGTGGGCT 478
Db 136 ----- 135
QY 479 GCTGTGCGCGCGGTGGCGAGCAGCTGTGTTACCTGCTGCGACGCTGCGCTT 538
Db 136 ----- 135
QY 539 TGTGCTGTGCTCCACAGCTGCGCTACAGAGTGTGCGGGCGCGCTGTACAGCTCG 598
Db 136 ----- 135
QY 599 CGCTCCACTCAGGCGCGCGCCCGCCACAGCTAGTGGACCCGGAAGCGCTTGGGATG 658
Db 136 ----- 135

```


GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 16, 2003, 19:50:52 : Search time 8230 Seconds
(without alignments)
12238.251 Million cell updates/sec

Title: US-09-424-686B-1DEL

Perfect score: 4006
Sequence: 1 gttcagcgacgcgtgcgtc.....aaaaaaaaaaaaaaaaaaaaa 4006

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.0

Searched: 24791104 segs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

Pending_Patents_NA_Main:*

1: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
8: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
9: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
10: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
11: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
12: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
13: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
14: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
15: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
16: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
17: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
18: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
19: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
20: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
21: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
22: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
23: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
24: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
25: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
26: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
27: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
28: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
29: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
30: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
31: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
32: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
33: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
34: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
35: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
36: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
37: /cgn2_6/ptodata/1/pna/US09_COMB.seq:*
38: /cgn2_6/ptodata/1/pna/US10_COMB.seq:*
39: /cgn2_6/ptodata/1/pna/US10_COMB.seq:*
40: /cgn2_6/ptodata/1/pna/US10_COMB.seq:*
41: /cgn2_6/ptodata/1/pna/US10_COMB.seq:*
42: /cgn2_6/ptodata/1/pna/US10_COMB.seq:*
43: /cgn2_6/ptodata/1/pna/US10_COMB.seq:*

44: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
45: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
46: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
47: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
48: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
49: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
50: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
51: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
52: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
53: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
54: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
55: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
56: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
57: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
58: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
59: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
60: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
61: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
62: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
63: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
64: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
65: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
66: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
67: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
68: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
69: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
70: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
71: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
72: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
73: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
74: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
75: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
76: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
77: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
78: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
79: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
80: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
81: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
82: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
83: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
84: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
85: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3982.6	99.4	4037	US-08-974-549-343	Sequence 343, App
2	3982.6	99.4	4037	US-09-402-181B-343	Sequence 343, App
3	3982.6	99.4	4037	US-09-402-181B-343	Sequence 343, App
4	3982.6	99.4	4037	US-09-432-503-343	Sequence 343, App
5	3982.6	99.4	4037	US-09-721-477-343	Sequence 343, App
6	3982.6	99.4	4037	US-09-721-506-343	Sequence 343, App
7	3982.6	99.4	4038	US-08-974-524E-117	Sequence 117, App
8	3982.6	99.4	4038	US-08-974-584C-117	Sequence 117, App
9	3973.8	99.2	4023	US-09-026-981-35	Sequence 35, App
10	3970	99.1	7029	US-08-911-312A-1	Sequence 1, Appl
11	3970	99.1	7029	US-08-911-312A-1	Sequence 1, Appl
12	3969	99.1	4015	PCT-US01-15774-3	Sequence 3, Appl
13	3969	99.1	4015	PCT-US01-14867-1	Sequence 1, Appl
14	3969	99.1	4015	PCT-US99-06898-1	Sequence 1, Appl
15	3969	99.1	4015	PCT-US99-07097-1	Sequence 1, Appl
16	3969	99.1	4015	PCT-US99-07160-1	Sequence 1, Appl
17	3969	99.1	4015	US-08-912-951-1	Sequence 1, Appl
18	3969	99.1	4015	US-08-974-549-1	Sequence 1, Appl
19	3969	99.1	4015	US-09-052-864-1	Sequence 1, Appl
20	3969	99.1	4015	US-09-402-181B-1	Sequence 1, Appl
21	3969	99.1	4015	US-09-402-181B-1	Sequence 1, Appl

Sequence 1, Appl1
Sequence 1, Appl1
Sequence 10, Appl1
Sequence 10, Appl1
Sequence 10, Appl1
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 3, Appl1
Sequence 224, Appl1
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 224, Appl1
Sequence 224, Appl1
Sequence 224, Appl1
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 817, App
Sequence 817, Appl1
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 3, Appl1
Sequence 1, Appl1

PRIOR APPLICATION DATA: US 08/911,312
APPLICATION NUMBER: 14-AUG-1997
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA: US 08/912,951
APPLICATION NUMBER: 14-AUG-1997
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA: US 08/915,503
APPLICATION NUMBER: 14-AUG-1997
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA: WO PCT/US97/17618
APPLICATION NUMBER: 01-OCT-1997
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA: WO PCT/US97/17885
APPLICATION NUMBER: 01-OCT-1997
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION: NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US1
TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEO ID NO: 343:
SEQUENCE CHARACTERISTICS: LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

```

1      PRIOR APPLICATION DATA:
2      APPLICATION NUMBER: US 08/911,312
3      FILING DATE: 14-AUG-1997
4      PRIOR APPLICATION DATA:
5      APPLICATION NUMBER: US 08/912,951
6      FILING DATE: 14-AUG-1997
7      PRIOR APPLICATION DATA:
8      APPLICATION NUMBER: US 08/915,503
9      FILING DATE: 14-AUG-1997
10     PRIOR APPLICATION DATA:
11     APPLICATION NUMBER: WO PCT/US97/17618
12     FILING DATE: 01-OCT-1997
13     PRIOR APPLICATION DATA:
14     APPLICATION NUMBER: WO PCT/US97/17885
15     FILING DATE: 01-OCT-1997
16     ATTORNEY/AGENT INFORMATION:
17     NAME: Apple, Randolph Ted
18     REGISTRATION NUMBER: 36,429
19     REFERENCE/DOCKET NUMBER: 015389-002610US
20     TELECOMMUNICATION INFORMATION:
21     TELEPHONE: (415) 576-0200
22     TELEFAX: (415) 576-0300
23     INFORMATION FOR SEQ ID NO: 343:
24     SEQUENCE CHARACTERISTICS:
25     LENGTH: 4037 base pairs
26     TYPE: nucleic acid
27     STRANDEDNESS: single
28     TOPOLOGY: linear
29     MOLECULE TYPE: cDNA
30     FEATURE:
31     NAME/KEY: CDS
32     LOCATION: 56..3454
33     OTHER INFORMATION: /note="refined sequence of hNRT cDNA"
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957

```

[illegible]

Db 481 CCGCTGGGCGACACAGCTGCTGTTACCTGCTGACAGCTGCCGCCCTTTTGTCTGCT 540
QY 548 GGGTCCACAGCTGCGCTACACAGTGTGGGGGCGCGCTGTACACAGCTGCGCTGCCAC 607
Db 541 GGGTCCACAGCTGCGCTACACAGTGTGGGGGCGCGCTGTACACAGCTGCGCTGCCAC 600
QY 608 TCAGGCGCGCGCGCGCGCACACAGCTAGTGAACCCGGAAGGCTGTGGATGCGAAGCGGC 667
Db 601 TCAGGCGCGCGCGCGCGCACACAGCTAGTGAACCCGGAAGGCTGTGGATGCGAAGCGGC 660
QY 668 CTGGAACCATAGCTCAGGAGGCGCGGGGTCCCTGTGGGCTGTCCAGGCCCGGGTGCAG 727
Db 661 CTGGAACCATAGCTCAGGAGGCGCGGGGTCCCTGTGGGCTGTCCAGGCCCGGGTGCAG 720
QY 728 GAGGCGCGGGGCGAGTGCAGCCGGAAGTGTGCGCTGCGCCAAAGAGCCCGAGCGTGGCG 787
Db 721 GAGGCGCGGGGCGAGTGCAGCCGGAAGTGTGCGCTGCGCCAAAGAGCCCGAGCGTGGCG 780
QY 788 TGGCCCTGAGCGGAGGAGCGCGCTTGGGAGGGGTCTGGGGCCCGAGCGGAGGAGC 847
Db 781 TGGCCCTGAGCGGAGGAGCGCGCTTGGGAGGGGTCTGGGGCCCGAGCGGAGGAGC 840
QY 848 GGTGAGACCGAGTACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
Db 841 GGTGAGACCGAGTACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 908 CACCTCTTTGAGAGGTGCGCTCTGTGGACAGCGGCACTCCCACTCCCTGTGGGCGGCCA 967
Db 901 CACCTCTTTGAGAGGTGCGCTCTGTGGACAGCGGCACTCCCACTCCCTGTGGGCGGCCA 960
QY 968 GCACACGCGGCG 1027
Db 961 GCACACGCGGCG 1020
QY 1028 CCGGCTGTACGCGGAGACAAAGCACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCTCT 1087
Db 1021 CCGGCTGTACGCGGAGACAAAGCACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCTCT 1080
QY 1088 GCGCT 1147
Db 1081 GCGCT 1140
QY 1148 GACCATCTTTTGTGGTTCAGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1207
Db 1141 GACCATCTTTTGTGGTTCAGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
QY 1208 GCGCCAGGCGTACTGTGGAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1267
Db 1201 GCGCCAGGCGTACTGTGGAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
QY 1268 GTGGCGCGTACGCGGTGCTCTCTCAAGACGACTGCGCGCTGCGAGCTGCGTACCGCG 1327
Db 1261 GTGGCGCGTACGCGGTGCTCTCTCAAGACGACTGCGCGCTGCGAGCTGCGTACCGCG 1320
QY 1328 AGCGGCTGT 1387
Db 1321 AGCGGCTGT 1380
QY 1388 CACAGACCCCGTGTGCTGT 1447
Db 1381 CACAGACCCCGT 1440
QY 1448 CCGCTTCTGTGGGCGCTGT 1507
Db 1441 CCGCTTCTGTGGGCGCTGT 1500
QY 1508 CAACGAGCGCGCTTCTCTCAGGAACACCAAGAAAGTTATCTCTCTCTCTCTCTCTCTCT 1567
Db 1501 CAACGAGCGCGCTTCTCTCAGGAACACCAAGAAAGTTATCTCTCTCTCTCTCTCTCTCT 1560
QY 1568 GCTCTGT 1627
Db 1561 GCTCTGT 1620

QY 1628 GAGCCAGGCGT 1687
Db 1621 GAGCCAGGCGT 1680
QY 1688 CAAGTTCCTGTACGT 1747
Db 1681 CAAGTTCCTGTACGT 1740
QY 1748 TGTCAAGGAGACAGCTTTTCAAAAGACAGGCTTTTTCCTACCGGAAGAGTGTCTGAAG 1807
Db 1741 TGTCAAGGAGACAGCTTTTCAAAAGACAGGCTTTTTCCTACCGGAAGAGTGTCTGAAG 1800
QY 1808 CAAGTTCGAAAGCTTTGGAATCAGACACACTTGAAGAGGAGTGTGTGTGTGTGTGTGTGT 1867
Db 1801 CAAGTTCGAAAGCTTTGGAATCAGACACACTTGAAGAGGAGTGTGTGTGTGTGTGTGTGT 1860
QY 1868 GGAAGCAGAGT 1927
Db 1861 GGAAGCAGAGT 1920
QY 1928 CTTGATCCCGCAAGCTGT 1987
Db 1921 CTTGATCCCGCAAGCTGT 1980
QY 1988 CAGAACTTCCGAGAGAAAGAGGCGCGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2047
Db 1981 CAGAACTTCCGAGAGAAAGAGGCGCGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
QY 2048 CAGCGTGTCTAACTAGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2107
Db 2041 CAGCGTGTCTAACTAGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2100
QY 2108 CCGT 2167
Db 2101 CCGT 2160
QY 2168 GCGCGCTGT 2191
Db 2161 GCGCGCTGT 2190
QY 2192 GAGCAGGCTGT 2251
Db 2221 GAGCAGGCTGT 2280
QY 2252 TGGGTATGCGGT 2311
Db 2281 TGGGTATGCGGT 2340
QY 2312 GGTCTGT 2371
Db 2341 GGTCTGT 2400
QY 2372 GACACAGCGCGT 2431
Db 2401 GACACAGCGCGT 2460
QY 2432 CAGT 2491
Db 2461 CAGT 2520
QY 2492 CAAGTTCGATGT 2551
Db 2521 CAAGTTCGATGT 2580
QY 2552 CAGCTGT 2611
Db 2581 CAGCTGT 2640
QY 2612 GCTCTGT 2671
Db 2641 GCTCTGT 2700

```

QY 2672 CTTCCTCAGACACCTGTCGAGGTGTCCCTGATGATGCTGCGTGTGAACCTTGCGGAA 2731
    |||||||
Db 2701 CTTCCTCAGACACCTGTCGAGGTGTCCCTGATGATGCTGCGTGTGAACCTTGCGGAA 2760
QY 2732 GACAGTGTGTAACCTTCCTGTGAGAGAGAGCCCTGGGTGGCAGAGCTTTTGTCAAT 2791
    |||||||
Db 2761 GACAGTGTGTAACCTTCCTGTGAGAGAGAGCCCTGGGTGGCAGAGCTTTTGTCAAT 2820
QY 2792 GCCGGCCACAGGCTTATTCCTGTCGGGCTGCTGTGTGATACCCGAGACCTGGAGT 2851
    |||||||
Db 2821 GCCGGCCACAGGCTTATTCCTGTCGGGCTGCTGTGTGATACCCGAGACCTGGAGT 2880
QY 2852 GCAGAGCAGTACTTCACCTATGCCCCGAGCTCCATCAGAGCCACTCACCTTCAACCG 2911
    |||||||
Db 2881 GCAGAGCAGTACTTCACCTATGCCCCGAGCTCCATCAGAGCCACTCACCTTCAACCG 2940
QY 2912 CGGCTTCAAGGCTGGGAGAGAACTGCTGCAACTCTTTGGGGCTTTGGCGCTGAAGTG 2971
    |||||||
Db 2941 CGGCTTCAAGGCTGGGAGAGAACTGCTGCAACTCTTTGGGGCTTTGGCGCTGAAGTG 3000
QY 2972 TCACAGCCTGTTTCGATTTGAGGTGACAGCCTCCAGAGGCTGACCAACATCTA 3031
    |||||||
Db 3001 TCACAGCCTGTTTCGATTTGAGGTGACAGCCTCCAGAGGCTGACCAACATCTA 3060
QY 3032 CAAGATCCTCTGCTGTCAGAGGCTGACAGGTTTCAGCATGTGCTGACAGCTCCATTCA 3091
    |||||||
Db 3061 CAAGATCCTCTGCTGTCAGAGGCTGACAGGTTTCAGCATGTGCTGACAGCTCCATTCA 3120
QY 3092 TCAGCAAGTTTGGAGAAACCCACATTTTCTGCGCTCATCTGTACAGCGCTCCCT 3151
    |||||||
Db 3121 TCAGCAAGTTTGGAGAAACCCACATTTTCTGCGCTCATCTGTACAGCGCTCCCT 3180
QY 3152 CTGCTACTCCATCCCTGAAAGCCAGAAACGAGGATGTCGGTGGGGGGCCAGAGGCGCGC 3211
    |||||||
Db 3181 CTGCTACTCCATCCCTGAAAGCCAGAAACGAGGATGTCGGTGGGGGGCCAGAGGCGCGC 3240
QY 3212 CGGCTCTGCTGCTGTCGAGAGGCTGTCAGTGGCTGTGCCAAGCATTCCTGCTCAACT 3271
    |||||||
Db 3241 CGGCTCTGCTGCTGTCGAGAGGCTGTCAGTGGCTGTGCCAAGCATTCCTGCTCAACT 3300
QY 3272 GACTGACACCGTGTACACTGACCTGACCTGCTGGGGTCACTCAGAGACGCCAGAGCCA 3331
    |||||||
Db 3301 GACTGACACCGTGTACACTGACCTGACCTGCTGGGGTCACTCAGAGACGCCAGAGCCA 3360
QY 3332 GCTGAGTGGAGAGCTCCCGGGGAGAGAGCTGACCTGTCGAGAGGCGGAGCAACCGCGC 3391
    |||||||
Db 3361 GCTGAGTGGAGAGCTCCCGGGGAGAGAGCTGACCTGTCGAGAGGCGGAGCAACCGCGC 3420
QY 3392 ACTGCCCTCAGACTTCAAGACATCTGATGATGAGCCACCGCCACAGCCAGAGCGCA 3451
    |||||||
Db 3421 ACTGCCCTCAGACTTCAAGACATCTGATGATGAGCCACCGCCACAGCCAGAGCGCA 3480
QY 3452 GAGCAGACACCCAGAGCCCTGTACAGCGCGGCTCTAGCTCCAGAGGAGAGGGCGCGC 3511
    |||||||
Db 3481 GAGCAGACACCCAGAGCCCTGTACAGCGCGGCTCTAGCTCCAGAGGAGAGGGCGCGC 3540
QY 3512 CACAGCCAGGCGCCAGAGCTGGAGTGTGAGGCTGAGTGTGAGTGTGGCCGAGGCGCTG 3571
    |||||||
Db 3541 CACAGCCAGGCGCCAGAGCTGGAGTGTGAGGCTGAGTGTGAGTGTGGCCGAGGCGCTG 3600
QY 3572 CATGTCCGGCTGAAGGCTGATGTCGGGCTGAGGCTGAGGAGTGTCCAGCAAGGAGCT 3631
    |||||||
Db 3601 CATGTCCGGCTGAAGGCTGATGTCGGGCTGAGGCTGAGGAGTGTCCAGCAAGGAGCT 3660
QY 3632 GAGTGTCCAGACACCTGCTTCACTTCCACAGGCTGGGCTGGCTCCAGCCCA 3691
    |||||||
Db 3661 GAGTGTCCAGACACCTGCTTCACTTCCACAGGCTGGGCTGGCTCCAGCCCA 3720
QY 3692 GGGCCAGCTTTTCTCAGAGAGAGCCGGCTTCACTCCCAATAGAAATAGTCATCC 3751
    |||||||
Db 3721 GGGCCAGCTTTTCTCAGAGAGAGCCGGCTTCACTCCCAATAGAAATAGTCATCC 3780
QY 3752 CCAAGATTCGCAATGTTCACCCCTGCGCTGCTTTCCTTTCACCCCAACATCC 3811

```

```

Db 3781 CCAGATTCGCAATGTTCACCCCTGCGCTGCTTTCCTTCCACCCCAACATCC 3840
QY 3812 AGGTGAGACACCTGAGAGAGACCCCTGGAGAGCTGCTGGGAATTTGAGTACCAAGGTGTG 3871
    |||||||
Db 3841 AGGTGAGACACCTGAGAGAGACCCCTGGAGAGCTGCTGGGAATTTGAGTACCAAGGTGTG 3900
QY 3872 CCTGTACACAGGAGAGACCCCTGACCTGATGGGGTCCCTGTGGGTCAAAATTTGGGGG 3931
    |||||||
Db 3901 CCTGTACACAGGAGAGACCCCTGACCTGATGGGGTCCCTGTGGGTCAAAATTTGGGGG 3960
QY 3932 GAGTGTCTGTGGAGTAAATATCTGAATATATGACTTTTTCAGTTTGGAAAAA 3991
    |||||||
Db 3961 GAGTGTCTGTGGAGTAAATATCTGAATATATGACTTTTTCAGTTTGGAAAAA 4020
QY 3992 AAAAAAAAAAAAAA 4006
    |||||||
Db 4021 AAAAAAAAAAAAAA 4035

```

```

RESULT 2
US-09-402-181A-343
; Sequence 343, Application US/09402181A
;
; GENERAL INFORMATION:
;
; APPLICANT: Cech, Thomas R.
;               Lingner, Joachim
;               Nakamura, Toru
;               Chapman, Karen B.
;               Morin, Gregg B.
;               Harley, Calvin B.
;               Andrews, William H.
;
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
;
; NUMBER OF SEQUENCES: 633
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Townsend and Townsend and Crew LLP
;
; STREET: Two Embarcadero Center, Eighth Floor
;
; CITY: San Francisco
;
; STATE: California
;
; COUNTRY: USA
;
; ZIP: 94111-3834
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/09/402,181A
;
; FILING DATE: 29-Sep-1997
;
; CLASSIFICATION: <unknown>
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US 08/724,643
;
; FILING DATE: 01-OCT-1996
;
; APPLICATION NUMBER: US 08/844,419
;
; FILING DATE: 18-APR-1997
;
; APPLICATION NUMBER: US 08/846,017
;
; FILING DATE: 25-APR-1997
;
; APPLICATION NUMBER: US 08/851,843
;
; FILING DATE: 06-MAY-1997
;
; APPLICATION NUMBER: US 08/854,050
;
; FILING DATE: 09-MAY-1997
;
; APPLICATION NUMBER: US 08/911,312
;
; FILING DATE: 14-AUG-1997
;
; APPLICATION NUMBER: US 08/912,951
;
; FILING DATE: 14-AUG-1997
;
; APPLICATION NUMBER: US 08/915,503
;
; FILING DATE: 14-AUG-1997
;
; APPLICATION NUMBER: WO PCT/US97/17885
;
; FILING DATE: 01-OCT-1997
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Ausenhus, Scott L.
;
; REGISTRATION NUMBER: 42,271
;
; REFERENCE/DOCKET NUMBER: 015389-00262005
;
; TELECOMMUNICATION INFORMATION:
;

```


Dh 1861 GGAAGCAAGGTCAAGGACATCGGGAGCCAGGCGCCCTGCTGACATCCAGACTCG 1920
Qy 1928 CTTATCCCAAGCCTGAGGGGCTGGGCGATTTGTGAACAATGACTACGTGCTGGAGC 1987
Dh 1921 CTTATCCCAAGCCTGAGGGGCTGGGCGATTTGTGAACAATGACTACGTGCTGGAGC 1980
Qy 1988 CAGAACGTTCCGAGAGAAAGAGGGCGAGCGTCTCACTCGAGGGGGAAGGCACTTT 2047
Dh 1981 CAGAACGTTCCGAGAGAAAGAGGGCGAGCGTCTCACTCGAGGGGGAAGGCACTTT 2040
Qy 2048 CAGCGTCTCAACTACGAGCGGGGCGGCGCCCGGCTCTGGGGGCTCTGTCTGGG 2107
Dh 2041 CAGCGTCTCAACTACGAGCGGGGCGGCGCCCGGCTCTGGGGGCTCTGTCTGGG 2100
Qy 2108 CCGAGGATATCCACAGGGGCTGGGCGACTGTGCTGTGGTGGGGGCGCCAGGAGCC 2167
Dh 2101 CCGAGGATATCCACAGGGGCTGGGCGACTGTGCTGTGGTGGGGGCGCCAGGAGCC 2160
Qy 2168 GCCGCTGAGCTGTA-----CATCCCCA 2191
Dh 2161 GCCGCTGAGCTGTACTTTGTCAAGGTGATGTAGCGGGCGGCTACGACACCATCCCA 2220
Qy 2192 GGACAGGCTCAGAGAGTCAATGCCAGCATATCAAAACCCAGAAACAGTACTGCTGG 2251
Dh 2221 GGACAGGCTCAGAGAGTCAATGCCAGCATATCAAAACCCAGAAACAGTACTGCTGG 2280
Qy 2252 TCGGATGCGGTGGTCCGAAGAGCGCCCATGGGCGAGTCCGCAAGGCGCTTCAAGAGCA 2311
Dh 2281 TCGGATGCGGTGGTCCGAAGAGCGCCCATGGGCGAGTCCGCAAGGCGCTTCAAGAGCA 2340
Qy 2312 CGTCTCACTTGAACAGACTTCAGCCGTACATGGGAGTTCGTGCTCACTTCAGAGA 2371
Dh 2341 CGTCTCACTTGAACAGACTTCAGCCGTACATGGGAGTTCGTGCTCACTTCAGAGA 2400
Qy 2372 GACCAGCCCGGTGAGGAGTGGCGTGTATGAGCAGAGCTCTCTCGAATGAGGCCAG 2431
Dh 2401 GACCAGCCCGGTGAGGAGTGGCGTGTATGAGCAGAGCTCTCTCGAATGAGGCCAG 2460
Qy 2432 CAGTGGCCTCTTGAACAGCTCTCACTACGCTTATGAGCCAGCAGCGCGTGCATCAGGG 2491
Dh 2461 CAGTGGCCTCTTGAACAGCTCTCACTACGCTTATGAGCCAGCAGCGCGTGCATCAGGG 2520
Qy 2492 CAACTCTCACTCACTGATGATGATTTCTTGTGTGATGATGATGATGATGATGATGAT 2551
Dh 2521 CAACTCTCACTCACTGATGATGATGATTTCTTGTGTGATGATGATGATGATGATGAT 2580
Qy 2552 CAGGCTGCTGATGAGGCGAGGAGAAACAAGCTGTTTCCGGGAGTTCGGCGGAGCGGCT 2611
Dh 2581 CAGGCTGCTGATGAGGCGAGGAGAAACAAGCTGTTTCCGGGAGTTCGGCGGAGCGGCT 2640
Qy 2612 GCTCTGCTGATGATGATGATTTCTTGTGTGATGATGATGATGATGATGATGATGAT 2671
Dh 2641 GCTCTGCTGATGATGATGATTTCTTGTGTGATGATGATGATGATGATGATGATGAT 2700
Qy 2672 CTTCTCAAGAACCTGGTCCGAGGTGTCCTGAGTATGCTGCTGCTGCTGCTGCTGCTG 2731
Dh 2701 CTTCTCAAGAACCTGGTCCGAGGTGTCCTGAGTATGCTGCTGCTGCTGCTGCTGCTG 2760
Qy 2732 GACAGTGTGAATTCCTCTGTAAGAAAGAGGCGCTGGTGGGAGCGGCTTTTGTTCATAT 2791
Dh 2761 GACAGTGTGAATTCCTCTGTAAGAAAGAGGCGCTGGTGGGAGCGGCTTTTGTTCATAT 2820
Qy 2792 GCCGCGCCACAGGCTATTCCTCTGTTGGGCGCTGCTGCTGATACCCGAGCCCTGAGGT 2851
Dh 2821 GCCGCGCCACAGGCTATTCCTCTGTTGGGCGCTGCTGCTGATACCCGAGCCCTGAGGT 2880
Qy 2852 GCAGAGGCACTACTCAGACTATGCCCGGACCTCATGAGAGCAGTCACTTCACCG 2911
Dh 2881 GCAGAGGCACTACTCAGACTATGCCCGGACCTCATGAGAGCAGTCACTTCACCG 2940
Qy 2912 CGGCTTCAAGGCTGGGAGAAACATGCTGCGAAACTCTTTGGGGCTTGGGGCTGAATG 2971
Dh 2941 CGGCTTCAAGGCTGGGAGAAACATGCTGCGAAACTCTTTGGGGCTTGGGGCTGAATG 3000

Qy 2972 TCACAGCCTGTTTCTGATTTGAGGTGAGAACAGCCTCCAGACGGTGTGACCAACATCTA 3031
Dh 3001 TCACAGCCTGTTTCTGATTTGAGGTGAGAACAGCCTCCAGACGGTGTGACCAACATCTA 3060
Qy 3032 CAAGATCTCTCTGCTGAGGGGTACAGGTTTCAGGCATGTGTGCTGACGTCCCAATTTC 3091
Dh 3061 CAAGATCTCTCTGCTGAGGGGTACAGGTTTCAGGCATGTGTGCTGACGTCCCAATTTC 3120
Qy 3092 TCAGCAATTTTGAAGAACCCACATTTTCTGCGGCTCATCTCTGACAGGGCTCCCT 3151
Dh 3121 TCAGCAATTTTGAAGAACCCACATTTTCTGCGGCTCATCTCTGACAGGGCTCCCT 3180
Qy 3152 CTGCTACTTCATCTCTGAAGAGCAAGAACGACGAGGATGTGCTGGGGGCGCAAGGGCGCG 3211
Dh 3181 CTGCTACTTCATCTCTGAAGAGCAAGAACGACGAGGATGTGCTGGGGGCGCAAGGGCGCG 3240
Qy 3212 CGGCGCTCTGCTCCGAGGGCGTGCAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3271
Dh 3241 CGGCGCTCTGCTCCGAGGGCGTGCAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
Qy 3272 GACTTGACACCGGTGTCACTTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3331
Dh 3301 GACTTGACACCGGTGTCACTTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360
Qy 3332 GCTGAGTGGAAAGCTCCCGGGGAGACGCTGACTGCTGCTGAGGCGCGAGCCCAACCGCG 3391
Dh 3361 GCTGAGTGGAAAGCTCCCGGGGAGACGCTGACTGCTGCTGAGGCGCGAGCCCAACCGCG 3420
Qy 3392 ACTGCGCTCAGACTTCAAGACATCTGACTGATGGCCACCCCGCCACAGCCAGCGCGGA 3451
Dh 3421 ACTGCGCTCAGACTTCAAGACATCTGACTGATGGCCACCCCGCCACAGCCAGCGCGGA 3480
Qy 3452 GAGCAGAACACGAGCCCTGTCAAGCGCGGCTCTACTGCTCCAGAGAGGAGGGCGGCG 3511
Dh 3481 GAGCAGAACACGAGCCCTGTCAAGCGCGGCTCTACTGCTCCAGAGAGGAGGGCGGCG 3540
Qy 3512 CACACCCAGGCGCCGAGCGCTGGAGTGTGAGGCGCTGATGATGATGATGATGATGATGAT 3571
Dh 3541 CACACCCAGGCGCCGAGCGCTGGAGTGTGAGGCGCTGATGATGATGATGATGATGATGAT 3600
Qy 3572 CATGTCCGGCTGAAGGCTGAGTGTCCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3631
Dh 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
Qy 3632 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCGTGGGCGTGGCTCCACCCCA 3691
Dh 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCGTGGGCGTGGCTCCACCCCA 3720
Qy 3692 GGGCCAGCTTTTCTCACACAGAGCGCGCTTCCACTCCCAATAGGAATAGTCCATCC 3751
Dh 3721 GGGCCAGCTTTTCTCACACAGAGCGCGCTTCCACTCCCAATAGGAATAGTCCATCC 3780
Qy 3752 CCAGATTTGCCATTTGTTACCCCTGCGCTGCTCTTGTGCTTCCACCCCAACATCC 3811
Dh 3781 CCAGATTTGCCATTTGTTACCCCTGCGCTGCTCTTGTGCTTCCACCCCAACATCC 3840
Qy 3812 AGGTGGAGACCTGAGAGGACCTGGAGGCTGGGGAATTTGGAGTACCAAAAGGTG 3871
Dh 3841 AGGTGGAGACCTGAGAGGACCTGGAGGCTGGGGAATTTGGAGTACCAAAAGGTG 3900
Qy 3872 CCCTGTACACAGGAGGAGCCCTGACCTGATGGGGTCCCTGCTGCTGCTGCTGCTGCTGCTG 3931
Dh 3901 CCCTGTACACAGGAGGAGCCCTGACCTGATGGGGTCCCTGCTGCTGCTGCTGCTGCTGCTG 3960
Qy 3932 GAGTGTCTGTGGAGTAAATACGATATATGAGTCTTTAGTTTGAATTAATTAATTAATTA 3991
Dh 3961 GAGTGTCTGTGGAGTAAATACGATATATGAGTCTTTAGTTTGAATTAATTAATTAATTA 4020
Qy 3992 AAAAAAAAAAAAAA 4006
Dh 4021 AAAAAAAAAAAAAA 4035

```

1      RESULT 3
2      US-09-402-181B-343
3      ; Sequence 343, Application US/09402181B
4      GENERAL INFORMATION:
5      APPLICANT: Cecch, Thomas R.
6      Linfert, Joachim
7      Nakamura, Toru
8      Chapman, Karen B.
9      Morin, Gregg B.
10     Hailey, William B.
11     Andrews, William H.
12     TITLE OF INVENTION: Human Telomerase Catalytic Subunit
13     NUMBER OF SEQUENCES: 633
14     CORRESPONDENCE ADDRESS:
15     ADDRESSEE: Townsend and Townsend and Crew LLP
16     STREET: Two Embarcadero Center, Eighth Floor
17     CITY: San Francisco
18     STATE: California
19     COUNTRY: USA
20     ZIP: 94111-3834
21     COMPUTER READABLE FORM:
22     MEDIUM TYPE: Floppy disk
23     COMPUTER: IBM PC compatible
24     OPERATING SYSTEM: PC-DOS/MS-DOS
25     SOFTWARE: Patent Release #1.0, Version #1.30
26     CURRENT APPLICATION DATA:
27     APPLICATION NUMBER: US/09/402,181B
28     FILING DATE: 29-Sep-1997
29     CLASSIFICATION: <Unknown>
30     PRIOR APPLICATION DATA:
31     APPLICATION NUMBER: US 08/724,643
32     FILING DATE: 01-OCT-1996
33     APPLICATION NUMBER: US 08/844,419
34     FILING DATE: 18-APR-1997
35     APPLICATION NUMBER: US 08/846,017
36     FILING DATE: 25-APR-1997
37     APPLICATION NUMBER: US 08/851,843
38     FILING DATE: 06-MAY-1997
39     APPLICATION NUMBER: US 08/854,050
40     FILING DATE: 09-MAY-1997
41     APPLICATION NUMBER: US 08/911,312
42     FILING DATE: 14-AUG-1997
43     APPLICATION NUMBER: US 08/912,951
44     FILING DATE: 14-AUG-1997
45     APPLICATION NUMBER: US 08/915,503
46     FILING DATE: 14-AUG-1997
47     APPLICATION NUMBER: WO PCT/US97/17885
48     FILING DATE: 01-OCT-1997
49     ATTORNEY/AGENT INFORMATION:
50     NAME: Ausenhus, Scott L.
51     REGISTRATION NUMBER: 42,271
52     REFERENCE/DOCKET NUMBER: 015389-002620US
53     TELECOMMUNICATION INFORMATION:
54     TELEPHONE: (415) 576-0200
55     TELEFAX: (415) 576-0300
56     INFORMATION FOR SEQ ID NO: 343:
57     SEQUENCE CHARACTERISTICS:
58     LENGTH: 4037 base pairs
59     TYPE: nucleic acid
60     STRANDEDNESS: single
61     TOPOLOGY: linear
62     MOLECULE TYPE: cdna
63     FEATURE:
64     NAME/KEY: CDS
65     LOCATION: 56..3454
66     OTHER INFORMATION: /note="refined sequence of hTERT cDNA"
67     ;
68     ;
69     ;
70     ;
71     ;
72     ;
73     ;
74     ;
75     ;
76     ;
77     ;
78     ;
79     ;
80     ;
81     ;
82     ;
83     ;
84     ;
85     ;
86     ;
87     ;
88     ;
89     ;
90     ;
91     ;
92     ;
93     ;
94     ;
95     ;
96     ;
97     ;
98     ;
99     ;
100    ;
101    ;
102    ;
103    ;
104    ;
105    ;
106    ;
107    ;
108    ;
109    ;
110    ;
111    ;
112    ;
113    ;
114    ;
115    ;
116    ;
117    ;
118    ;
119    ;
120    ;
121    ;
122    ;
123    ;
124    ;
125    ;
126    ;
127    ;
128    ;
129    ;
130    ;
131    ;
132    ;
133    ;
134    ;
135    ;
136    ;
137    ;
138    ;
139    ;
140    ;
141    ;
142    ;
143    ;
144    ;
145    ;
146    ;
147    ;
148    ;
149    ;
150    ;
151    ;
152    ;
153    ;
154    ;
155    ;
156    ;
157    ;
158    ;
159    ;
160    ;
161    ;
162    ;
163    ;
164    ;
165    ;
166    ;
167    ;
168    ;
169    ;
170    ;
171    ;
172    ;
173    ;
174    ;
175    ;
176    ;
177    ;
178    ;
179    ;
180    ;
181    ;
182    ;
183    ;
184    ;
185    ;
186    ;
187    ;
188    ;
189    ;
190    ;
191    ;
192    ;
193    ;
194    ;
195    ;
196    ;
197    ;
198    ;
199    ;
200    ;
201    ;
202    ;
203    ;
204    ;
205    ;
206    ;
207    ;
208    ;
209    ;
210    ;
211    ;
212    ;
213    ;
214    ;
215    ;
216    ;
217    ;
218    ;
219    ;
220    ;
221    ;
222    ;
223    ;
224    ;
225    ;
226    ;
227    ;
228    ;
229    ;
230    ;
231    ;
232    ;
233    ;
234    ;
235    ;
236    ;
237    ;
238    ;
239    ;
240    ;
241    ;
242    ;
243    ;
244    ;
245    ;
246    ;
247    ;
248    ;
249    ;
250    ;
251    ;
252    ;
253    ;
254    ;
255    ;
256    ;
257    ;
258    ;
259    ;
260    ;
261    ;
262    ;
263    ;
264    ;
265    ;
266    ;
267    ;
268    ;
269    ;
270    ;
271    ;
272    ;
273    ;
274    ;
275    ;
276    ;
277    ;
278    ;
279    ;
280    ;
281    ;
282    ;
283    ;
284    ;
285    ;
286    ;
287    ;
288    ;
289    ;
290    ;
291    ;
292    ;
293    ;
294    ;
295    ;
296    ;
297    ;
298    ;
299    ;
300    ;
301    ;
302    ;
303    ;
304    ;
305    ;
306    ;
307    ;
308    ;
309    ;
310    ;
311    ;
312    ;
313    ;
314    ;
315    ;
316    ;
317    ;
318    ;
319    ;
320    ;
321    ;
322    ;
323    ;
324    ;
325    ;
326    ;
327    ;
328    ;
329    ;
330    ;
331    ;
332    ;
333    ;
334    ;
335    ;
336    ;
337    ;
338    ;
339    ;
340    ;
341    ;
342    ;
343    ;
344    ;
345    ;
346    ;
347    ;
348    ;
349    ;
350    ;
351    ;
352    ;
353    ;
354    ;
355    ;
356    ;
357    ;
358    ;
359    ;
360    ;
361    ;
362    ;
363    ;
364    ;
365    ;
366    ;
367    ;
368    ;
369    ;
370    ;
371    ;
372    ;
373    ;
374    ;
375    ;
376    ;
377    ;
378    ;
379    ;
380    ;
381    ;
382    ;
383    ;
384    ;
385    ;
386    ;
387    ;
388    ;
389    ;
390    ;
391    ;
392    ;
393    ;
394    ;
395    ;
396    ;
397    ;
398    ;
399    ;
400    ;
401    ;
402    ;
403    ;
404    ;
405    ;
406    ;
407    ;
408    ;
409    ;
410    ;
411    ;
412    ;
413    ;
414    ;
415    ;
416    ;
417    ;
418    ;
419    ;
420    ;
421    ;
422    ;
423    ;
424    ;
425    ;
426    ;
427    ;
428    ;
429    ;
430    ;
431    ;
432    ;
433    ;
434    ;
435    ;
436    ;
437    ;
438    ;
439    ;
440    ;
441    ;
442    ;
443    ;
444    ;
445    ;
446    ;
447    ;
448    ;
449    ;
450    ;
451    ;
452    ;
453    ;
454    ;
455    ;
456    ;
457    ;
458    ;
459    ;
460    ;
461    ;
462    ;
463    ;
464    ;
465    ;
466    ;
467    ;
468    ;
469    ;
470    ;
471    ;
472    ;
473    ;
474    ;
475    ;
476    ;
477    ;
478    ;
479    ;
480    ;
481    ;
482    ;
483    ;
484    ;
485    ;
486    ;
487    ;
488    ;
489    ;
490    ;
491    ;
492    ;
493    ;
494    ;
495    ;
496    ;
497    ;
498    ;
499    ;
500    ;
501    ;
502    ;
503    ;
504    ;
505    ;
506    ;
507    ;
508    ;
509    ;
510    ;
511    ;
512    ;
513    ;
514    ;
515    ;
516    ;
517    ;
518    ;
519    ;
520    ;
521    ;
522    ;
523    ;
524    ;
525    ;
526    ;
527    ;
528    ;
529    ;
530    ;
531    ;
532    ;
533    ;
534    ;
535    ;
536    ;
537    ;
538    ;
539    ;
540    ;
541    ;
542    ;
543    ;
544    ;
545    ;
546    ;
547    ;
548    ;
549    ;
550    ;
551    ;
552    ;
553    ;
554    ;
555    ;
556    ;
557    ;
558    ;
559    ;
560    ;
561    ;
562    ;
563    ;
564    ;
565    ;
566    ;
567    ;
568    ;
569    ;
570    ;
571    ;
572    ;
573    ;
574    ;
575    ;
576    ;
577    ;
578    ;
579    ;
580    ;
581    ;
582    ;
583    ;
584    ;
585    ;
586    ;
587    ;
588    ;
589    ;
590    ;
591    ;
592    ;
593    ;
594    ;
595    ;
596    ;
597    ;
59
```

QY	8	GGAGGCGGCTGCTGACGACAGTGGAGAACCCCTGAGCCGAGCCACCCCGCATGAGC	67
Db	1	GCAGGCTGGCTGCTGCTGCGCAGCATGTGGAAACCTTGCCCGCGGACACCCCGCATGAGC	60
QY	68	GGGCGCTCCCGCTGCGAGCGGCGGCTCCCTGTCGCGAGCAGCATGACGAGCGGT	127
Db	61	GGGCGCTCCCGCTGCGAGCGGCGGCTCCCTGTCGCGAGCAGCATGCGAGGCTGCT	120
QY	128	GGCGGTGACCAGTTGCTGTGGGCGCCCGCGGAGCCCGAGGTGAGCGCTGTGGACGCG	187
Db	121	GGCGGTGACCAGTTGCTGTGGGCGCCCGCGGAGCCCGAGGTGAGCGCTGTGGACGCG	180
QY	188	GGACCCGCGCGCTTTTCCGCGCGCTGTGGCCAGTGGCTGTGTCTGCTGTGGACGCG	247
Db	181	GGACCCGCGCGCTTTTCCGCGCGCTGTGGCCAGTGGCTGTGTCTGCTGTGGACGCG	240
QY	248	AGGAGCGCGCCCGCGCGCCCTCTCTTCCGCGAGGTGTCTGTGTGAAGAGCGGTGGC	307
Db	241	AGGAGCGCGCCCGCGCGCCCTCTCTTCCGCGAGGTGTCTGTGTGAAGAGCGGTGGC	300
QY	308	CCGAGTGTCTCAAGGCTGTGTCCAGCGCGGCGCCCAAGAAAGTGTGTGTGCTTCCGCTTGC	367
Db	301	CCGAGTGTCTCAAGGCTGTGTCCAGCGCGGCGCCCAAGAAAGTGTGTGTGCTTCCGCTTGC	360
QY	368	GGTGTGAGCGGGGCCCCCGGGGCCCCCGAGAGCTTACACACAGCTGTGGCAGCTA	427
Db	361	GGTGTGTGAGCGGGGCCCCCGGGGCCCCCGAGAGCTTACACACAGCTGTGGCAGCTA	420
QY	428	CCTGTGCCAAGACGTTGACCGAGCGACTGTGGGGGAGAGGGGGGCTGGTGTGTGCG	487
Db	421	CCTGTGCCAAGACGTTGACCGAGCGACTGTGGGGGAGAGGGGGGCTGTGTGTGCG	480
QY	488	CGGCGTGGGGGAGAGAGTGTGTGCTACCTGTGTGGCAGGCTGTGGGCTTGTGTGTGT	547
Db	481	CGGCGTGGGGGAGAGAGTGTGTGCTACCTGTGTGGCAGGCTGTGGGCTTGTGTGTGT	540
QY	548	GGCTTCCACGCTGTGCTTACAGAGTGTGTGGGCGCGCTCGCTTACAGCTGTGGCTGTCC	607
Db	541	GGCTTCCACGCTGTGCTTACAGAGTGTGTGGGCGCGCGCTCGCTTACAGCTGTGGCTGTCC	600
QY	608	TCAGGCGCGGCCCCCGCCAGCAGCTGTGTGAGCCCGAGAGGCGTCTGGGATGTGGAAGGCG	667
Db	601	TCAGGCGCGGCCCCCGCCAGCAGCTGTGTGAGCCCGAGAGGCGTCTGGGATGTGGAAGGCG	660
QY	668	CTGGAACCATAGCTGTAGGAGGAGCGCGGGTTCGCCCTGTGGGCTTCCAGCGCCCGGATGTG	727
Db	661	CTGGAACCATAGCTGTAGGAGGAGCGCGGGTTCGCCCTGTGGGCTTCCAGCGCCCGGATGTG	720
QY	728	GAGGCGGCGGGGAGTGTGACAGCGAAGTGTGTGCTGTGTGCCAAGAGGCCAAGGCTGTGGCG	787
Db	721	GAGGCGGCGGGGAGTGTGACAGCGAAGTGTGTGCTGTGTGCCAAGAGGCCAAGGCTGTGGCG	780
QY	788	TGCGCTGTGAGCGGAGCGGACGCGCGTTGGGCGAGGGGTCTGTGGGCCACCCGGGCGAGC	847
Db	781	TGCGCTGTGAGCGGAGCGGACGCGCGTTGGGCGAGGGGTCTGTGGGCCACCCGGGCGAGC	840
QY	848	GGGTGTGACAGTGAACCTGT	907
Db	841	GGGTGTGACAGTGAACCTGT	900
QY	908	CACCTCTTGTGAGGGT	967
Db	901	CACCTCTTGTGAGGGT	960
QY	968	GGAGCAGCGGGGCCCCCATCTCATGTGGGGGCGACAGGTCTGTGGAGCAGGCTTGTGC	1027
Db	961	GGAGCAGCGGGGCCCCCATCTCATGTGGGGGCGACAGGTCTGTGGAGCAGGCTTGTGC	1020
QY	1028	CCCGGTGTGAGCGGAGACCAAGCATTTCTCTACTCTCTCAAGCGAGCAGAGAGCAGCTGTG	1087
Db	1021	CCCGGTGTGAGCGGAGACCAAGCATTTCTCTACTCTCTCAAGCGAGCAGAGAGCAGCTGTG	1080

Thu Apr 17 08:21:56 2003

us-09-424-686b-1del.rnpm

Page 9

Dh	3241	CGGGCCCTCTCCCTCCGAGGCGCCGACGAGTGGGCTGGCCACCAAGCATCTCGCTCAAGCT	3303
Qy	3272	GACGTGACACCGTGGTACCTTACGTACGGCCATCTCGTGGGTCACATCAGACAGCCGACAGCA	3331
Dh	3301	GACTGACACCGTGGTACCTTACGTGGCCACTCGTGGGTCACATCAGACAGCCGACAGCA	3360
Qy	3332	GCTGAGTCGGAAGCTCCCGGGAGAGACGCTGACGCTCGCTGAGGGCGGAGCAACCGGCG	3391
Dh	3361	GCTGAGTCGGAAGCTCCCGGGAGAGACGCTGACGCTCGCTGAGGGCGGAGCAACCGGCG	3420
Qy	3392	ACTGCGCTCAGACTTCAAGACATCTGGATGATGGCCACCGGCCACAGCAGGCTCGA	3451
Dh	3421	ACTGCGCTCAGACTTCAAGACATCTGGATGATGGCCACCGGCCACAGCAGGCTCGA	3480
Qy	3452	GAGCAGACACACAGACCGCTGTACACCCCGGGCTGTACGTGCCAGGAGAGAGGGGGGCGC	3511
Dh	3481	GAGCAGACACACAGACCGCTGTACACCCCGGGCTGTACGTGCCAGGAGAGAGGGGGGCGC	3540
Qy	3512	CACACACAGGCGCGACCGCTGGGAGCTGAGAGCCTAGTGAATGTTTGGCGAGGCTCG	3571
Dh	3541	CACACACAGGCGCGACCGCTGGGAGCTGAGAGCCTAGTGAATGTTTGGCGAGGCTCG	3600
Qy	3572	CATGTCGGGTGAAGCTGATGTGCGGGCTGAGGCTCAGACAGTGTGCAGACCAAGGCT	3631
Dh	3601	CATGTCGGGTGAAGCTGATGTGCGGGCTGAGGCTCAGACAGTGTGCAGACCAAGGCT	3660
Qy	3632	GAGTGTCCAGCACACCTGCGGTCTTACTTCCACAGCTGGCGCTGGCTCCACCCA	3691
Dh	3661	GAGTGTCCAGCACACCTGCGGTCTTACTTCCACAGCTGGCGCTGGCTCCACCCA	3720
Qy	3692	GGGCGACCTTTCCTCCACAGAGACCCGGCTTCACACTCCCAATAGGAATGTCCATCC	3751
Dh	3721	GGGCGACCTTTCCTCCACAGAGACCCGGCTTCACACTCCCAATAGGAATGTCCATCC	3780
Qy	3752	CCAGATTCCGCAATGTTCACCCCTGCGCCCTCTTGTGCTTCACCCCAACATCC	3811
Dh	3781	CCAGATTCCGCAATGTTCACCCCTGCGCCCTCTTGTGCTTCACCCCAACATCC	3840
Qy	3812	AGGTGGAGACCCCTGAGAGAGACCTGGAGGCTCTGGGAATTTTGGATACCAAGAGTGTG	3871
Dh	3841	AGGTGGAGACCCCTGAGAGAGACCTGGAGGCTCTGGGAATTTTGGATACCAAGAGTGTG	3900
Qy	3872	CCGTGTACACAGGCGAGGACCCCTGACCTGATATGGGGTCCCTGTGGGTCAAAATTTGGGG	3931
Dh	3901	CCGTGTACACAGGCGAGGACCCCTGACCTGATATGGGGTCCCTGTGGGTCAAAATTTGGGG	3960
Qy	3932	GAGGTGCTGTGGAGTAATAATATCGAATATATGAGTTTTCAGTTTGAATAAAAAAAAAAAAA	3991
Dh	3961	GAGGTGCTGTGGAGTAATAATATCGAATATATGAGTTTTCAGTTTGAATAAAAAAAAAAAAA	4020
Qy	3992	AAAAAAAAAAAAAAAAAAAA 4006	
Dh	4021	AAAAAAAAAAAAAAAAAAAA 4035	

RESULT 4
US-09-432-503-343
Sequence 343, Application US/0932503.
GENERAL INFORMATION:
APPLICANT: Cecchi, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California

```

COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,549
FILING DATE: <unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /note="refined sequence of hTERT cDNA"

US-09-432-503-343
DB 18; Length 4037;
Query Match 99.4%; Score 3982.6;
Best Local Similarity 98.9%; Pred. No. 6,4e-140;
Matches 3992; Conservative 4; Mismatches 3; Indels 36; Gaps

```


Db 2401 GACCAAGCCGCTGAGGATGCCGTGTCATGACAGAGCTCCTCTGTAATGAGCCAG 2460
 QY 2432 CAGTGGCTCTTGAGAGCTTCTTCTACGCTTCATGTGTCACACAGCCGCTGCATCAGAGG 2491
 Db 2461 CAGTGGCTCTTGAGAGCTTCTTCTACGCTTCATGTGTCACACAGCCGCTGCATCAGAGG 2520
 QY 2492 CAAATCTTACGCTCAGTGGCAGAGGATCCGACAGGGCTCCATCTCTCTCAGAGCTGCTG 2551
 Db 2521 CAAATCTTACGCTCAGTGGCAGAGGATCCGACAGGGCTCCATCTCTCTCAGAGCTGCTG 2580
 QY 2552 CAGCTGTGTAGGAGGAGATGAGAACAGAGCTGTTGGGGGATGTTGGGGGAGGGGGCT 2611
 Db 2581 CAGCTGTGTAGGAGGAGATGAGAACAGAGCTGTTGGGGGATGTTGGGGGAGGGGGCT 2640
 QY 2612 GCTCTGCTGTTGGTGGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2671
 Db 2641 GCTCTGCTGTTGGTGGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2700
 QY 2672 CTTCCTCAGAGACCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2731
 Db 2701 CTTCCTCAGAGACCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
 QY 2732 GACAGTGTAACTTCTCTGTAGAAAGAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 2791
 Db 2761 GACAGTGTAACTTCTCTGTAGAAAGAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820
 QY 2792 GCCGGCCACAGGCTATTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2851
 Db 2821 GCCGGCCACAGGCTATTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
 QY 2852 GCAGAGGAGTACTCCAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2911
 Db 2881 GCAGAGGAGTACTCCAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
 QY 2912 CGGCTTCAAGGCTGGAGGAGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2971
 Db 2941 CGGCTTCAAGGCTGGAGGAGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000
 QY 2972 TCACAGGCTGTTCTGATTTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 3031
 Db 3001 TCACAGGCTGTTCTGATTTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 3060
 QY 3032 CAAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3091
 Db 3061 CAAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3120
 QY 3092 TCAGCAAGTTTGAAGAACCCCACTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3151
 Db 3121 TCAGCAAGTTTGAAGAACCCCACTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3180
 QY 3152 CTGCTACTCATCTTAAAGCCAAAGAGCAGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3211
 Db 3181 CTGCTACTCATCTTAAAGCCAAAGAGCAGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3240
 QY 3212 CGGCTCTCTGCTCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3271
 Db 3241 CGGCTCTCTGCTCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
 QY 3272 GACTGAGACCGTGTACCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3331
 Db 3301 GACTGAGACCGTGTACCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360
 QY 3332 GCTGAGTGTGAGAGCTCCGCGGAGAGAGCTGAGCTGCTGAGAGGCTGAGAGGCTGAGAGGCT 3391
 Db 3361 GCTGAGTGTGAGAGCTCCGCGGAGAGAGCTGAGCTGCTGAGAGGCTGAGAGGCTGAGAGGCT 3420
 QY 3392 ACTGCTCTGAGAGTCTAAAGACATCTGAGAGTATGAGAGGCTGAGAGGCTGAGAGGCTGAG 3451
 Db 3421 ACTGCTCTGAGAGTCTAAAGACATCTGAGAGTATGAGAGGCTGAGAGGCTGAGAGGCTGAG 3480
 QY 3452 GAGCAGACACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3511
 Db 3481 GAGCAGACACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3540

QY 3512 CACACCCAGGCCCCGACACCGCTGAGAGCTGAGGCTGAGTATGTTGGCCGAGGCTG 3571
 Db 3541 CACACCCAGGCCCCGACACCGCTGAGAGCTGAGGCTGAGTATGTTGGCCGAGGCTG 3600
 QY 3572 CATGTCCGGCTGAGAGCTGAGAGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3631
 Db 3601 CATGTCCGGCTGAGAGCTGAGAGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3660
 QY 3632 GAGTGTACAGACACCTGCGCTTTCACCTTCCACAGAGGCTGAGAGGCTGAGAGGCTGAG 3691
 Db 3661 GAGTGTACAGACACCTGCGCTTTCACCTTCCACAGAGGCTGAGAGGCTGAGAGGCTGAG 3720
 QY 3692 GGGCAGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3751
 Db 3721 GGGCAGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3780
 QY 3752 CCAGATTCGCTATGTTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3811
 Db 3781 CCAGATTCGCTATGTTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3840
 QY 3812 AGGTGAGACCTTGAGAGAGACCTGAGAGCTGAGAGTGTGAGAGTGTGAGAGTGTGAG 3871
 Db 3841 AGGTGAGACCTTGAGAGAGACCTGAGAGCTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 3900
 QY 3872 CCCTGTACAGAGGCGAGAGACCTGACCTGATGAGAGGCTGCTGCTGCTGCTGCTGCTGCTG 3931
 Db 3901 CCCTGTACAGAGGCGAGAGACCTGACCTGATGAGAGGCTGCTGCTGCTGCTGCTGCTGCTG 3960
 QY 3932 GAGTGTCTGCTGAGAGAAATATGAAATATGATGTTTTCAGTTTGAAGAGAGAGAGAG 3991
 Db 3961 GAGTGTCTGCTGAGAGAAATATGAAATATGATGATGTTTTCAGTTTGAAGAGAGAGAGAG 4020
 QY 3992 AAAAAAAAAAAAAA 4006
 Db 4021 AAAAAAAAAAAAAA 4035

RESULT 5
 US-09-721-477-343
 Sequence 343 Application US/09721477
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/721,477
 FILING DATE: 22-Nov-2000
 CLASSIFICATION: <unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/974,549
 FILING DATE: <unknown>
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-Apr-1997
 APPLICATION NUMBER: US 08/846,017

Db 1561 GCTCTCGTCGAGAGAGCTGACGTGAGAGATGACGCTGCGGAGATGCGCTGTGCTGCGCAG 1620
QY 1628 GAGCCCAAGGGGTGGCTGTGTTTCCGGCCGACAGACACCGTCTGCTGAGAGATGCTGAGC 1687
Db 1621 GAGCCCAAGGGGTGGCTGTGTTTCCGGCCGACAGACACCGTCTGCTGAGAGATGCTGAGC 1680
QY 1688 CAAAGTCTGCTGAGCTGCTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1747
Db 1681 CAAAGTCTGCTGAGCTGCTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740
QY 1748 TGTCAAGGAGACACAGCTTTCAAAAAGACAGGCTTTTCTTACCGAGAGAGTGTCTGAG 1807
Db 1741 TGTCAAGGAGACACAGCTTTCAAAAAGACAGGCTTTTCTTACCGAGAGAGTGTCTGAG 1800
QY 1808 CAAAGTTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1867
Db 1801 CAAAGTTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
QY 1868 GGAACAGAGAGGTGAGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1927
Db 1861 GGAACAGAGAGGTGAGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
QY 1928 CTTCATCCCAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1987
Db 1921 CTTCATCCCAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
QY 1988 CAGACGCTTCGGAG 2047
Db 1981 CAGACGCTTCGGAG 2040
QY 2048 CAGCGTCTCAACTAG 2107
Db 2041 CAGCGTCTCAACTAG 2100
QY 2108 CCGTAGAGATATCCACAG 2167
Db 2101 CCGTAGAGATATCCACAG 2160
QY 2168 GCGGCTGAGCTGTA-----CATCCGCCA 2191
Db 2161 GCGGCTGAGCTGTA-----CATCCGCCA 2220
QY 2192 GAGACAGGCTTCAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2251
Db 2221 GAGACAGGCTTCAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2280
QY 2252 TCGGATGCGGTGTCAG 2311
Db 2281 TCGGATGCGGTGTCAG 2340
QY 2312 GGTCTCTACCTTGACAG 2371
Db 2341 GGTCTCTACCTTGACAG 2400
QY 2372 GACACAGCCGCTGAG 2431
Db 2401 GACACAGCCGCTGAG 2460
QY 2432 CAGTGCGCTTGTGAG 2491
Db 2461 CAGTGCGCTTGTGAG 2520
QY 2492 CAAAGTCTACAGTGTGAG 2551
Db 2521 CAAAGTCTACAGTGTGAG 2580
QY 2552 CAGCGTGTGACAG 2611
Db 2581 CAGCGTGTGACAG 2640
QY 2612 GGTCTCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2671
Db 2641 GGTCTCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2700

QY 2672 CTTCCTACAGACCTTGTGTCAG 2731
Db 2701 CTTCCTACAGACCTTGTGTCAG 2760
QY 2732 GACAGTGTGTAACCTTGTGTAAG 2791
Db 2761 GACAGTGTGTAACCTTGTGTAAG 2820
QY 2792 GCGGAGCCAGAGGCTATTTCCCTGTGCGGAGCTGTGATGATGATGATGATGATGATGATGAT 2851
Db 2821 GCGGAGCCAGAGGCTATTTCCCTGTGCGGAGCTGTGATGATGATGATGATGATGATGATGAT 2880
QY 2852 GCAGAGGAGACTTCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2911
Db 2881 GCAGAGGAGACTTCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940
QY 2912 CCGCTTCAGAGGCTGAG 2971
Db 2941 CCGCTTCAGAGGCTGAG 3000
QY 2972 TCACAGGCTGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3031
Db 3001 TCACAGGCTGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060
QY 3032 CAAAGTCTCTGCTGTCAG 3091
Db 3061 CAAAGTCTCTGCTGTCAG 3120
QY 3092 TCAGCAATTTGGAAGAACCCACATTTTCTGCGGCTCATCTGTGACAGAGGCTCCCT 3151
Db 3121 TCAGCAATTTGGAAGAACCCACATTTTCTGCGGCTCATCTGTGACAGAGGCTCCCT 3180
QY 3152 CTGCTATCTCATCTCTGTAAG 3211
Db 3181 CTGCTATCTCATCTCTGTAAG 3240
QY 3212 CCGGCTCTGTGCTGCGAG 3271
Db 3241 CCGGCTCTGTGCTGCGAG 3300
QY 3272 GACTGAGACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3331
Db 3301 GACTGAGACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360
QY 3332 GCTGAGTGGAGAGTCCCGGGAG 3391
Db 3361 GCTGAGTGGAGAGTCCCGGGAG 3420
QY 3392 ACTGCGCTGAGACTGTAAG 3451
Db 3421 ACTGCGCTGAGACTGTAAG 3480
QY 3452 GAGCAGACACAG 3511
Db 3481 GAGCAGACACAG 3540
QY 3512 CACACCCAGGCGGACAGCGCTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3571
Db 3541 CACACCCAGGCGGACAGCGCTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3600
QY 3572 CATGTCCGCTGAAAGGCTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3631
Db 3601 CATGTCCGCTGAAAGGCTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3660
QY 3632 GAGTGTCCAGACACAG 3691
Db 3661 GAGTGTCCAGACACAG 3720
QY 3692 GGGCGAGGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 3751
Db 3721 GGGCGAGGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 3780

[illegible]

QY	1868	GGAGACGAGGTCAGGCACGATCGGGAGACAGGCCGCCCTGCTGACGTCCAGACTCCG	1927
Db	1861	GGAAACAGAGGTCAGGCACACTCGGGAGACAGGCCGCCCTCTGACGTCCAGACTCCG	1920
QY	1928	CTTTCATCCCAAGCTCGAAGGGCTGCGCGCCGATTGTGAACATGACATGCTCGTGGAC	1987
Db	1921	CTTTCATCCCAAGCTCGAAGGGCTGCGCGCCGATTGTGAACATGACATGCTCGTGGAC	1980
QY	1988	CAGAAAGTTCGCGAGAAAGAGAGGGCCGAGGTCTACCTGAGGGTGAAGGACACTGTT	2047
Db	1981	CAGAAAGTTCGCGAGAAAGAGAGGGCCGAGGTCTACCTGAGGGTGAAGGACACTGTT	2040
QY	2048	CAGCGGTGCTAACTACAGAGCGGGGCGGCCGCCCTCTGAGGGCTGTGCTGGGG	2107
Db	2041	CAGCGGTGCTAACTACAGAGCGGGGCGGCCGCCCTCTGAGGGCTGTGCTGGGG	2100
QY	2108	CCTGGACGATATCCACAGGCGCTTGCGACATTGCTGCTGTGCGGGCCAGACCC	2167
Db	2101	CCTGGACGATATCCACAGGCGCTTGCGACATTGCTGCTGTGCGGGCCAGACCC	2160
QY	2168	GGCGGCTGAGCTGATTTGTCAAGTGGATGTGACGGGGCGCGTACGACACATCCGCCA	2191
Db	2161	GGCGGCTGAGCTGATTTGTCAAGTGGATGTGACGGGGCGCGTACGACACATCCGCCA	2220
QY	2192	GGACAGGCTCACGAGAGTATACGCGACAGATCATCTAAACCCCAAGACAGTACTCGTGG	2251
Db	2221	GGACAGGCTCACGAGAGTATACGCGACAGATCATCTAAACCCCAAGACAGTACTCGTGG	2280
QY	2252	TGCGATATCCGCTGATCCAGAAAGGCGGCCATGGGACGTGCGCAAGAGGCTTCAAGAGCA	2311
Db	2281	TGCGATATCCGCTGATCCAGAAAGGCGGCCATGGGACGTGCGCAAGAGGCTTCAAGAGCA	2340
QY	2312	CGGTCATCTACATGACAGACATCCACGCGTACATGACAGATTTGATGGCTCACCTGAGGA	2371
Db	2341	CGTCTCATCTACATGACAGACATCCACGCGTACATGACAGATTTGATGGCTCACCTGAGGA	2400
QY	2372	GACACAGCCCGTAGGAGATGCCGTGTCATGACGACAGAGCTCTCTCTGAATGAGCGCA	2431
Db	2401	GACACAGCCCGTAGGAGATGCCGTGTCATGACGACAGAGCTCTCTCTGAATGAGCGCA	2460
QY	2432	CAGTGGCCCTTGGAGAGCTTCTCTACAGCTTCTCATGTGCGACACAGCGCGTGGCATAGGGGG	2491
Db	2461	CAGTGGCCCTTGGAGAGCTTCTCTACAGCTTCTCATGTGCGACACAGCGCGTGGCATAGGGGG	2520
QY	2492	CAGATGCTACAGTCCAGTGTGCGAGGGAGTCCCGAGAGGCTCCATCTCTCCACAGCGCTCG	2551
Db	2521	CAGATGCTACAGTCCAGTGTGCGAGGGAGTCCCGAGAGGCTCCATCTCTCCACAGCGCTCG	2580
QY	2552	CAGCGTGTGCTACGAGGAGATGAGAGAAACAGCTGTTTGCGGGGATTTCGCGGGAGAGGGCT	2611
Db	2581	CAGCGTGTGCTACGAGGAGATGAGAGAAACAGCTGTTTGCGGGGATTTCGCGGGAGAGGGCT	2640
QY	2612	GCTCTCGGTTTGGTGGATGATTTCTTGTGTGTGACACTCAGCTCAGCCACGCGGAAAC	2671
Db	2641	GCTCTCGGTTTGGTGGATGATTTCTTGTGTGTGACACTCAGCTCAGCCACGCGGAAAC	2700
QY	2672	CTTTCCTCAGAGACCTGCTCGAGGTGTCCCTGAGTATGAGCTGCGGTGTGAATCTTGGGAA	2731
Db	2701	CTTTCCTCAGAGACCTGCTCGAGGTGTCCCTGAGTATGAGCTGCGGTGTGAATCTTGGGAA	2760
QY	2732	GACATGTGTAATCTTCCCTGTAGAGAAACAGAGCCCTGGGTGCGACGCTTGTGTACAGAT	2791
Db	2761	GACATGTGTAATCTTCCCTGTAGAGAAACAGAGCCCTGGGTGCGACGCTTGTGTACAGAT	2820
QY	2792	GGCGGCCACAGGGCTATTTCCTCGTGGTGGGCGCTGTGCTGGATACCGGACCCGGAGGT	2851
Db	2821	GGCGGCCACAGGGCTATTTCCTCGTGGTGGGCGCTGTGCTGGATACCGGACCCGGAGGT	2880
QY	2852	GGAGAGGCACTACTCCAGTATGACCGCGACATCTACAGAGCAGTCTACATTCACCG	2911
Db	2881	GGAGAGGCACTACTCCAGTATGACCGCGACATCTACAGAGCAGTCTACATTCACCG	2940

OY	2108	CCTGGACGATATTCACAGAGGCTCGGGACACTTCGTCGTGCGTGGGGGCCACGAGACC	2167
Db	2101	CCTGGACGATATTCACAGAGGCTCGGGACACTTCGTCGTGCGTGGGGGCCACGAGACC	2160
OY	2168	GGCGCTGAGCTGTA-----CATCCCCA	2191
Db	2161	GGCGCTGAGCTGACTTTGTCAAGGTGATGACGGGGGTTACGACACATCCCCCA	2220
OY	2192	GGACAGGCTACAGAGGTCTATCGCAGACATCATCAAAACCCAGAACAGTACTGCTGCG	2251
Db	2221	GGACAGGCTACAGAGGTCTATCGCAGACATCATCAAAACCCAGAACAGTACTGCTGCG	2280
OY	2252	TGCGATAGCCGTGGTCCAGAAAGCCGCCCATGGGGACGTGCGCAAGGGCTTCAGAGCA	2311
Db	2281	TGCGATATCCGTGGTCCAGAAAGCCGCCCATGGGGACGTGCGCAAGGGCTTCAGAGCA	2340
OY	2312	CGTCTTACCTTGCACAGACCTCCAGCCGTAACATGCGACAGTTCGTGGCTCACCTGACAGA	2371
Db	2341	CGTCTTACCTTGCACAGACCTCCAGCCGTAACATGCGACAGTTCGTGGCTCACCTGACAGA	2400
OY	2372	GACCAGCCCGCTGAGGGATATCCGTGCTCATCGACAGAGACTCCTCCGTGATGAGCCAG	2431
Db	2401	GACCAGCCCGCTGAGGGATATCCGTGCTCATCGACAGAGACTCCTCCGTGATGAGCCAG	2460
OY	2432	CAGTGGCCTCTGCACGCTCTTCCCTAGCGTTCATGTCCACACGGCGTGGCGATCAGGG	2491
Db	2461	CAGTGGCCTCTGCACGCTCTTCCCTAGCGTTCATGTCCACACGGCGTGGCGATCAGGG	2520
OY	2492	CAAGTCTTACGTCCAGTGCACAGGGGATCCCGCAGGGCTTCATCTCTCACGCTGCTCTG	2551
Db	2521	CAAGTCTTACGTCCAGTGCACAGGGGATCCCGCAGGGCTTCATCTCTCACGCTGCTCTG	2580
OY	2552	CAGGCTGTGCTACGGGCGACATGGAAGAACAAAGCTGTTGCGGGGATTCGGCGGACGGGCT	2611
Db	2581	CAGGCTGTGCTACGGGCGACATGGAAGAACAAAGCTGTTGCGGGGATTCGGCGGACGGGCT	2640
OY	2612	GCTCCTCGTTGGTGGATATTTCTTGTGGGACACCTCACACACCCAGCGGAAAC	2671
Db	2641	GCTCCTCGTTGGTGGATATTTCTTGTGGGACACCTCACACACCCAGCGGAAAC	2700
OY	2672	CTTCCCTCAGGACCCGTGGTCCGAGGTGCCCTGAGTATGGCTCCGTGGAACTTGGCGAA	2731
Db	2701	CTTCCCTCAGGACCCGTGGTCCGAGGTGCCCTGAGTATGGCTCCGTGGAACTTGGCGAA	2760
OY	2732	GACAGTGTGAATCTCCCTGTAGAGACGAGGCCCTGGGTGGACGCTTTTGTTCAGAT	2791
Db	2761	GACAGTGTGAATCTCCCTGTAGAGACGAGGCCCTGGGTGGACGCTTTTGTTCAGAT	2820
OY	2792	GGCGGCCACAGGGCTATTCGCCGGTGGGGGCGCTGCTGCGGTATACCGGACCTGGAGGT	2851
Db	2821	GGCGGCCACAGGGCTATTCGCCGGTGGGGGCGCTGCTGCGGTATACCGGACCTGGAGGT	2880
OY	2852	GCAGAGCGACTACTCCAGCTATCCCGGACCTTCATACAGAGCAGTCTCACCTTCAACG	2911
Db	2881	GCAGAGCGACTACTCCAGCTATCCCGGACCTTCATACAGAGCAGTCTCACCTTCAACG	2940
OY	2912	CGGCTTAAAGCTGGGAGAACATGCGTGCACAACTCTTTGGGGCTTGGCGGTGAAGTG	2971
Db	2941	CGGCTTAAAGCTGGGAGAACATGCGTGCACAACTCTTTGGGGCTTGGCGGTGAAGTG	3000
OY	2972	TTCACAGCTTCTTGATTTGGAGGTGAACAGCCTCCAGACGGTGTGACCAACATCTA	3031
Db	3001	TTCACAGCTTCTTGATTTGGAGGTGAACAGCCTCCAGACGGTGTGACCAACATCTA	3060
OY	3032	CAAGATCTCTGCTCAGAGCGTACAGGTTTACAGCATGTGTCGACAGTCCCATTTCA	3091
Db	3061	CAAGATCTCTGCTCAGAGCGTACAGGTTTACAGCATGTGTCGACAGTCCCATTTCA	3120
OY	3092	TCAAGCATTTTGAAGAACCCACATTTTCCCTGGCGCTCATCTCTGACAGGCGCTCCCT	3151
Db	3121	TCAAGCATTTTGAAGAACCCACATTTTCCCTGGCGCTCATCTCTGACAGGCGCTCCCT	3180
OY	3152	CTGCTACTCATCTCTGAAGCCAGAACGACGAGATGTGCTGGGGGCCAAGGGCGCCG	3211

Db	3181	CTGCTACTCCATCTCTGAAACCGAAGAACGAGGATGTGCTGGGGGCCCAAGGGCGCCG	3240
Qy	3212	CGGGCCCTGTGCCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCATTTCTGCTCAAGCT	3271
Db	3241	CGGGCCCTGTGCCCTCCGAGGCGGTGCAAGTGGGTGTGCCACCAAGCATTTCTGCTCAAGCT	3300
Qy	3272	GACTTCGACACCGGTGTACCTTACCTAGCTGCCACTCCTGGGGGTCACTCAGACAGCCCAAGCGCA	3331
Db	3301	GACTTCGACACCGGTGTACCTTACCTAGCTGCCACTCCTGGGGGTCACTCAGACAGCCCAAGCGCA	3360
Qy	3332	GCTAAGTTCGGAAGGTCCCGGGGAGACAGCGGTGAGTGGCCCTGGAGGGCGGAGCAACCCGGC	3391
Db	3361	GCTAAGTTCGGAAGGTCCCGGGGAGACAGCGGTGAGTGGCCCTGGAGGGCGGAGCAACCCGGC	3420
Qy	3392	ACTGCCCCAGACTTTCAAAGACCAATCTGTGATGTAGTGCCACCCGCCACAGCCAGCGCGA	3451
Db	3421	ACTGCCCCAGACTTTCAAAGACCAATCTGTGATGTAGTGCCACCCGCCACAGCCAGCGCGA	3480
Qy	3452	GAGCAGACACCCAGCAGCAGCCCTGTACACCCCGGGCTCTACGTCCCAAGGAGAGAGGGCGCC	3511
Db	3481	GAGCAGACACCCAGCAGCAGCCCTGTACACCCCGGGCTCTACGTCCCAAGGAGAGAGGGCGCC	3540
Qy	3512	CACACCCAGGCGCCGACACCGTGTGGAGTCTGAGGCGCTGAGTGAAGTATTGGCCGAGAGCGTG	3571
Db	3541	CACACCCAGGCGCCGACACCGTGTGGAGTCTGAGGCGCTGAGTGAAGTATTGGCCGAGAGCGTG	3600
Qy	3572	CATGTCCGGCTGAAAGGCTGAGTGTCCGGCTGAGGGCTGAGCGAGTGTCCACAGCAAGGAGCT	3631
Db	3601	CATGTCCGGCTGAAAGGCTGAGTGTCCGGCTGAGGGCTGAGCGAGTGTCCACAGCAAGGAGCT	3660
Qy	3632	GAGTGTCCAGCACAACCTGCGCTTACTTCTCCACAGGCTGTGGCGCTGGCTCCACCCCA	3691
Db	3661	GAGTGTCCAGCACAACCTGCGCTTACTTCTCCACAGGCTGTGGCGCTGGCTCCACCCCA	3720
Qy	3692	GGGCGACCTTTTCTTCCACAGAGGCCGGGCTTCCACTCCCCACATAGGAATATGTCCATTC	3751
Db	3721	GGGCGACCTTTTCTTCCACAGAGGCCGGGCTTCCACTCCCCACATAGGAATATGTCCATTC	3780
Qy	3752	CCAGATTTGGCATTGTTTCAACCCCTCGCCCTGCTTTGGCTTCCACCCCAACATTC	3811
Db	3781	CCAGATTTGGCATTGTTTCAACCCCTCGCCCTGCTTTGGCTTCCACCCCAACATTC	3840
Qy	3812	AGGTGAGACCCCTGAGAGAGACCTCTGGAGCTCTGGGAATTTGGAGTACCACCAAGGTGTG	3871
Db	3841	AGGTGAGACCCCTGAGAGAGACCTCTGGAGCTCTGGGAATTTGGAGTACCACCAAGGTGTG	3900
Qy	3872	CCCTGTACACAGCGAGAGACCTCGACCTGGAATGGGGGTCCCTGTGGGTCAAAATTTGGGG	3931
Db	3901	CCCTGTACACAGCGAGAGACCTCGACCTGGAATGGGGGTCCCTGTGGGTCAAAATTTGGGG	3960
Qy	3932	GAGTGTGCTGTGGAGTAAATACTGAATATATGAGTATTTTTCAGTTTGGAAAAA	3991
Db	3961	GAGTGTGCTGTGGAGTAAATACTGAATATATGAGTATTTTTCAGTTTGGAAAAA	4020
Qy	3992	AAAAAAAAAAAAAAAA 4006	
Db	4021	AAAAAAAAAAAAAAAA 4035	
RESULT 8			
US-08-974-584C-117			
Sequence 117, Application US/08974584C			
GENERAL INFORMATION:			
APPLICANT: Cech, Thomas R.			
Lingner, Joachim			
Nakamura, Toru			
Chapman, Karen B.			
Morin, Gregg B.			
Harley, Calvin B.			
Andrews, William H.			
TITLE OF INVENTION: Telomerase Reverse Transcriptase			
NUMBER OF SEQUENCES: 479			

OY	1268	GTCCCTCAGGSGGTGCTCTCTCAAGACGACTGCCGTGCGAGCTGGGGTACCCACAGC	1327
Db	1261	GTGCCCTCAGGSGGTGCTCTCTCAAGACGACTGCCGTGCGAGCTGGGGTACCCACAGC	1320
OY	1328	AGCCGGTCTGTGTCGCCGGGAGAAAGCCCAAGGGCTCTGTGGGGGGCCCCGAGAGAGAGA	1387
Db	1321	AGCCGGTCTGTGTCGCCGGGAGAAAGCCCAAGGGCTCTGTGGGGGGCCCCGAGAGAGAGA	1380
OY	1388	CACAGACCCCCCGGACCTTGGGTGCGAGCTGTCCGCCACAGCAGACCCCTGTGCAAGTGA	1447
Db	1381	CACAGACCCCCCGGACCTTGGGTGCGAGCTGTCCGCCACAGCAGACCCCTGTGCAAGTGA	1440
OY	1448	CGGCTTGTGTGGGGCTTGCTCGCGCGGGCTGGTGTCCCGAGCCCTCTGTGGGCTCCAGCA	1507
Db	1441	CGGCTTGTGTGGGGCTTGCTCGCGCGGGCTGGTGTCCCGAGCCCTCTGTGGGCTCCAGCA	1500
OY	1508	CAAGGAACGGCGCTTCTCAAGGAACCAAGAAAGTTCAATCTCCCTGGGGAAGCATGCCAA	1567
Db	1501	CAAGGAACGGCGCTTCTCAAGGAACCAAGAAAGTTCAATCTCCCTGGGGAAGCATGCCAA	1560
OY	1568	GCTCTCGCTGCAGAGAGTGAAGTGAAGATGAAGCGGCGGAGCTCGGCTGGGCTCCGAG	1627
Db	1561	GCTCTCGCTGCAGAGAGTGAAGTGAAGATGAAGCGGCGGAGCTCGGCTGGGCTCCGAG	1620
OY	1628	GAGCCACAGGGGTGGCTGTTCGGGCCGACAGCAGCTGTGCGTGAAGAGATCTGGC	1687
Db	1621	GAGCCACAGGGGTGGCTGTTCGGGCCGACAGCAGCTGTGCGTGAAGAGATCTGGC	1680
OY	1688	CAAGTTCTGCACCTGGCTGATGAGTGTGTAAGTCTGTGACGCTGTCAAGCTCTTCTTTTA	1747
Db	1681	CAAGTTCTGCACCTGGCTGATGAGTGTGTAAGTCTGTGACGCTGTCAAGCTCTTCTTTTA	1740
OY	1748	TGTACAGGAGACCAAGTTGAAAAAAGAGGGCTCTTTTTCACGCGGAAGAGTCTGGAG	1807
Db	1741	TGTACAGGAGACCAAGTTGAAAAAAGAGGGCTCTTTTTCACGCGCGAGTGTCTGGAG	1800
OY	1808	CAAGTTCAAAGCAATTGGAAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTC	1867
Db	1801	CAAGTTCAAAGCAATTGGAAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTC	1860
OY	1868	GGAGCAGAGAGTCAAGCAGATGGGGAAGCCAGAGCCCGCCCTGTGACAGTCCAGACTCCG	1927
Db	1861	GGAGCAGAGAGTCAAGCAGATGGGGAAGCCAGAGCCCGCCCGCTGTGACAGTCCAGACTCCG	1920
OY	1928	CTTCATCTCCCAAGCTCAGCGGCTGCGGCGCGATGTGGAACATGAGCTACGTCTGGGAGC	1987
Db	1921	CTTCATCTCCCAAGCTCAGCGGCTGCGGCGCGATGTGGAACATGAGCTACGTCTGGGAGC	1980
OY	1988	CAGAACTTCGCGCAGAGAAAAAGAGGGCCGAGGCTCTCACCTCGAGGGTGAAGGCACTGTT	2047
Db	1981	CAGAACTTCGCGCAGAGAAAAAGAGGGCCGAGGCTCTCACCTCGAGGGTGAAGGCACTGTT	2040
OY	2048	CAGGCTGCTCAACTAGAGAGGGGGCGGGCGCCCGGCTCTGTGGGCGCTCTGTGTGCG	2107
Db	2041	CAGGCTGCTCAACTAGAGAGGGGGCGGGCGCCCGGCTCTGTGGGCGCTCTGTGTGCG	2100
OY	2108	CCTGAGAGATATCCACAGGGCTGCGGCGCACTTCGTCGTGCGGTGCGGGGCCAGAGACC	2167
Db	2101	CCTGAGAGATATCCACAGGGCTGCGGCGCACTTCGTCGTGCGGTGCGGGGCCAGAGACC	2160
OY	2168	GCCGCGCTGAGCTGA-----CATCCGCCA	2191
Db	2161	GCCGCGCTGAGCTGA-----CATCCGCCA	2220
OY	2192	GGAGAGGCTCAGGAGGTCAATGCCAGCATCATCAAAACCCAGAAACAGTACTGCTGCG	2251
Db	2221	GGAGAGGCTCAGGAGGTCAATGCCAGCATCATCAAAACCCAGAAACAGTACTGCTGCG	2280
OY	2252	TTCGGTATCCGCTGCTCAGAAAGGCCCGCATATGGGCAAGTCCGCAAGGGCTTCAAGAGCA	2311
Db	2281	TTCGGTATCCGCTGCTCAGAAAGGCCCGCATATGGGCAAGTCCGCAAGGGCTTCAAGAGCA	2340
OY	2312	CGTCTTACCTTGACAGACCTCCAGCCGTAACATGGACAGTTCGTGGCTCACTGTGACGA	2371

Db	2341	CGTCTCACTTGGACAACGCTCCAGCGCGTATCAATGCGACAAGTTCTGTGGCTCACTCCAGCA	2400
QY	2372	GACCGAGCCCGGTGAGGGATGGCCGTCGATCGAGACAGACTCTCCCTCAATGAGGCGAC	2431
Db	2401	GACCAAGCCCGGTGAGGGATGCCGTGTCATCGACGACAGAGCTCTCTCTAATGAGGCGAC	2460
QY	2432	CAGTGGCCCTCTTCGACGCTCTTCCCTACGCTTCATGTGCGCACACAGCGCCGTGCGCATCAGGGG	2491
Db	2461	CAGTGGCCCTCTTCGACGCTCTTCCCTACGCTTCATGTGCGCACACAGCGCCGTGCGCATCAGGGG	2520
QY	2492	CAAGTCTTACGTTCCAGTGCACAGGGGATCCCGCAGGGGCTCCATCTCTCTCCAGCTCTCTG	2551
Db	2521	CAAGTCTTACGTTCCAGTGCACAGGGGATCCCGCAGGGGCTCCATCTCTCTCCAGCTCTCTG	2580
QY	2552	CAGCCTGTGCTAAGGGGACACATGGAGAACAGCTGTTGGGGGGATTTCCGCGGGAGGGGCT	2611
Db	2581	CAGCCTGTGCTAAGGGGACACATGGAGAACAGCTGTTGGGGGGATTTCCGCGGGAGGGGCT	2640
QY	2612	GCTCCTGTGCTTGGTGTGATATTTCTGTGTGTGATCACTCACCTCACACGCGCAAAAC	2671
Db	2641	GCTCCTGTGCTTGGTGTGATATTTCTGTGTGTGATCACTCACCTCACACGCGCAAAAC	2700
QY	2672	CTTCTCTAGAGACCCCTGTGCTCCGAGGTGTCCCTGAGTATGAGCTCCGTGTGTAACTTCCGGA	2731
Db	2701	CTTCTCTAGAGACCCCTGTGCTCCGAGGTGTCCCTGAGTATGAGCTCCGTGTGTAACTTCCGGA	2760
QY	2732	GACAGTGTGATCTTCCCTGTAGAAGACAGAGCCCTTGGGTGGCAGGCTTTTGTTCAT	2791
Db	2761	GACAGTGTGATCTTCCCTGTAGAAGACAGAGCCCTTGGGTGGCAGGCTTTTGTTCAT	2820
QY	2792	GCCGAGCCACAGGCTTATTTCCCTGTGATGACGCGCTGTGTGTGATATCCCGACCTCGAGAGT	2851
Db	2821	GCCGAGCCACAGGCTTATTTCCCTGTGATGACGCGCTGTGTGTGATATCCCGACCTCGAGAGT	2880
QY	2852	GCAGAGCAGCTACTCCAGCTATGCCCCGAGACCTTCATCAGAGCCAGTCTTCACTTCAACCG	2911
Db	2881	GCAGAGCAGCTACTCCAGCTATGCCCCGAGACCTTCATCAGAGCCAGTCTTCACTTCAACCG	2940
QY	2912	CGGCTTCAAGGCTGGGAGAACATGGTGTGCAAACTTTTGGGGTCTTGGCGCTGTGAAGT	2971
Db	2941	CGGCTTCAAGGCTGGGAGAACATGGTGTGCAAACTTTTGGGGTCTTGGCGCTGTGAAGT	3000
QY	2972	TCACAGCCTGTTTGTGATTTTGCAGGTGAGGACACCTTCCAGAGGGTGTGCAACACATCTA	3031
Db	3001	TCACAGCCTGTTTGTGATTTTGCAGGTGAGGACACCTTCCAGAGGGTGTGCAACACATCTA	3060
QY	3032	CAAGATCCTCTCTGTGTCGAGGCGTACAGAGTTTCACGCGATGTGTGTGTCAGCTCCCAATTTCA	3091
Db	3061	CAAGATCCTCTCTGTGTCGAGGCGTACAGAGTTTCACGCGATGTGTGTGTCAGCTCCCAATTTCA	3120
QY	3092	TCACAGAGTTTGGAGAAACCCCAACATTTTTCCTGCGCGCTCATCTCTGACAGGGCTCCCT	3151
Db	3121	TCACAGAGTTTGGAGAAACCCCAACATTTTTCCTGCGCGCTCATCTCTGACAGGGCTCCCT	3180
QY	3152	CTGCTACTCCATCTCTGAAACCCCAAGAACGAGGAGTGTGCTGGGGGCAAGGGGCGCGC	3211
Db	3181	CTGCTACTCCATCTCTGAAACCCCAAGAACGAGGAGTGTGCTGGGGGCAAGGGGCGCGC	3240
QY	3212	CGGCGCTCTGTGCGCCGAGGCGGTGACGTGTGTGTCACACAGCAATTTCTGTCTCAAGCT	3271
Db	3241	CGGCGCTCTGTGCGCCGAGGCGGTGACGTGTGTGTCACACAGCAATTTCTGTCTCAAGCT	3300
QY	3272	GACTGTGACACCGTGTACACTTACCTGTCCCTGTGGGGGTACTTCAGACAGCCCAAGACCA	3331
Db	3301	GACTGTGACACCGTGTACACTTACCTGTCCCTGTGGGGGTACTTCAGACAGCCCAAGACCA	3360
QY	3332	GCTGTGTGTGAAAGTCTCCCGGGAGACAGCGTGTGCTGTGAGGGCGGACAGCCACCGGCG	3391
Db	3361	GCTGTGTGTGAAAGTCTCCCGGGAGACAGCGTGTGCTGTGAGGGCGGACAGCCACCGGCG	3420
QY	3392	ACTGCGCTCAAGACTTTCAAAGACATCTCTGACTGATGGCACCGGCGCCACAGCAGGCGGA	3451

Db 2821 GATGCCGGCCGACGCTATTTCCCTGTCGGGCTGCTGCTGATACCCGACCTGGA 2880
Qy 2849 GGTGACAGAGCCTACTCTACAGCTATGCCCCGACCTCTACAGACAGCTCTCA 2908
Db 2881 GGTGACAGAGCCTACTCTACAGCTATGCCCCGACCTCTACAGACAGCTCTCA 2940
Qy 2909 CGCGGGCTTCAAGGCTGGAGAAACATGCTGCAACTCTTTGGGGCTCTGAA 2968
Db 2941 CCGCGGCTTCAAGGCTGGAGAAACATGCTGCAACTCTTTGGGGCTCTGAA 3000
Qy 2969 GGTGACAGAGCCTGATTTCTGATTTGAGTGAACACCTCCAGAGCTGACACACAT 3028
Db 3001 GGTGACAGAGCCTGATTTCTGATTTGAGTGAACACCTCCAGAGCTGACACACAT 3060
Qy 3029 CTACAGATCTCTCTGTCAGAGCTGATGCTTTCAGCATGCTGCTGAGTCTCCAT 3088
Db 3061 CTACAGATCTCTCTGTCAGAGCTGATGCTTTCAGCATGCTGCTGAGTCTCCAT 3120
Qy 3089 TCTATGAGAGTTTGGAGAAACCCACATTTTCTGCGGCTCATCTGTACAGGCTC 3148
Db 3121 TCTATGAGAGTTTGGAGAAACCCACATTTTCTGCGGCTCATCTGTACAGGCTC 3180
Qy 3149 CCTCTGCTACTCTCTGTAAGAACCCAGAGATGCTGCTGGGGCCAGAGGCTC 3208
Db 3181 CCTCTGCTACTCTCTGTAAGAACCCAGAGATGCTGCTGGGGCCAGAGGCTC 3240
Qy 3209 CGCGGGCTTCCCTCGAGGCTGACAGTGTGCTGACACACATTTCTGCTCA 3268
Db 3241 CGCGGGCTTCCCTCGAGGCTGACAGTGTGCTGACACACATTTCTGCTCA 3300
Qy 3269 GGTGACAGAGCCTGATTTCTGATTTGAGTGAACACCTCCAGAGCTGACACACAT 3328
Db 3301 GGTGACAGAGCCTGATTTCTGATTTGAGTGAACACCTCCAGAGCTGACACACAT 3360
Qy 3329 GCAGCTGAGTGAAGTCTCCGGGGGACGAGCTGATCTCCCTGGAGGCTGACACACAT 3388
Db 3361 GCAGCTGAGTGAAGTCTCCGGGGGACGAGCTGATCTCCCTGGAGGCTGACACACAT 3420
Qy 3389 GGTGACAGAGCCTGATTTCTGATTTGAGTGAACACCTCCAGAGCTGACACACAT 3448
Db 3421 GGTGACAGAGCCTGATTTCTGATTTGAGTGAACACCTCCAGAGCTGACACACAT 3480
Qy 3449 CGAGAGAGAGACACAGAGCCTGATGAGGCTGATGCTGACAGAGAGAGGCTC 3508
Db 3481 CGAGAGAGAGACACAGAGCCTGATGAGGCTGATGCTGACAGAGAGAGGCTC 3540
Qy 3509 GGTGACAGAGCCTGATTTCTGATTTGAGTGAACACCTCCAGAGCTGACACACAT 3568
Db 3541 GGTGACAGAGCCTGATTTCTGATTTGAGTGAACACCTCCAGAGCTGACACACAT 3600
Qy 3569 GGTGACAGAGCCTGATTTCTGATTTGAGTGAACACCTCCAGAGCTGACACACAT 3628
Db 3601 GGTGACAGAGCCTGATTTCTGATTTGAGTGAACACCTCCAGAGCTGACACACAT 3660
Qy 3629 GGTGACAGAGCCTGATTTCTGATTTGAGTGAACACCTCCAGAGCTGACACACAT 3688
Db 3661 GGTGACAGAGCCTGATTTCTGATTTGAGTGAACACCTCCAGAGCTGACACACAT 3720
Qy 3689 CGAGAGAGAGACACAGAGCCTGATGAGGCTGATGCTGACAGAGAGAGGCTC 3748
Db 3721 CGAGAGAGAGACACAGAGCCTGATGAGGCTGATGCTGACAGAGAGAGGCTC 3780
Qy 3749 TCCCGAGATTTGCGATTTTCAACCTTGGCTGCTGCTTCTTTCACACCTCCACCA 3808
Db 3781 TCCCGAGATTTGCGATTTTCAACCTTGGCTGCTGCTTCTTTCACACCTCCACCA 3840
Qy 3809 TCCCGAGATTTGCGATTTTCAACCTTGGCTGCTGCTTCTTTCACACCTCCACCA 3868
Db 3841 TCCCGAGATTTGCGATTTTCAACCTTGGCTGCTGCTTCTTTCACACCTCCACCA 3900
Qy 3869 GGTGACAGAGCCTGATTTCTGATTTGAGTGAACACCTCCAGAGCTGACACACAT 3928
Db 3901 GGTGACAGAGCCTGATTTCTGATTTGAGTGAACACCTCCAGAGCTGACACACAT 3960

Qy 3929 GGGAGAGTCTGTGGAGTAATACTGATATATGAGTTTTCAGTTTGA 3988
Db 3961 GGGAGAGTCTGTGGAGTAATACTGATATATGAGTTTTCAGTTTGA 4020
Qy 3989 AAA 3991
Db 4021 AAA 4023

RESULT 10
US-08-911-312-1
Sequence 1, Application US/08911312
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morlin, Gregg B.
APPLICANT: Harley, Calvin B.
TITLE OF INVENTION: Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-Aug-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
ATTORNEY/AGENT INFORMATION:
NAME: Binhorn, Gregory P.
REGISTRATION/DOCKET NUMBER: 38,440
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 782..417
OTHER INFORMATION: /product= "human telomerase reverse transcriptase (hTR)"
OTHER INFORMATION: /note= "cDNA contained in plasmid"
OTHER INFORMATION: pGRN121
US-08-911-312-1

Query Match 99.1%; Score 3970; DB 13; Length 7029;
Best Local Similarity 99.1%; Pred. No. 1.7e-139;
Matches 3980; Conservative 0; Mismatches 1; Indels 36; Gaps 1;

Qy 6 AGGACAGCGCTGCTCTGCTGCGACAGTGGAGAGCCCTGCGCCAGCCAGCCCGCGATG 65
Db 725 ACGGAGCGGTGCTCTGCTGCGACAGTGGAGAGCCCTGCGCCAGCCAGCCCGCGATG 784
Qy 66 CCGCGCGCTCCCGCTGCGGAGCGCTGCGCTCTGCTGCGGACGACCTACCGGAGGTG 125
Db 785 CCGCGCGCTCCCGCTGCGGAGCGCTGCGCTCTGCTGCGGACGACCTACCGGAGGTG 844
Qy 126 CTGCCGTGCGGACGCTGCTGCGGAGCGCTGCGGAGCGCTGCGGAGCGCTGCGGAGCG 185
Db 845 CTGCCGTGCGGACGCTGCTGCGGAGCGCTGCGGAGCGCTGCGGAGCGCTGCGGAGCG 904
Qy 186 GGGAGACCGGCGGCTTTCGCGCGCTGCTGCGGAGCGCTGCGGAGCGCTGCGGAGCG 245
Db 905 GGGAGACCGGCGGCTTTCGCGCGCTGCTGCGGAGCGCTGCGGAGCGCTGCGGAGCG 964
Qy 246 GCAGCG 305
Db 965 GCAGCG 1024
Qy 306 GCCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 365
Db 1025 GCCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1084
Qy 366 GCGCTGTGTGAGCG 425
Db 1085 GCGCTGTGTGAGCG 1144
Qy 426 TACCTGCGGACAGGTCAGCGGACGCTGCGGAGCGCGCGCGCGCGCGCGCGCGCG 485
Db 1145 TACCTGCGGACAGGTCAGCGGACGCTGCGGAGCGCGCGCGCGCGCGCGCGCGCG 1204
Qy 486 CGCGCGGTGCGGAGCGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 545
Db 1205 CGCGCGGTGCGGAGCGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1264
Qy 546 GTGCTGTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 605
Db 1265 GTGCTGTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1324
Qy 606 ACTAGGCG 665
Db 1325 ACTAGGCG 1384
Qy 666 GCGTGGAAACATAGGTCAGGAGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 725
Db 1385 GCGTGGAAACATAGGTCAGGAGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1444
Qy 726 AGGAGCG 785
Db 1445 AGGAGCG 1504
Qy 786 GCTGCG 845
Db 1505 GCTGCG 1564
Qy 846 ACGGTCGAGCGAGTGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 905
Db 1565 ACGGTCGAGCGAGTGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1624

Qy 906 GCCACTCTTTGGAGGTGCGCTCTGCGACGCGCCACCTCCACCCATCCGTGGGCGCG 965
Db 1625 GCCACTCTTTGGAGGTGCGCTCTGCGACGCGCCACCTCCACCCATCCGTGGGCGCG 1684
Qy 966 CAGCACACG 1025
Db 1685 CAGCACACG 1744
Qy 1026 CCGCGCGGTGTCGCGGAGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1085
Db 1745 CCGCGCGGTGTCGCGGAGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1804
Qy 1086 CCGCGCGCTCTCTACTAGCTCTGTCGAGGCGCCAGCTGCTGCTGCTGCTGCTGCTG 1145
Db 1805 CCGCGCGCTCTCTACTAGCTCTGTCGAGGCGCCAGCTGCTGCTGCTGCTGCTGCTG 1864
Qy 1146 GAGACCATCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1205
Db 1865 GAGACCATCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1924
Qy 1206 CTGCCCGAGCGCTACTGCGCAATGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 1265
Db 1925 CTGCCCGAGCGCTACTGCGCAATGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 1984
Qy 1266 CAGTCCCGCTACGCGGCTCTCTCAAGACGACCTGCGCGCTGCGAGCTGCGGTCACCCCA 1325
Db 1985 CAGTCCCGCTACGCGGCTCTCTCAAGACGACCTGCGCGCTGCGAGCTGCGGTCACCCCA 2044
Qy 1326 GCAGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1385
Db 2045 GCAGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2104
Qy 1386 GACACAGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1445
Db 2105 GACACAGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2164
Qy 1446 TACGCGCTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1505
Db 2165 TACGCGCTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2224
Qy 1506 CACAACGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1565
Db 2225 CACAACGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2284
Qy 1566 AAGCTCTGCTGACAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1625
Db 2285 AAGCTCTGCTGACAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2344
Qy 1626 AGGAGCGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1685
Db 2345 AGGAGCGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2404
Qy 1686 GCCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1745
Db 2405 GCCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2464
Qy 1746 TATGTCAGGAGACACCTTTCAAAGAACAGGCTCTTTCCTACCGGAAGATGCTGCG 1805
Db 2465 TATGTCAGGAGACACCTTTCAAAGAACAGGCTCTTTCCTACCGGAAGATGCTGCG 2524
Qy 1806 AGCAAGTTGCAAGCATTGGAATCAGACAGCATTGGAAGAGGCTGCTGCTGCTGCTG 1865
Db 2525 AGCAAGTTGCAAGCATTGGAATCAGACAGCATTGGAAGAGGCTGCTGCTGCTGCTG 2584
Qy 1866 TCGGAGAGAGGTCAGGACACATCGGGAACCGCGCGCGCGCGCGCGCGCGCGCGCG 1925
Db 2585 TCGGAGAGAGGTCAGGACACATCGGGAACCGCGCGCGCGCGCGCGCGCGCGCGCG 2644
Qy 1926 CGCTTCATCCCAAGCGCTGAGCGGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1985
Db 2645 CGCTTCATCCCAAGCGCTGAGCGGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTG 2704

Db 1865 GAGACCATCTTTTGTGGTTCCAGGCCCCGTGATGCCAGGACATCCCCGAGTTGCCCCGC 1924
 QY 1206 CTGCCCCAGCCCTACTGGCAAAATGCGGCCCTGTTTCTGGAGCTGTTTGGAAACACGCG 1265
 Db 1925 CTGCCCCAGCCCTACTGGCAAAATGCGGCCCTGTTTCTGGAGCTGTTTGGAAACACGCG 1984
 QY 1266 CAGTCCCCCTAGGGGGTGTCTCTCAAGACGACAGTCCGCTGAGACTCCGCTCACCCCA 1325
 Db 1985 CAGTCCCCCTAGGGGGTGTCTCTCAAGACGACAGTCCGCTGAGACTCCGCTCACCCCA 2044
 QY 1326 GCAGCCGCTGTGTGTGCCCCGAGAAAGCCAGAGGCTCTGTGCGGCCGCCAGAGAGAG 1385
 Db 2045 GCAGCCGCTGTGTGTGCCCCGAGAAAGCCAGAGGCTCTGTGCGGCCGCCAGAGAGAG 2104
 QY 1386 GACACAGACCCCCGCTGCGCTGTGTCAGAGCTGTCGCCAGACACAGACCCCCCTGCGAGGTG 1445
 Db 2105 GACACAGACCCCCGCTGCGCTGTGTCAGAGCTGTCGCCAGACACAGACCCCCCTGCGAGGTG 2164
 QY 1446 TACGGCTTCGTGCGGGGCTGCGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 1505
 Db 2165 TACGGCTTCGTGCGGGGCTGCGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 2224
 QY 1506 CACAAACGAGCGCGCTTCTCTAGAGAACACCAAGATTCTCTCCCTGGGGAAGCATGCC 1565
 Db 2225 CACAAACGAGCGCGCTTCTCTAGAGAACACCAAGATTCTCTCCCTGGGGAAGCATGCC 2284
 QY 1566 AAGCTCTGCTGACAGAGCTGAGCTGGAAGATGAGCGTGGGGACTGCGCTTGGCTGCGC 1625
 Db 2285 AAGCTCTGCTGACAGAGCTGAGCTGGAAGATGAGCGTGGGGACTGCGCTTGGCTGCGC 2344
 QY 1626 AAGAGCCCCAGGGGTTGGCTGTGTTCCGGCCGACAGAGACCGTGTGCGTAGAGATCTCG 1685
 Db 2345 AAGAGCCCCAGGGGTTGGCTGTGTTCCGGCCGACAGAGACCGTGTGCGTAGAGATCTCG 2404
 QY 1686 GCCAAGTCTGCACTGGCTGATGATGTGTACCTGCTGAGCTGCTCAGGCTTCTT 1745
 Db 2405 GCCAAGTCTGCACTGGCTGATGATGTGTACCTGCTGAGCTGCTCAGGCTTCTT 2464
 QY 1746 TATGTACAGAGAGACACGCTTAAAGAAACAGGCTCTTTTCTACCGGAAGTCTCG 1805
 Db 2465 TATGTACAGAGAGACACGCTTAAAGAAACAGGCTCTTTTCTACCGGAAGTCTCG 2524
 QY 1806 ACGAAGTTGCAAAACATTGGAATCAGACAGCACTTTGAAGAGGTTGAGTGGGGAGTGG 1865
 Db 2525 ACGAAGTTGCAAAACATTGGAATCAGACAGCACTTTGAAGAGGTTGAGTGGGGAGTGG 2584
 QY 1866 TGGGAAGAGAGGTCAGGCAAGTCGGAAGCCAGGCGCCCTGCTGACGTCAGACTC 1925
 Db 2585 TGGGAAGAGAGGTCAGGCAAGTCGGAAGCCAGGCGCCCTGCTGACGTCAGACTC 2644
 QY 1926 CCGTTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACATGACTGTGGGA 1985
 Db 2645 CCGTTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACATGACTGTGGGA 2704
 QY 1986 GCCAGAACGTTCCGACAGAAAAAGAGGCGCAGCGTCTACCTCAGCTGAGGAGGAAAGCACTG 2045
 Db 2705 GCCAGAACGTTCCGACAGAAAAAGAGGCGCAGCGTCTACCTCAGCTGAGGAGGAAAGCACTG 2764
 QY 2046 TTTACGCTGCTCAACTAGAGCGGGGCGGGGCCCGCCCTCTCTGGGCGCTCTGTGTG 2105
 Db 2765 TTTACGCTGCTCAACTAGAGCGGGGCGGGGCCCGCCCTCTCTGGGCGCTCTGTGTG 2824
 QY 2106 GGCCTGAGAGATATCAGAGGCGCTGGCGACCTTCTGCTGTGTGTGGGCGCCAGAGAC 2165
 Db 2825 GGCCTGAGAGATATCAGAGGCGCTGGCGACCTTCTGCTGTGTGTGGGCGCCAGAGAC 2884
 QY 2166 CCGCGCGCTGAGCTGTA-----CATGCC 2189
 Db 2885 CCGCGCGCTGAGCTGTA-----CATGCC 2944
 QY 2190 CAGGACAGGCTCAGGAGGTCATGCGCAGCAATCATCAAAACCCAGAAACAGTACGCTG 2249
 Db 2945 CAGGACAGGCTCAGGAGGTCATGCGCAGCAATCATCAAAACCCAGAAACAGTACGCTG 3004

QY 2250 CGTGGTATGCGCGTGGTCCAGAAAGCCGCCATGGGCACGTCCGCAAGGCTTCCAAAGAG 2309
 Db 3005 CGTGGTATGCGCGTGGTCCAGAAAGCCGCCATGGGCACGTCCGCAAGGCTTCCAAAGAG 3064
 QY 2310 CAGCTCTACCTTGAACAAGACCTCCAGCCGCTACATGCGACATGCTGTGGCTCACCTCAG 2369
 Db 3065 CAGCTCTACCTTGAACAAGACCTCCAGCCGCTACATGCGACATGCTGTGGCTCACCTCAG 3124
 QY 2370 GAGACACAGCCCGGAGGGGATGCGCTGTCATGAGAGAGAGTCCCTCCCTGAAGAGAGCC 2429
 Db 3125 GAGACACAGCCCGGAGGGGATGCGCTGTCATGAGAGAGAGTCCCTCCCTGAAGAGAGCC 3184
 QY 2430 ACGAGTGGCTCTTTCAGACTCTTTCATGCTTACGCTTACATGTCACACAGCCGTCGATACAG 2489
 Db 3185 ACGAGTGGCTCTTTCAGACTCTTTCATGCTTACGCTTACATGTCACACAGCCGTCGATACAG 3244
 QY 2490 GGCAGATCTACGTCAGAGTCGAGGGATCCCGCAGGGCTCCATCTCTCCAGCTGTCTC 2549
 Db 3245 GGCAGATCTACGTCAGAGTCGAGGGATCCCGCAGGGCTCCATCTCTCCAGCTGTCTC 3304
 QY 2550 TGCAGCTGTGCTACGCGCAATGAGAAACAGCTGTTTCCGGGATTTCCGGGAGCGG 2609
 Db 3305 TGCAGCTGTGCTACGCGCAATGAGAAACAGCTGTTTCCGGGATTTCCGGGAGCGG 3364
 QY 2610 CTGCTCTGCGGTTTGGTGGATGATTTCTTGTGGTGACACTCACCTCACCGCGAA 2669
 Db 3365 CTGCTCTGCGGTTTGGTGGATGATTTCTTGTGGTGACACTCACCTCACCGCGAA 3424
 QY 2670 ACGTTCCTCAGAGACCTGCGTCCGAGGTGCTCCGATGATGAGTGGCTGCTGATGATGCGG 2729
 Db 3425 ACGTTCCTCAGAGACCTGCGTCCGAGGTGCTCCGATGATGAGTGGCTGCTGATGATGCGG 3484
 QY 2730 AAGACAGTGGTGAACCTTCCCTGTAGAAACAGAGCCCTGGGAGGACAGGCTTTTGTTCAG 2789
 Db 3485 AAGACAGTGGTGAACCTTCCCTGTAGAAACAGAGCCCTGGGAGGACAGGCTTTTGTTCAG 3544
 QY 2790 ATGCGGGCCACGAGCCATTTCCCTGATGCGGGCCCTGCTGTGATACCCGAGACCTGGAG 2849
 Db 3545 ATGCGGGCCACGAGCCATTTCCCTGATGCGGGCCCTGCTGTGATACCCGAGACCTGGAG 3604
 QY 2850 GTGCGAGGCGACTACTCAGCTATGCTCCGGACCTCCATGAGAGCCAGTCTCACTTAC 2909
 Db 3605 GTGCGAGGCGACTACTCAGCTATGCTCCGGACCTCCATGAGAGCCAGTCTCACTTAC 3664
 QY 2910 GCGGCTTCAAGGCTGGGAGGAACATGCTGCGCAACTCTTGGGCTGTGCGGCTGAG 2969
 Db 3665 GCGGCTTCAAGGCTGGGAGGAACATGCTGCGCAACTCTTGGGCTGTGCGGCTGAG 3724
 QY 2970 TGTACAGCTGTTTCTGATTTGAGTGTGAACAGCTCCAGACGGTGTGACCAATC 3029
 Db 3725 TGTACAGCTGTTTCTGATTTGAGTGTGAACAGCTCCAGACGGTGTGACCAATC 3784
 QY 3030 TTAAGAATCTCTCTGCTGACAGGCTACAGGTTTACAGCATGTGTGCTCAGCTCCCATTT 3089
 Db 3785 TTAAGAATCTCTCTGCTGACAGGCTACAGGTTTACAGCATGTGTGCTCAGCTCCCATTT 3844
 QY 3090 CATCAGCAAGTTTGAAGAAACCCACATTTTCTCGGCGTATCTCTGACACGGCTCC 3149
 Db 3845 CATCAGCAAGTTTGAAGAAACCCACATTTTCTCGGCGTATCTCTGACACGGCTCC 3904
 QY 3150 CTCTGCTACTCATTCTGAAGAACCAAGAACCAAGAGATGCTGTGGGGCCCAAGGGCGCC 3209
 Db 3905 CTCTGCTACTCATTCTGAAGAACCAAGAACCAAGAGATGCTGTGGGGCCCAAGGGCGCC 3964
 QY 3210 GCGGCGCTTGGCTGCTCCAGAGGCGGTGAGTGGCTGTGCGACACAGCAATTCCTCTCAG 3269
 Db 3965 GCGGCGCTTGGCTGCTCCAGAGGCGGTGAGTGGCTGTGCGACACAGCAATTCCTCTCAG 4024
 QY 3270 CTGACTGACACCGTGTACATCTGACGCTGCTGAGGCTGCTGAGGACAGCCAGAGC 3329
 Db 4025 CTGACTGACACCGTGTACATCTGACGCTGCTGAGGCTGCTGAGGACAGCCAGAGC 4084

Qy	1088	GGCCCTCCTTCATCTACCTCTCTGAGGGCCAGCCATCAGCGGCTCGAGAGCTCGTGGAA	1147
Db	1081	GGCCCTCCTTCATCTACCTCTCTGAGGGCCAGCCATCAGCGGCTCGAGAGCTCGTGGAA	1140
Qy	1148	GACCACTCTTCCTGGGTTCCAGAGCCCTGAAATGCAAGGAGATCCCGGAGTTCGCCCGCT	1207
Db	1141	GACCACTCTTCCTGGGTTCCAGAGCCCTGAAATGCAAGGAGATCCCGGAGTTCGCCCGCT	1200
Qy	1208	GGCCGAGCGCTACTGGCAAAATGAGGGCCCTGTTTCTTGAGACTGCTTTGGGAAACAGCGCA	1267
Db	1201	GGCCGAGCGCTACTGGCAAAATGAGGGCCCTGTTTCTTGAGACTCTTTGGGAAACAGCGCA	1260
Qy	1268	GTGGCCCTACGGGGGTGTCCTCAAGAGAGCAATCGCCGTGCGAGACTGGGTCACCCAGC	1327
Db	1261	GTGGCCCTACGGGGGTGTCCTCAAGAGAGCAATCGCCGTGCGAGACTGGGTCACCCAGC	1320
Qy	1328	AACCGGTGTCTGTGCCCGGAGAAAGCCCAAGGCTCTGTGGCGGCCCCGAGAGAGAGA	1387
Db	1321	AACCGGTGTCTGTGCCCGGAGAAAGCCCAAGGCTCTGTGGCGGCCCCGAGAGAGAGA	1380
Qy	1388	CACAGACCCCGTGCAGCTGATGTGCAGCTGTCTCCGACACAGAGAGCCCTTGACAGTGTGA	1447
Db	1381	CACAGACCCCGTGCAGCTGATGTGCAGCTGTCTCCGACACAGAGAGCCCTTGACAGTGTGA	1440
Qy	1448	CGGCTTGTCGAGGACCTGCCTGCACCGCGCTGGTGCCCGCAGGCTCTGGGGCTCTCAGACA	1507
Db	1441	CGGCTTGTCGAGGACCTGCCTGCACCGCGCTGGTGCCCGCAGGCTCTGGGGCTCTCAGACA	1500
Qy	1508	CACAGAACGCCGCTTCTCAGAGAAACACCAAGAAATATCTCCCTGGGGAGACATGACAA	1567
Db	1501	CACAGAACGCCGCTTCTCAGAGAAACACCAAGAAATATCTCCCTGGGGAGACATGACAA	1560
Qy	1568	GCTCTCCGCTCAGAGAGCTGAGAGTGAAGATGAGCGTCGGGGAATGTCGCTTGCGCGCAG	1627
Db	1561	GCTCTCCGCTCAGAGAGCTGAGAGTGAAGATGAGCGTCGGGGAATGTCGCTTGCGCGCAG	1620
Qy	1628	GAGCCCAAGGGGTGGCTGTGTCCGGGCCAGAGACCGCTCTCGGAGAGATATCCGAGC	1687
Db	1621	GAGCCCAAGGGGTGGCTGTGTCCGGGCCAGAGACCGCTCTCGGAGAGATATCCGAGC	1680
Qy	1688	CAGTGTCTCTCATCTGGCTGATGATGTGTAATGCTGTGAGACTGTCTCAGTCTTTCTTTA	1747
Db	1681	CAGTGTCTCTCATCTGGCTGATGATGTGTAATGCTGTGAGACTGTCTCAGTCTTTCTTTA	1740
Qy	1748	TGTCAAGGAAACAGCTTTCAAAAAGAAAGAGCTCTTTTCTACCGAAGAGTGTCTGGAG	1807
Db	1741	TGTCAAGGAAACAGCTTTCAAAAAGAAAGAGCTCTTTTCTACCGAAGAGATGTCTGGAG	1800
Qy	1808	CAGTGTCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGAGAGCTGT	1867
Db	1801	CAGTGTCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGAGAGCTGT	1860
Qy	1868	GGAAGCAGAGGTTGAGCAGCATCGGGAAACCGAGCCGCCCTCTGTAGCTCAACATCCG	1927
Db	1861	GGAAGCAGAGGTTGAGCAGCATCGGGAAACCGAGCCGCCCTCTGTAGCTCAACATCCG	1920
Qy	1928	CTTTCATCCCCAAACCTGCAGGGGCTGGCGCGATTTGTAAATGATGACTGCTGCGAGAC	1987
Db	1921	CTTTCATCCCCAAACCTGCAGGGGCTGGCGCGATTTGTAAATGATGACTGCTGCGAGAC	1980
Qy	1988	CAGAAAGCTTCCGAGAGAAAGAGAGGCGAGGCTCTCACTCAGAGGGTGAAGGACATGTT	2047
Db	1981	CAGAAAGCTTCCGAGAGAAAGAGAGGCGAGGCTCTCACTCAGAGGGTGAAGGACATGTT	2040
Qy	2048	CAGCGTGTCTAAATGAGAGGGGGTGGGGCCCGCGGCTCTGAGGGCTCTGTGTGGGG	2107
Db	2041	CAGCGTGTCTAAATGAGAGGGGGTGGGGCCCGCGGCTCTGAGGGCTCTGTGTGGGG	2100
Qy	2108	CCTGGAGAGATATCAAGAGGCTGAGGCAACTTGTGTCTGCTGTGCGGCGCCAGAGACC	2167
Db	2101	CCTGGAGAGATATCAAGAGGCTTGTGGCAACTTGTGTGTCTGCTGTGCGGCGCCAGAGACC	2160
Qy	2168	CGCGCTGTAGCTGTGA-----CATCCGCCA	2191

Db	2161	GGCGGCTGACCTCTATCTTTGTCAGAGGGAATGTGACGGGGCGGTACAGCAACATCCGCCCA			2220
Oy	2192	GGACAGGCTACGAGAGTCATCGCAGACATCATCTAAACCCCAACACAGCTACCTCGGG			2251
Db	2221	GGACAGGCTCAGGAGATCATCGCAGCATCATCAAAACCCCAACACAGCTACCTCGGG			2280
Oy	2252	TGGGATGCGGTGTCGCAAGAAAGGCGCCGACGTGACGTCCGAAGGGCTTCGAAGAGCA			2311
Db	2281	TGGGATGCGGTGTCGCAAGAAAGGCGCCGACGTGACGTCCGAAGGGCTTCGAAGAGCA			2340
Oy	2312	GCTCTTACCTTTCACAGACCTCCAGCCGTCATCTGAGACATTTGTGTGCTACCTCGAGCA			2371
Db	2341	GCTCTTACCTTTCACAGACCTCCAGCCGTCATCTGAGACATTTGTGTGCTACCTCGAGCA			2400
Oy	2372	GACACGCCCCGTAGGGATGCCGTGTCATCGACGACGATCTCTCCGTGAATGAGCCAG			2431
Db	2401	GACACGCCCCGTAGGGATGCCGTGTCATCGACGACGATCTCTCCGTGAATGAGCCAG			2460
Oy	2432	CAGTGGCTCTTGACAGCTTCTTCACGCTTCATGTGCCACACAGCCGTGTGCATCAGGG			2491
Db	2461	CAGTGGCTCTTGACAGCTTCTTCACGCTTCATGTGCCACACAGCCGTGTGCATCAGGG			2520
Oy	2492	CAGGCTCAGCTCAGTGCATAGTGCACAGGGGATCCCGCAGAGGCTCCATCTCTCCAGCTGCTG			2551
Db	2521	CAGGCTCAGCTCAGTGCATAGTGCACAGGGGATCCCGCAGAGGCTCCATCTCTCCAGCTGCTG			2580
Oy	2552	CAGCCTGTGCTACGAGGACATGAGAAACAAGCTGTTTTGCGGGGATTCGCGCGGACGGCT			2611
Db	2581	CAGCCTGTGCTACGAGGACATGAGAAACAAGCTGTTTTGCGGGGATTCGCGCGGACGGCT			2640
Oy	2612	GCTCTCGGTTTTGTGATGATGATTTCTGTGGTGTGACACCTCACCTACCCAGCGGAAAC			2671
Db	2641	GCTCTCGGTTTTGTGATGATGATTTCTGTGGTGTGACACCTCACCTACCCAGCGGAAAC			2700
Oy	2672	CTTCTCCAGGACCTCGTCGAGAGGTGCCCTAGATAGGCTGGCGTGTGTAATCTGGGAA			2731
Db	2701	CTTCTCCAGGACCTCGTCGAGAGGTGCCCTAGATAGGCTGGCGTGTGTAATCTGGGAA			2760
Oy	2732	GACAGTGTGATCTCCCTGATGAGAAAGCAGAGGCTCGGTGTGTGAGCGCTTTGTTCAGAT			2791
Db	2761	GACAGTGTGATCTCCCTGATGAGAAAGCAGAGGCTCGGTGTGTGAGCGCTTTGTTCAGAT			2820
Oy	2792	GCGGGCCACAGGCTATTTCCCTGTGTGCGGCTCGTGTGTGATATCCGAGACCTGTGAGGT			2851
Db	2821	GCGGGCCACAGGCTATTTCCCTGTGTGCGGCTCGTGTGTGATATCCGAGACCTGTGAGGT			2880
Oy	2852	GCAGAGCAGCTACTCCAGCTATGACCAGGACCTCATCAGAGCCAGTCTACCTTCAACCG			2911
Db	2881	GCAGAGCAGCTACTCCAGCTATGACCAGGACCTCATCAGAGCCAGTCTACCTTCAACCG			2940
Oy	2912	CGGCTTCAGGCTGGGAGGAACATGCGCTGCAAACTCTTTGGGGGCTTTCGCGCTGAAGTG			2971
Db	2941	CGGCTTCAGGCTGGGAGGAACATGCGCTGCAAACTCTTTGGGGGCTTTCGCGCTGAAGTG			3000
Oy	2972	TACACAGCTTTCTTGATTTGACAGTGAAGAACGCTCCACAGCGTGTGACACATCTA			3031
Db	3001	TACACAGCTTTCTTGATTTGACAGTGAAGAACGCTCCACAGCGTGTGACACATCTA			3060
Oy	3032	CAGAATCCTCTCTGACAGGGGTACAGGTTTACGACATGTGTCTGACAGCTCCCATTTCA			3091
Db	3061	CAGAATCCTCTCTGACAGGGGTACAGGTTTACGACATGTGTGTCTGACAGCTCCCATTTCA			3120
Oy	3092	TACAGAGTTTGGAAAGAACCCCAATTTTCTGGCGGTATCTGTGACAGCGCTCCCT			3151
Db	3121	TACAGAGTTTGGAAAGAACCCCAATTTTCTGGCGGTATCTGTGACAGCGCTCCCT			3180
Oy	3152	CTGCTACTCATCTGTAAAGCAAGAACGCAAGGATGTCCCTGTGGGGCCAAAGGGCTCCG			3211
Db	3181	CTGCTACTCATCTGTAAAGCAAGAACGCAAGGATGTCCCTGTGGGGCCAAAGGGCTCCG			3240
Oy	3212	GCGGCTCTGCGCTCCGAGGCGGTGACAGTGGCTGTGCCACCAAGCATTCCTGTCAAGCT			3271

```

Db 3241 CGGCCCTTGCCCTCCGAGGCCGTGAGTGGCTGTGCCACCAAGCATTTCTGCTCAAGCT 3300
QY 3272 GACTGACACCGGTGTACCTACGTGCGACTCTCTGGGGTCACTCAGACAGCCAGACGCA 3331
Db 3301 GACTGACACCGGTGTACCTACGTGCGACTCTCTGGGGTCACTCAGACAGCCAGACGCA 3360
QY 3332 GCTGAGTGGAAAGCTCCCGGGGAGACGCTGACTGCTCCCTGGAGGCCGAGCCACCCGCG 3391
Db 3361 GCTGAGTGGAAAGCTCCCGGGGAGACGCTGACTGCTCCCTGGAGGCCGAGCCACCCGCG 3420
QY 3392 ACTGCCCCACACTTCAAGACCATCTGTGAGTGGCCACCCGCGCACAGCCAGCCGCA 3451
Db 3421 ACTGCCCCACACTTCAAGACCATCTGTGAGTGGCCACCCGCGCACAGCCAGCCGCA 3480
QY 3452 GAGCAGACACGACGAGCCCTGTACAGCCGGGCTACGTCTCCAGGAGGAGGAGGGCGCC 3511
Db 3481 GAGCAGACACGACGAGCCCTGTACAGCCGGGCTACGTCTCCAGGAGGAGGAGGGCGCC 3540
QY 3512 CACACCCAGGCCCCGACCGCTGGAGTGTGAGGCGCTGAGTGGCTTTGGCCGAGCGCTG 3571
Db 3541 CACACCCAGGCCCCGACCGCTGGAGTGTGAGGCGCTGAGTGGCTTTGGCCGAGCGCTG 3600
QY 3572 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGGCGCTGAGTGGCTTTGG 3631
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGGCGCTGAGTGGCTTTGG 3660
QY 3632 GAGTGTCCAGACACACTGCTGCTTCACTTCCCAAGGCTGGCGCTGCTCAGCCCA 3691
Db 3661 GAGTGTCCAGACACACTGCTGCTTCACTTCCCAAGGCTGGCGCTGCTCAGCCCA 3720
QY 3692 GGGCAGGCTTTTCTCACCAGAGCGCGGCTTCCACTCCCAATAGAAATAGTCCATCC 3751
Db 3721 GGGCAGGCTTTTCTCACCAGAGCGCGGCTTCCACTCCCAATAGAAATAGTCCATCC 3780
QY 3752 CCAGATTTGCCATTGTTCACCCCTGGCCCTGCTTGGCTTCCACCCCAACATCC 3811
Db 3781 CCAGATTTGCCATTGTTCACCCCTGGCCCTGCTTGGCTTCCACCCCAACATCC 3840
QY 3812 AGGTGAGACCCCTGAGAAAGAACCTGGAGGCTGGGAAATTTGAGTGAAGGAGTGTG 3871
Db 3841 AGGTGAGACCCCTGAGAAAGAACCTGGAGGCTGGGAAATTTGAGTGAAGGAGTGTG 3900
QY 3872 CCCTGTACACAGCGAGACCTGTGACTGGATGGGGTCCCTGTGGGTCAATTTGGGGG 3931
Db 3901 CCCTGTACACAGCGAGACCTGTGACTGGATGGGGTCCCTGTGGGTCAATTTGGGGG 3960
QY 3932 GAGTGTCTGGAGTAAATATCTGAATATAGATTTTTCAGTTTGAATTTGAAAAA 3986
Db 3961 GAGTGTCTGGAGTAAATATCTGAATATAGATTTTTCAGTTTGAATTTGAAAAA 4015

RESULT 13
PCT-US02-14867-1
: Sequence 1, Application PC/TUS0214867
: GENERAL INFORMATION:
: APPLICANT: Genon Corporation
: APPLICANT: Jiang, Xu-Rong
: APPLICANT: Chiu, Choy-Pik
: APPLICANT: Harley, Calvin B.
: TITLE OF INVENTION: Treatment for Wounds
: FILE REFERENCE: 120/200
: CURRENT APPLICATION NUMBER: PCT/US02/14867
: CURRENT FILING DATE: 2002-05-09
: PRIOR APPLICATION NUMBER: 60/289,903
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: Patent version 3.1
: SEQ ID NO 1
: LENGTH: 4015
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS

```

```

: LOCATION: (56)..(3454)
: OTHER INFORMATION:
: PCT-US02-14867-1

Query Match          99.1%; Score 3969; DB 1; Length 4015;
Best Local Similarity 99.1%; Pred. No. 2,1e-139;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 8 GCAGGCGTGGCGTTCGTCGCGCAGCTGAGGAAAGCCCTGGGCCCCGGGACACCCCGCATGCG 67
Db 1 GCAGGCGTGGCGTTCGTCGCGCAGCTGAGGAAAGCCCTGGGCCCCGGGACACCCCGCATGCG 60
QY 68 GCGCGCTCCCGCTGCGCGAGCCGCTGCTCCCTGCTGCGCAACCACTACCGGAGTGTCT 127
Db 61 GCGCGCTCCCGCTGCGCGAGCCGCTGCTCCCTGCTGCGCAACCACTACCGGAGTGTCT 120
QY 128 GCGCGTGGCCACGTTGCTGCGCGGCGCTGGGGGCCCAAGGGCTGGCGGCTGTGTGCAACGGG 187
Db 121 GCGCGTGGCCACGTTGCTGCGCGGCGCTGGGGGCCCAAGGGCTGGCGGCTGTGTGCAACGGG 180
QY 188 GGACCCGGGCGCTTCCGCGGCGCTGTGTGAGCCAGTGCCTGTGTGTGCTGTGGGAGCGC 247
Db 181 GGACCCGGGCGCTTCCGCGGCGCTGTGTGAGCCAGTGCCTGTGTGTGCTGTGGGAGCGC 240
QY 248 ACGGCGGCCCCCGCGCGCCCTCTCCCGCAGGTGTCTGCTGCAAGAGAGCTGTGGC 307
Db 241 ACGGCGGCCCCCGCGCGCCCTCTCCCGCAGGTGTCTGCTGCAAGAGAGCTGTGGC 300
QY 308 CCGAATGTGTGAGAGGCTGTGTGAGCGGGGCGGCAAGAAAGTGTGTGGCTTGTGGCTTGGC 367
Db 301 CCGAATGTGTGAGAGGCTGTGTGAGCGGGGCGGCAAGAAAGTGTGTGGCTTGTGGCTTGGC 360
QY 368 GCTGTGACAGGGGGCGCGCGGGGGCGCCCGAGAGCTTTCACACACAGCTGTGCGAGCTA 427
Db 361 GCTGTGACAGGGGGCGCGCGGGGGCGCCCGAGAGCTTTCACACACAGCTGTGCGAGCTA 420
QY 428 CCGTCCCAACAGGTGTGACGACGACTCGGGGGAGCGGGCGGTGTGCTGTGCG 487
Db 421 CCGTCCCAACAGGTGTGACGACGACTCGGGGGAGCGGGCGGTGTGCTGTGCG 480
QY 488 CCGCGTGGGCGACGAGGTGTGTGACCTGTGTGACGAGTGTGTGCGGCTTGTGTGCTGTG 547
Db 481 CCGCGTGGGCGACGAGGTGTGTGACCTGTGTGACGAGTGTGTGCGGCTTGTGTGCTGTG 540
QY 548 GGGTCCACAGCTGCGCTCAACAGGTGTGCGGGCGCGCTGTACACAGCTGTGCGGCTGTGCG 607
Db 541 GGGTCCACAGCTGCGCTCAACAGGTGTGCGGGCGCGCTGTACACAGCTGTGCGGCTGTGCG 600
QY 608 TCAGGCGCGGCGCGCGCGCACACAGCTAGTGTGACCCCGAAGGCGTGTGAGTGTGGAACGGGCG 667
Db 601 TCAGGCGCGGCGCGCGCGCACACAGCTAGTGTGACCCCGAAGGCGTGTGAGTGTGGAACGGGCG 660
QY 668 CTGGAACCATATAGCGTCAGGAGAGCGCGGGTCCCGCTGTGAGCGCTGTGAGCGCGGGGCGAG 727
Db 661 CTGGAACCATATAGCGTCAGGAGAGCGCGGGTCCCGCTGTGAGCGCTGTGAGCGCGGGGCGAG 720
QY 728 GAGGCGCGGGGCGCACTGTGACGCGCAAGTCTGCGCTTGTGCGCAAGAGGCCAGCGGTGGCGC 787
Db 721 GAGGCGCGGGGCGCACTGTGACGCGCAAGTCTGCGCTTGTGCGCAAGAGGCCAGCGGTGGCGC 780
QY 788 TGCCCTTACAGCGGAGCGGAGCGCGCGTGTGGGAGGAGGCTGTGTGCGGCGCGCGGAGAGAC 847
Db 781 TGCCCTTACAGCGGAGCGGAGCGCGCGTGTGGGAGGAGGCTGTGTGCGGCGCGCGGAGAGAC 840
QY 848 GCGTGTGACGAGTGTGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
Db 841 GCGTGTGACGAGTGTGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 908 CACCTCTTTGAGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 967
Db 901 CACCTCTTTGAGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
QY 968 GCACACGCGGGCGCGCGCATTCACATCGCGGCGCACACAGCTGCTGTGTGTGTGTGTGTGTGT 1027

```

Db 961 GCACACAGGCGGCCCCCATCATGCGGGCCACAGCTCCCTGGAGCACGGCTGTCC 1020
 Oy 1028 CCCGGTGTAGGCGGAGACCAAGCACTTCTCTACTCTCTAGGCGACAAAGAGAGCTGGC 1087
 Db 1021 CCCGGTGTAGGCGGAGACCAAGCACTTCTCTACTCTCTAGGCGACAAAGAGAGCTGGC 1080
 Oy 1088 GCCCTCTCTACTACTAGCTCTCTGAGGCGGAGACCTGAGTGGGCTGGAGGCTGTGGA 1147
 Db 1081 GCCCTCTCTACTACTAGCTCTCTGAGGCGGAGACCTGAGTGGGCTGTGGA 1140
 Oy 1148 GACCATCTTCTGGGTTCCAGGCGGCGGAGTCCCGGAGGAGTCCCGGAGTGGCGGCT 1207
 Db 1141 GACCATCTTCTGGGTTCCAGGCGGCGGAGTCCCGGAGGAGTCCCGGAGTGGCGGCT 1200
 Oy 1208 GCCCGAGGCTACTGGCAATGCGGCGGCTCTTCTGAGAGTCTCTGGGAACCAAGCGGA 1267
 Db 1201 GCCCGAGGCTACTGGCAATGCGGCGGCTCTTCTGAGAGTCTCTGGGAACCAAGCGGA 1260
 Oy 1268 GTGCGCTTACGGGGTGTCTCTCAAGAGCACTGCGCGAGCTGCGAGTCCAGCCAGC 1327
 Db 1261 GTGCGCTTACGGGGTGTCTCTCAAGAGCACTGCGCGAGCTGCGAGTCCAGCCAGC 1320
 Oy 1328 AGCGGTGTCTGTGCGCGGAGAAAGCCCGAGGCTCTGTGCGGCGCCCGAGGAGAGGA 1387
 Db 1321 AGCGGTGTCTGTGCGCGGAGAAAGCCCGAGGCTCTGTGCGGCGCCCGAGGAGAGGA 1380
 Oy 1388 CAGAGACCCCGCTGCGCTGTGTGAGTGTCTGCGGAGCAAGAGAGCCCTGAGGAGTGA 1447
 Db 1381 CAGAGACCCCGCTGCGCTGTGTGAGTGTCTGCGGAGCAAGAGAGCCCTGAGGAGTGA 1440
 Oy 1448 CGGGTCTGTGCGGAGGCTGTGCGCGGCTGTGCGGCGCCCGAGGAGTCTGAGGGA 1507
 Db 1441 CGGGTCTGTGCGGAGGCTGTGCGCGGCTGTGCGGCGCCCGAGGAGTCTGAGGGA 1500
 Oy 1508 CAGCGAAGCGCGCTTCTCTCAAGAGCAAGAGTCTCTCTGCGGAGAGAGATGCGAA 1567
 Db 1501 CAGCGAAGCGCGCTTCTCTCAAGAGCAAGAGTCTCTCTGCGGAGAGATGCGAA 1560
 Oy 1568 GCTCTGCTGTGAGAGTGTGAGAGATGAGCTGTGCGGAGAGTCTGCTGTGCGAG 1627
 Db 1561 GCTCTGCTGTGAGAGTGTGAGAGATGAGCTGTGCGGAGAGTCTGCTGTGCGAG 1620
 Oy 1628 GAGCCAGAGGGTGTGCTGTGCTGCGGCGGAGAGCAAGCTGTGAGAGAGATCTGTGC 1687
 Db 1621 GAGCCAGAGGGTGTGCTGTGCTGCGGCGGAGAGCAAGCTGTGAGAGAGATCTGTGC 1680
 Oy 1688 CAAATTCTGTGACTGTGATGATGTGTACGTCTGTGAGAGTGTCTGTCTTTTA 1747
 Db 1681 CAAATTCTGTGACTGTGATGATGTGTACGTCTGTGAGAGTGTCTGTCTTTTA 1740
 Oy 1748 TGTACGAGAGACAGCTTTCAAAAGAACAGGCTCTTTTCTACGCGAAGAGTGTGAG 1807
 Db 1741 TGTACGAGAGACAGCTTTCAAAAGAACAGGCTCTTTTCTACGCGAAGAGTGTGAG 1800
 Oy 1808 CAAATTGCAAACTTGGAAATCAGAGAGCACTTGAAGAGGGTGTGAGTGGGGAGTGTG 1867
 Db 1801 CAAATTGCAAACTTGGAAATCAGAGAGCACTTGAAGAGGGTGTGAGTGGGGAGTGTG 1860
 Oy 1868 GGAAGAGAGGCTGAGAGAGATGCGGGAAGCGAGGCGGCTGCTGTGAGCTCAAGATCCG 1927
 Db 1861 GGAAGAGAGGCTGAGAGAGATGCGGGAAGCGAGGCGGCTGCTGTGAGCTCAAGATCCG 1920
 Oy 1928 CTTATCTCCCAAGCTGAGGCGGCTGTGCGGCGGATGTGAACATGACGTCTGTGAGC 1987
 Db 1921 CTTATCTCCCAAGCTGAGGCGGCTGTGCGGCGGATGTGAACATGACGTCTGTGAGC 1980
 Oy 1988 CAGAACTTCTGAGAGAGAGAGAGGCGGAGCTCTCACTCTGAGAGGTGAAGGCACTGTT 2047
 Db 1981 CAGAACTTCTGAGAGAGAGAGAGGCGGAGCTCTCACTCTGAGAGGTGAAGGCACTGTT 2040
 Oy 2048 CAGGCTGTCTACTAGAGAGGCGGCGGCGGCTCTCTGTGAGGCTCTCTGTGTGGG 2107
 |||||||

Db 2041 CAGGCTGTCTACTAGAGAGGCGGCGGCGGCGGCGGCTCTGTGAGGCTCTGTGTG 2100
 Oy 2108 CTTGAGAGATATCCACAGAGGCTGTGGCGACCTTCTGTGTGTGTGTGTGGGCGGCGAGACC 2167
 Db 2101 CTTGAGAGATATCCACAGAGGCTGTGGCGACCTTCTGTGTGTGTGTGTGGGCGGCGAGACC 2160
 Oy 2168 GCGGCTGAGCTGTG-----CATCCCA 2191
 Db 2161 GCGGCTGAGCTGTGATCTTTCAGAGGTGATGTGAGGCGGCGGCGGCGGCGGCGGCGGCGG 2220
 Oy 2192 GAGAGGCTCTACAGAGGATGATGCGCAGCATCATCAAAACCCAGAGAGAGTGTGTGCG 2251
 Db 2221 GAGAGGCTCTACAGAGGATGATGCGCAGCATCATCAAAACCCAGAGAGAGTGTGTGCG 2280
 Oy 2252 TCGGTATGCGGCTGTGCGAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2311
 Db 2281 TCGGTATGCGGCTGTGCGAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2340
 Oy 2312 GCTCTCTACTGTGAGAGAGCTTCCAGGCGGCTGACAGTGTGTGTGTGTGTGTGTGTGTGT 2371
 Db 2341 GCTCTCTACTGTGAGAGAGCTTCCAGGCGGCTGACAGTGTGTGTGTGTGTGTGTGTGTGT 2400
 Oy 2372 GACACAGCCGCTGAGAGGATGCGCTGTCTATCGAGCAGAGCTCTCTCTATGAGGCGAG 2431
 Db 2401 GACACAGCCGCTGAGAGGATGCGCTGTCTATCGAGCAGAGCTCTCTCTATGAGGCGAG 2460
 Oy 2432 CAGTGGCTCTCTGAGAGCTTCTCTACGCTTCAATGTGTGTGTGTGTGTGTGTGTGTGT 2491
 Db 2461 CAGTGGCTCTCTGAGAGCTTCTCTACGCTTCAATGTGTGTGTGTGTGTGTGTGTGTGT 2520
 Oy 2492 CAAATCTCTACGCTTCTGAGAGGATGCGGAGGATGCGGAGGCGGCGGCGGCGGCGGCGG 2551
 Db 2521 CAAATCTCTACGCTTCTGAGAGGATGCGGAGGATGCGGAGGCGGCGGCGGCGGCGGCGG 2580
 Oy 2552 CAGCTGTGCTACGCGGAG 2611
 Db 2581 CAGCTGTGCTACGCGGAG 2640
 Oy 2612 GCTCTGCTGT 2671
 Db 2641 GCTCTGCTGT 2700
 Oy 2672 CTTCTCTACAGAGAGCTGTGCGAGGATGCTCTGAGTGTGTGTGTGTGTGTGTGTGTGT 2731
 Db 2701 CTTCTCTACAGAGAGCTGTGCGAGGATGCTCTGAGTGTGTGTGTGTGTGTGTGTGTGT 2760
 Oy 2732 GACAGTGTGAGACTTCCCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2791
 Db 2761 GACAGTGTGAGACTTCCCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2820
 Oy 2792 GCGGCGGCGGAGGCTATTTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2851
 Db 2821 GCGGCGGCGGAGGCTATTTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2880
 Oy 2852 GAGAGAGAGCTACTCTGAGAGATGCGGAGAGCTCTGATGAGAGAGAGAGAGAGAGAGAG 2911
 Db 2881 GAGAGAGAGCTACTCTGAGAGATGCGGAGAGCTCTGATGAGAGAGAGAGAGAGAGAGAG 2940
 Oy 2912 GCGGCTTCAAGGCTGTGAG 2971
 Db 2941 GCGGCTTCAAGGCTGTGAG 3000
 Oy 2972 TCAAGAGCTGT 3031
 Db 3001 TCAAGAGCTGT 3060
 Oy 3032 CAAAGATCTCTGT 3091
 Db 3061 CAAAGATCTCTGT 3120
 Oy 3092 TCAGCAAGTTTGTGAG 3151
 Db 3121 TCAGCAAGTTTGTGAG 3180

```

QY 3152 CTGCTACTCATCTCTGAAGCCAGACGAGGATGCTGCTGGGGCCCAAGGGCGCCG 3211
D 3181 CTGCTACTCATCTCTGAAGCCAGACGAGGATGCTGCTGGGGCCCAAGGGCGCCG 3240
QY 3212 CGGCGCTCTGCGCTCCGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3271
D 3241 CGGCGCTCTGCGCTCCGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
QY 3272 GACTGACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3331
D 3301 GACTGACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
QY 3332 GCTGAGTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3391
D 3361 GCTGAGTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
QY 3392 ACTGCGCTCAGCTCTGAGACCATCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 3451
D 3421 ACTGCGCTCAGCTCTGAGACCATCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 3480
QY 3452 GAGCAGACACCGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3511
D 3481 GAGCAGACACCGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
QY 3512 CACACCCAGGCGCCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3571
D 3541 CACACCCAGGCGCCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
QY 3572 CATGTCGCGCTGAGAGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3631
D 3601 CATGTCGCGCTGAGAGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
QY 3632 GAGTGTCCAGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3691
D 3661 GAGTGTCCAGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
QY 3692 GGGCAGCTTTTCTCTACACGAGGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 3751
D 3721 GGGCAGCTTTTCTCTACACGAGGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 3780
QY 3752 CGAGATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3811
D 3781 CGAGATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
QY 3812 AGGTGAGACCTTGAGAGGACCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 3871
D 3841 AGGTGAGACCTTGAGAGGACCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 3900
QY 3872 CCGTGTACAGAGGCGAGGACCTGACCTGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 3931
D 3901 CCGTGTACAGAGGCGAGGACCTGACCTGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 3960
QY 3932 GAGGTGCTGTGGAGTAATAATCTGAATATGAGTTTCTGAGTTTCTGAGTTTCTGAG 3986
D 3961 GAGGTGCTGTGGAGTAATAATCTGAATATGAGTTTCTGAGTTTCTGAGTTTCTGAG 4015

```

RESULT 14 PCT-US99-06898-1

```

: Sequence 1, Application PC/TUS9906898
: GENERAL INFORMATION:
: APPLICANT: Gaeta, Federico C.A.
: TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
: TITLE OF INVENTION: Response to a Telomerase Antigen
: FILE REFERENCE: 015389-003500PC
: CURRENT APPLICATION NUMBER: PCT/US99/06898
: EARLIER FILING DATE: 1999-03-30
: EARLIER APPLICATION NUMBER: US 08/911,312
: EARLIER FILING DATE: 1997-08-14
: EARLIER APPLICATION NUMBER: US 08/912,951
: EARLIER FILING DATE: 1997-08-14

```

```

: EARLIER APPLICATION NUMBER: US 08/915,503
: EARLIER FILING DATE: 1997-08-14
: EARLIER APPLICATION NUMBER: WO PCT/US97/17618
: EARLIER FILING DATE: 1997-10-01
: EARLIER APPLICATION NUMBER: WO PCT/US/17885
: EARLIER FILING DATE: 1997-10-01
: EARLIER APPLICATION NUMBER: US 08/974,549
: EARLIER FILING DATE: 1997-11-19
: EARLIER APPLICATION NUMBER: US 08/974,584
: EARLIER FILING DATE: 1997-11-19
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 4015
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (56)..(3454)
: OTHER INFORMATION: human telomerase reverse transcriptase (hTR)
PCT-US99-06898-1

```

```

Query Match 99.1% Score 3969; DB 1; Length 4015;
Best Local Similarity 99.1% Pred. No. 2,1e-139; Mismatches 0; Indels 36; Gaps 1;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

```

```

QY 8 GCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 67
D 1 GCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 68 GCGCGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 127
D 61 GCGCGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 128 GCGCGTGGCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187
D 121 GCGCGTGGCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 188 GGACCGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
D 181 GGACCGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 248 ACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 307
D 241 ACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 308 CCGAGTGTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 367
D 301 CCGAGTGTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 368 GCTGCTGAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 427
D 361 GCTGCTGAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 428 CCGCGCCCAACGAGTGAACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 487
D 421 CCGCGCCCAACGAGTGAACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 488 CCGCGTGGGAGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
D 481 CCGCGTGGGAGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 548 GCGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607
D 541 GCGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 608 TCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 667
D 601 TCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY 668 CTGGAACCATAGCGTCAAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 727
D 661 CTGGAACCATAGCGTCAAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 720

```


Qy	608	TCAGGCCGGCCCCCGCCACACGCTGATGTGACCCCGAAGGCTCTGGATATCCAGACGGCC	657
Db	601	TCAGGCCGGCCCCCGCCACACGCTATGTGACCCCGAAGGCGCTGGATATCCAGACGGCC	660
Qy	668	CTGGAACCAATAGCTGTACAGGAGAGCGGGGGTCCCTCTGGGCTGTGCCAGGCCGGGTGTGAG	727
Db	661	CTGGAACCAATAGCTGTACAGGAGAGCGGGGGTCCCTCTGGGCTGTGCCAGGCCGGGTGTGAG	720
Qy	728	GAGGCGGGGGGGGACATGCTCCACAGCAAGTGTGCCCTGTGACAGAGGCCAGGCGTGGCC	787
Db	721	GAGGCGGGGGGGGACATGCTCCACAGCAAGTGTGCCCTGTGACAGAGGCCAGGCGTGGCC	780
Qy	788	TGCCCTGTAGCCGGAGCGAGCGCCCTGTGGAGAGGGTCTGTGGGCCCAACCCGGGCGAGAC	847
Db	781	TGCCCTGTAGCCGGAGCGAGCGCCCTGTGGAGAGGGTCTGTGGGCCCAACCCGGGCGAGAC	840
Qy	848	GCGTGTGACCGAGTGACCGTGGTTTCTGTGTGTGTGTGCACCTGCACAGACCCGGCCAGAAAGAC	907
Db	841	GCGTGTGACCGAGTGACCGTGGTTTCTGTGTGTGTGTGTGCACCTGCACAGACCCGGCCAGAAAGAC	900
Qy	908	CACCTCTTTTGGAGGGTGGCGCTCTGTGGACAGGCGCACTGCCCAACCATCGTGGGGCGGCA	967
Db	901	CACCTCTTTTGGAGGGTGGCGCTCTGTGGACAGGCGCACTGCCCAACCATCGTGGGGCGGCA	960
Qy	968	GCACACAGCGGGGCCCCCATCATATCGGGGCAACACGTCCTCGTGGAGACAGCCCTGTGTC	1027
Db	961	GCACACAGCGGGGCCCCCATCATATCGGGGCAACACGTCCTCGTGGAGACAGCCCTGTGTC	1020
Qy	1028	CCCGGTTGTACGGCGAGACCAAGCAACTTCTCTACTCTCCAGGCTGAGCAGAGGACAGCTGGG	1087
Db	1021	CCCGGTTGTACGGCGAGACCAAGCAACTTCTCTACTCTCCAGGCTGAGCAGAGGACAGCTGGG	1080
Qy	1088	GGCCCTCTCTACTACACTCTGTGAGAGGCCAGCGCTGACGTGAGGCGTGTGGGAGGCTGTGGA	1147
Db	1081	GGCCCTCTCTACTACACTCTGTGAGAGGCCAGCGCTGACGTGAGGCGTGTGGGAGGCTGTGGA	1140
Qy	1148	GACCATCTTCTTGTGGGTTCAGAGGCCGTGTGATGTCCAGAGGACTCTCCCGAGGTTGCCCGGCT	1207
Db	1141	GACCATCTTCTTGTGGGTTCAGAGGCCGTGTGATGTCCAGAGGACTCTCCCGAGGTTGCCCGGCT	1200
Qy	1208	GGCCCAAGCGCTACTGGCAATATGGCGCCCTGTTTGTGTGAGATCTGTGGAGAACACAGCGCA	1267
Db	1201	GGCCCAAGCGCTACTGGCAATATGGCGCCCTGTTTGTGTGAGATCTGTGGAGAACACAGCGCA	1260
Qy	1268	GTGCCCTGTACGGGGTGTCTCTCAAGACGACACTGCCCTGTCCGAGCTGTGGGTCAACCCACAC	1327
Db	1261	GTGCCCTGTACGGGGTGTCTCTCAAGACGACACTGCCCTGTCCGAGCTGTGGGTCAACCCACAC	1320
Qy	1328	AAGCCGTTGTGTGTGCCCGGAGAAAGCCCAAGGGCTGTGTGGCGGCCCGCCGAGAGAGAGA	1387
Db	1321	AAGCCGTTGTGTGTGCCCGGAGAAAGCCCAAGGGCTGTGTGGCGGCCCGCCGAGAGAGAGA	1380
Qy	1388	CACAGACCCCCGTCGCTGTGTGTGACAGCTGTCCGCGACACACAGAGAGCCCTGTCCGAGGTGA	1447
Db	1381	CACAGACCCCCGTCGCTGTGTGTGACAGCTGTCCGCGACACACAGAGAGCCCTGTCCGAGGTGA	1440
Qy	1448	CGCGCTGTGTGGGGGCGTGTCCGCGCGGGGTGGTGTGCCCAAGGCTGTGTGGGGCTGTCAAGGA	1507
Db	1441	CGCGCTGTGTGGGGGCGTGTCCGCGCGGGGTGGTGTGCCCAAGGCTGTGTGGGGCTGTCAAGGA	1500
Qy	1508	CACGAGACGCCGCTGTCTCTCAGAGAAACACCAAGAAAGTATATCTCCGTGGGAGAACATATGCA	1567
Db	1501	CACGAGACGCCGCTGTCTCTCAGAGAAACACCAAGAAAGTATATCTCCGTGGGAGAAAGTATGCA	1560
Qy	1568	GCTCTCCCTCTCAGAGAGCTGTGAGTAATGTAGCGGTGCGGAGACTGTGCTTGGCTGCGCAG	1627
Db	1561	GCTCTCCCTCTCAGAGAGCTGTGAGTAATGTAGCGGTGCGGAGACTGTGCTTGGCTGCGCAG	1620
Qy	1628	GAGCCCAAGGGGTGAGTGTGTGTCCGGCGCAGAGACACCGTCTCCGTGTGAGAGAGATCTGTGC	1687
Db	1621	GAGCCCAAGGGGTGAGTGTGTGTCCGGCGCAGAGACACCGTCTCCGTGTGAGAGAGATCTGTGC	1680
Qy	1688	CAGATCTCTCACTGTGTGATGATGTGTGACACTGTGTGACACTGTGTGACACTGTGTCTTTT	1747

Db	1681	CAAGTTCCTCGACTGGCTGATGATGTGTGACCTCGTGCAGCTGTCTCAGTCTTTCTTTTAA	1740
Db	1748	TGTCAACGAGAACACAGCTTTCAAAGAAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1807
Db	1741	TGTCAACGAGAACACAGCTTTCAAAGAAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800
Db	1808	CAAGTTCGAAAGCATTTGGATGTACACAGCATTTGAAGAGGTGTACATCGCGAGCTGTCT	1867
Db	1801	CAAGTTGGAAAGCATTTGGAAATTCACACAGCATTTGAAGAGGTGTACAGCTGTGGAGAGCTGTCT	1860
Db	1868	GGAAACAGAGAGTCAAGCAGCATCTGGGAAGCCAGAGCCGCCCTGTCTGTAGCTTCACAACTCCG	1927
Db	1861	GGAAACAGAGAGTCAAGCAGCATCTGGGAAGCCAGAGCCGCCCTGTCTGTAGCTTCACAACTCCG	1920
Db	1928	CTTTCATCCCAACCCCTGACAGGGGCTGCGCGCGCGATTTGTAAANTGACATCGTCTGGAGAC	1987
Db	1921	CTTTCATCCCAACCCCTGACAGGGGCTGCGCGCGCGATTTGTAAANTGACATCGTCTGGAGAC	1980
Db	1988	CAGACAGTCTCCGAGAGAAAGAGAGGAGCCAGAGGTCTACCTCAGAGGTGTGAAGAGCACTGTT	2047
Db	1981	CAGACAGTCTCCGAGAGAAAGAGAGGAGCCAGAGGTCTACCTCAGAGGTGTGAAGAGCACTGTT	2040
Db	2048	CAGCGGTGTCAACTAAGAGAGCGAGGAGGAGGAGCCCGGCGCTCTGTGGAGGAGGAGGAGG	2107
Db	2041	CAGCGGTGTCAACTAAGAGAGCGAGGAGGAGGAGGAGCCCGGCGCTCTGTGGAGGAGGAGGAGG	2100
Db	2108	CCTGGAGATTTCCACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2167
Db	2101	CCTGGAGATTTCCACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2160
Db	2168	GCCGCTGTAGCTGTAA-----CATCCGCA 2191	
Db	2161	GCCGCTGTAGCTGTAA-----CATCCGCA 2191	
Db	2192	GGACAGGCTCAAGAGAGGTATCGCCAGCATCATCAACCCAGAAACAGTACTGCTGGC	2251
Db	2221	GGACAGGCTCAAGAGAGGTATCGCCAGCATCATCAACCCAGAAACAGTACTGCTGGC	2280
Db	2252	TGGATATCGCTGTGTCCAGAAAGGCGGCCCATGGAGCATCGTCCGAAAGGCTTCAAGAGCCA	2311
Db	2281	TGGATATCGCTGTGTCCAGAAAGGCGGCCCATGGAGCATCGTCCGAAAGGCTTCAAGAGCCA	2340
Db	2312	GCTCTCTACCTTACAGAGACCTCCAGCCGTCATGAGCATGAGCACTTGTGTGTCTACCTGTAGAGA	2371
Db	2341	GCTCTCTACCTTACAGAGACCTCCAGCCGTCATGAGCATGAGCACTTGTGTGTCTACCTGTAGAGA	2400
Db	2372	GACACAGCCCTCAGAGAGATGCGCGTGTCTATCAGAGAGAGAGTCTCTCCGTATGAGCCAG	2431
Db	2401	GACACAGCCCTCAGAGAGATGCGCGTGTCTATCAGAGAGAGAGTCTCTCCGTATGAGCCAG	2460
Db	2432	CAGTGGCCCTGTGAAGTCTTCTCAGACCTTCAATGTGACACACAGCCGTTGAGCCATCAAGGAG	2491
Db	2461	CAGTGGCCCTGTGAAGTCTTCTCAGACCTTCAATGTGACACACAGCCGTTGAGCCATCAAGGAG	2520
Db	2492	CAGTGTCTACGTCAAGTCCAGAGGAGATCCCGAGAGGCTCCATCTCTCAAGTGTCTG	2551
Db	2521	CAGTGTCTACGTCAAGTCCAGAGGAGATCCCGAGAGGCTCCATCTCTCAAGTGTCTG	2580
Db	2552	CAGCTGTGTCTACAGGAGACATGTGAACAACAGTCTTTTTCGGAGATTTCCGGCGGAGAGGAGCT	2611
Db	2581	CAGCTGTGTCTACAGGAGACATGTGAACAACAGTCTTTTTCGGAGATTTCCGGCGGAGAGGAGCT	2640
Db	2612	GCTGCTGT	2671
Db	2641	GCTGCTGT	2700
Db	2672	CTTTCCTCAAGAACCTGTGTCCAGAGGTGTCCCTCAGATGAGGCTGTGGTGTGAATCTTGGAGAA	2731
Db	2701	CTTTCCTCAAGAACCTGTGTCCAGAGGTGTCCCTCAGATGAGGCTGTGGTGTGAATCTTGGAGAA	2760
Db	2732	GACATGTGTGAATCTTCCCTGTAGAAAGACAGAGCCCTCGAGTGTGAGAGGCTTTTGTGAGAT	2791

Db 2761 GACAGTGTGAACCTCCCTGTAGAGAGAGGCCCCGTGGGTGGACGGCTTTTGTTCAGAT 2820
QY 2792 GCCGGCCACAGGCGCTATTTCCCTGTGGTGGGCGCTCTGTCTGTGATACCGGACCTGTGAGGT 2851
Db 2821 GCCGGCCACAGGCGCTATTTCCCTGTGGTGGGCGCTCTGTCTGTGATACCGGACCTGTGAGGT 2880
QY 2852 GCAGAGGAGACTACCTCCAGCTATGGCCGGAGCTCCATCAGAGCCAGTCTCACCTTCAACCG 2911
Db 2881 GCAGAGGAGACTACCTCCAGCTATGGCCGGAGCTCCATCAGAGCCAGTCTCACCTTCAACCG 2940
QY 2912 CGGCTTCAAGGCTGGAGGAACATGCTCGCAACTCTTTGGGGCTTTGGGGCTGAAGTG 2971
Db 2941 CGGCTTCAAGGCTGGAGGAACATGCTCGCAACTCTTTGGGGCTTTGGGGCTGAAGTG 3000
QY 2972 TCACAGCCTGTTTCTGTGATTTGACAGTGAACAGCCTCCAGAGGCTGTGCACCAACATCTA 3031
Db 3001 TCACAGCCTGTTTCTGTGATTTGACAGTGAACAGCCTCCAGAGGCTGTGCACCAACATCTA 3060
QY 3032 CAAGATCCTCTGTGTGAGGCGTACAGGTTTCACGCATGTGTGCTGCACTCCCATTTCA 3091
Db 3061 CAAGATCCTCTGTGTGAGGCGTACAGGTTTCACGCATGTGTGCTGCACTCCCATTTCA 3120
QY 3092 TCAGCAGTTTGGAGAAACCCCAATTTTCTGGGGCTCATCTGACACGGGCTGCT 3151
Db 3121 TCAGCAGTTTGGAGAAACCCCAATTTTCTGGGGCTCATCTGACACGGGCTGCT 3180
QY 3152 CTGCTACTCATCTCTGAAGCCAGAAAGCAGGAGTGTGCTGGGGGCCAAAGGGCGCGC 3211
Db 3181 CTGCTACTCATCTCTGAAGCCAGAAAGCAGGAGTGTGCTGGGGGCCAAAGGGCGCGC 3240
QY 3212 CGGCGCTCTGCTCCGAGGCGGTGGAGTGGTGTGTGACCAACAGATTTCTGCTCAAGCT 3271
Db 3241 CGGCGCTCTGCTCCGAGGCGGTGGAGTGGTGTGTGACCAACAGATTTCTGCTCAAGCT 3300
QY 3272 GACTCGACACCTGTGTACCTACGTGCTCTCTGGGGTCACTCAGGACAGCCAGAGCA 3331
Db 3301 GACTCGACACCTGTGTACCTACGTGCTCTCTGGGGTCACTCAGGACAGCCAGAGCA 3360
QY 3332 GCTGAGTGGAGACTCCCGGGGAGCAGAGCTGACCTGCGCTGAGGCGCCAGCCAAACCGGC 3391
Db 3361 GCTGAGTGGAGACTCCCGGGGAGCAGAGCTGACCTGCGCTGAGGCGCCAGCCAAACCGGC 3420
QY 3392 ACTGCCCTCAGACTTCAAGACCATCTGTGACTGATGGCCACCGCCACAGCCAGGCCGA 3451
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGTGACTGATGGCCACCGCCACAGCCAGGCCGA 3480
QY 3452 GAGCAGACACACAGAGCGCTGTACGCGCGGCTCTACGTCGCCAGGGAGGGGGGGGCC 3511
Db 3481 GAGCAGACACACAGAGCGCTGTACGCGCGGCTCTACGTCGCCAGGGAGGGGGGGGCC 3540
QY 3512 CACACCCAGGCGCGCAGCGCTGGAGTCTGAGGCTGAGTGAAGTGTGGCCGAGGCGCTG 3571
Db 3541 CACACCCAGGCGCGCAGCGCTGGAGTCTGAGGCTGAGTGAAGTGTGGCCGAGGCGCTG 3600
QY 3572 CATGTCCGGCTGAAGGCTAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAGGGCT 3631
Db 3601 CATGTCCGGCTGAAGGCTAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAGGGCT 3660
QY 3632 GAGTGTCAAGACACTGCGCTTCTCACTTCCACAGAGGCTGGGCTCCAGCCCA 3691
Db 3661 GAGTGTCAAGACACTGCGCTTCTCACTTCCACAGAGGCTGGGCTCCAGCCCA 3720
QY 3692 GGGCCAGCTTTTCTCACCAGAGAGCGCGGCTTCCACTCCACATAGAGATAGTCCATCC 3751
Db 3721 GGGCCAGCTTTTCTCACCAGAGAGCGCGGCTTCCACTCCACATAGAGATAGTCCATCC 3780
QY 3752 CCAGATTTCCCATTTTTCACCCCTCGCCCTCTTGGCTTCCACCCCATCC 3811
Db 3781 CCAGATTTCCCATTTTTCACCCCTCGCCCTCTTGGCTTCCACCCCATCC 3840
QY 3812 AGGTGAGACCCCTGAGAAAGACCTGGAGGCTTGGAAATTTGGAGTGAACCAAGGTG 3871
Db 3841 AGGTGAGACCCCTGAGAAAGACCTGGAGGCTTGGAAATTTGGAGTGAACCAAGGTG 3900

QY 3872 CCTGTACACAGGCGAGACCCCTGACCTGGATGGGGTCCCTGTGGTCAAAATTTGGGG 3931
Db 3901 CCTGTACACAGGCGAGAGACCCCTGACCTGGATGGGGTCCCTGTGGTCAAAATTTGGGG 3960
QY 3932 GAGTGTGAGGAGTAAATCTGAATATATGAGTTTTCAGTTTGAAGAAAA 3986
Db 3961 GAGTGTGAGGAGTAAATCTGAATATATGAGTTTTCAGTTTGAAGAAAA 4015

Search completed: April 17, 2003, 04:28:31
Job time : 8324 secs

PA (FARB) BAYER AG.

XX Hagen G, Siegmund H, Welchel W, Wick M, Zubov D;

XX WPI: 1999-081276/07.

DR P-PSDB; AAM90251.

XX New catalytically active subunit of human telomerase - used in the
 PT modulation of telomerase activity, particularly for treating cancer
 PT and ageing

PS Claim 4: Fig 1: 76pp: German.

XX This sequence encodes a novel human catalytic telomerase sub-unit
 CC (hTC). The encoded protein can be used in screening assays to identify
 CC modulators of telomerase and to treat or inhibit cellular disorders,
 CC death, defects and/or other pathological processes involving telomerase,
 CC particularly cancer and ageing (also suitable for this are agents that
 CC stimulate, inhibit or mimic the activity of the subunit). Antisense
 CC nucleic acids inhibit telomerase action (by binding to specific mRNA),
 CC particularly in neoplastic cells and may be expressed in vivo. Antibodies
 CC and fragments of the protein, used as probes or primers, are used to
 CC diagnose telomerase-related conditions (especially neoplasia) by (1)
 CC detecting abnormal levels of the subunit protein in body fluids or
 CC tissues or (11) by measuring the amount of the encoding nucleic acid.
 CC Expression of the nucleic acid encoding the subunit mRNA is confined to
 CC tumour cells, in contrast to the ubiquitous expression of the telomerase
 CC RNA subunit.

SQ Sequence 4042 Bp: 684 A; 1364 C; 1277 G; 717 T; 0 other;

Query Match 99.8%; Score 3996; DB 20; Length 4042;

Best Local Similarity 99.1%; Pred. No. 8.5e-148;

Matches 4006; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 1 GTTTAGGACGCGTGCCTCTGCTGCGACGCTGGAGACCTGGCCCCGCCACCCCG 60
 DB 1 GTTTAGGACGCGTGCCTCTGCTGCGACGCTGGAGACCTGGCCCCGCCACCCCG 60
 QY 61 CGATCCCGGCGCTCCCGGCTCCGAGCGGTGCTCCCTGCTGGCGACCTACCCGG 120
 DB 61 CGATCCCGGCGCTCCCGGCTCCGAGCGGTGCTCCCTGCTGGCGACCTACCCGG 120
 QY 121 AGTGTCTGCGCTGCGACGTTGCTGCGGCGCTGGGGCCCGAGGCTGGCGCTGTGC 180
 DB 121 AGTGTCTGCGCTGCGACGTTGCTGCGGCGCTGGGGCCCGAGGCTGGCGCTGTGC 180
 QY 181 AGCGGGGAGACCGCGGCTTCCGCGGCTGTGGCCCAAGTGGCTGTGCTGCTCCCT 240
 DB 181 AGCGGGGAGACCGCGGCTTCCGCGGCTGTGGCCCAAGTGGCTGTGCTGCTCCCT 240
 QY 241 GGGACGACGAGCGCGCGCGCGCGCGCTCTCCGCGAGTGTCTGCTGAGGAGAC 300
 DB 241 GGGACGACGAGCGCGCGCGCGCGCGCTCTCCGCGAGTGTCTGCTGAGGAGAC 300
 QY 301 TGTGTGCGCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGAGAAAGCTGTGCGCTTCG 360
 DB 301 TGTGTGCGCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGAGAAAGCTGTGCGCTTCG 360
 QY 361 GCTTGGCGCTGTGAGACGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 420
 DB 361 GCTTGGCGCTGTGAGACGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 420
 QY 421 GCAGCTACCTGCGCAACAGCGTGAACGACGACGCTGCGGGAGCGGGGCTGGGCTGC 480
 DB 421 GCAGCTACCTGCGCAACAGCGTGAACGACGACGCTGCGGGAGCGGGGCTGGGCTGC 480
 QY 481 TGTGTGCGCGCGTGGGCGACGAGTGTGCTTACCTGCTGGACGCTGCGCGCTTTTG 540
 DB 481 TGTGTGCGCGCGTGGGCGACGAGTGTGCTTACCTGCTGGACGCTGCGCGCTTTTG 540
 QY 541 TGTGTGCGCTTCCAGCTGCGCTTACGAGTGTGCGGGCGCGCGCTTACGAGCTCGGC 600
 DB 541 TGTGTGCGCTTCCAGCTGCGCTTACGAGTGTGCGGGCGCGCGCTTACGAGCTCGGC 600

DB 541 TGTGTGCGCTTCCAGCTGCGCTTACGAGTGTGCGGGCGCGCGCTTACGAGCTCGGC 600
 QY 601 CTGCACTACAGCG 660
 DB 601 CTGCACTACAGCG 660
 QY 661 AACGGGCTGGAACCATAGCGTCAAGGAGCGCGGGGCTCCCTGGGCTGCCAGCCCGG 720
 DB 661 AACGGGCTGGAACCATAGCGTCAAGGAGCGCGGGGCTCCCTGGGCTGCCAGCCCGG 720
 QY 721 GTGCGAGAGAGCG 780
 DB 721 GTGCGAGAGAGCG 780
 QY 781 GTGGGCTGCGCGCTGAGCG 840
 DB 781 GTGGGCTGCGCGCTGAGCG 840
 QY 841 GCAGAGCGGTGAGCGAGTACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
 DB 841 GCAGAGCGGTGAGCGAGTACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
 QY 901 AAGAGCCACCTTTTGTGAGGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
 DB 901 AAGAGCCACCTTTTGTGAGGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
 QY 961 GCGGCGAGCAGCAGCG 1020
 DB 961 GCGGCGAGCAGCAGCG 1020
 QY 1021 CTTGTCCCGCGGTGTACGCGCGAGCAAGCACTTCTTCTACTCTGAGCGCAAGAGAC 1080
 DB 1021 CTTGTCCCGCGGTGTACGCGCGAGCAAGCACTTCTTCTACTCTGAGCGCAAGAGAC 1080
 QY 1081 AGCTGCGCGCTCTTCTTCTACTACTCTCTGTAGAGCCCAAGCTGTGCTGTGCGAGCG 1140
 DB 1081 AGCTGCGCGCTCTTCTTCTACTACTCTCTGTAGAGCCCAAGCTGTGCTGTGCGAGCG 1140
 QY 1141 TGTGTGAGACATCTTTTGTGAGGCTGTGAGCGCTGTGAGCTGTGAGGCTGTGAGG 1200
 DB 1141 TGTGTGAGACATCTTTTGTGAGGCTGTGAGCGCTGTGAGCTGTGAGGCTGTGAGG 1200
 QY 1201 CCGCGCTGCG 1260
 DB 1201 CCGCGCTGCG 1260
 QY 1261 ACGCGCATGCG 1320
 DB 1261 ACGCGCATGCG 1320
 QY 1321 CCGCGAGCGCGGTGTGTGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
 DB 1321 CCGCGAGCGCGGTGTGTGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
 QY 1381 AGGAGGACACAGACCG 1440
 DB 1381 AGGAGGACACAGACCG 1440
 QY 1441 AGGTGTAGGCTGTGTGCG 1500
 DB 1441 AGGTGTAGGCTGTGTGCG 1500
 QY 1501 CCAGGACACAGAGCGCGCTTCTCTAGAGAACACCAAGTTATCTCTCTGAGGAGAC 1560
 DB 1501 CCAGGACACAGAGCGCGCTTCTCTAGAGAACACCAAGTTATCTCTCTGAGGAGAC 1560
 QY 1561 ATGCAAGCTCTGCTGTGAGAGCTGTGAGATGAGCTGTGCGGAGCTGTGCGGCTTGGC 1620
 DB 1561 ATGCAAGCTCTGCTGTGAGAGCTGTGAGATGAGCTGTGCGGAGCTGTGCGGCTTGGC 1620
 QY 1621 TGGCGAGAGCG 1680
 DB 1621 TGGCGAGAGCG 1680

```
QY 1681 TCCTGGCCAAAGTTCCTCAGCTGCTGATGAGTGTGTACGTCTGAGCTGCTCAGGCTCTT 1740
    |||||||
Db 1681 TCCTGGCCAAAGTTCCTCAGCTGCTGATGAGTGTGTGTACGTCTGAGCTGCTCAGGCTCTT 1740
QY 1741 TCTTTTATGTACGAGAGACCACTTTCAAAAGACAGGCTCTTTTCTCTACCGGAAAGATG 1800
    |||||||
Db 1741 TCTTTTATGTACGAGAGACCACTTTCAAAAGACAGGCTCTTTTCTCTACCGGAAAGATG 1800
QY 1801 TCTGGAGCAATGTCAGAAAGATGGAATCAGACAGCACTTGAGAGAGGTGTGAGCTGGGG 1860
    |||||||
Db 1801 TCTGGAGCAATGTCAGAAAGATGGAATCAGACAGCACTTGAGAGAGGTGTGAGCTGGGG 1860
QY 1861 AGCTGTGGAAGCAGAGAGTGTGAGGAGCATGCGGAAGCAGAGGCGCGCTGCTGAGCTGCA 1920
    |||||||
Db 1861 AGCTGTGGAAGCAGAGAGTGTGAGGAGCATGCGGAAGCAGAGGCGCGCTGCTGAGCTGCA 1920
QY 1921 GACTCGGCTTATCCCAACGCTGAGAGGCTGAGGCGCGGATGTTGAACATGGAATACGTCG 1980
    |||||||
Db 1921 GACTCGGCTTATCCCAACGCTGAGAGGCTGAGGCGCGGATGTTGAACATGGAATACGTCG 1980
QY 1981 TGGGAGCCAGAGAGTTCGCGAGAGAAAAGAGGCGCGAGCTCTCAGCTCTGAGAGGTGAAG 2040
    |||||||
Db 1981 TGGGAGCCAGAGAGTTCGCGAGAGAAAAGAGGCGCGAGCTCTCAGCTCTGAGAGGTGAAG 2040
QY 2041 CACTGTTCAGGCTGTCAACTACAGAGGCGCGGCGCGCGCTCTCTGAGGCGCTCTG 2100
    |||||||
Db 2041 CACTGTTCAGGCTGTCAACTACAGAGGCGCGGCGCGCGCTCTCTGAGGCGCTCTG 2100
QY 2101 TCTGTGGGCTGTGAGCATATCAGAGGCTGTGCGACCTTCGTGTGTGTGCGGGGCC 2160
    |||||||
Db 2101 TCTGTGGGCTGTGAGCATATCAGAGGCTGTGCGACCTTCGTGTGTGTGCGGGGCC 2160
QY 2161 AGGACCCGCGCTGAGCTGTGTA-----CA 2184
    |||||||
Db 2161 AGGACCCGCGCTGAGCTGTGTA-----CA 2184
QY 2185 TCCCCAGAGACAGGCTCAGCGAGAGTATCAGCAGCATATCAAAACCCAGAGACAGTACT 2244
    |||||||
Db 2185 TCCCCAGAGACAGGCTCAGCGAGAGTATCAGCAGCATATCAAAACCCAGAGACAGTACT 2244
QY 2221 TCCCCAGAGACAGGCTCAGCGAGAGTATCAGCAGCATATCAAAACCCAGAGACAGTACT 2280
    |||||||
Db 2221 TCCCCAGAGACAGGCTCAGCGAGAGTATCAGCAGCATATCAAAACCCAGAGACAGTACT 2280
QY 2245 GCGTGTGCGGTATGCGGTGTGAGAGAGGCGCGCATGAGGCGAGCTGCGCAAGGCTTCA 2304
    |||||||
Db 2245 GCGTGTGCGGTATGCGGTGTGAGAGAGGCGCGCATGAGGCGAGCTGCGCAAGGCTTCA 2304
QY 2281 GCGTGTGCGGTATGCGGTGTGAGAGAGGCGCGCATGAGGCGAGCTGCGCAAGGCTTCA 2340
    |||||||
Db 2281 GCGTGTGCGGTATGCGGTGTGAGAGAGGCGCGCATGAGGCGAGCTGCGCAAGGCTTCA 2340
QY 2305 AGAGCAGAGCTCTACCTTGAAGACCTCAGCGGTACAGAGAGTGTGAGGCTGACG 2364
    |||||||
Db 2305 AGAGCAGAGCTCTACCTTGAAGACCTCAGCGGTACAGAGAGTGTGAGGCTGACG 2364
QY 2341 AGAGCAGAGCTCTACCTTGAAGACCTCAGCGGTACAGAGAGTGTGAGGCTGACG 2400
    |||||||
Db 2341 AGAGCAGAGCTCTACCTTGAAGACCTCAGCGGTACAGAGAGTGTGAGGCTGACG 2400
QY 2365 TCGAGAGACAGAGCCGCTGAGGAGTGCCTGTGTATCAGAGACAGCTCTCTGTAATG 2424
    |||||||
Db 2365 TCGAGAGACAGAGCCGCTGAGGAGTGCCTGTGTATCAGAGACAGCTCTCTGTAATG 2424
QY 2401 TCGAGAGACAGAGCCGCTGAGGAGTGCCTGTGTATCAGAGACAGCTCTCTGTAATG 2460
    |||||||
Db 2401 TCGAGAGACAGAGCCGCTGAGGAGTGCCTGTGTATCAGAGACAGCTCTCTGTAATG 2460
QY 2425 AGGCGAGAGTGGCTTGTGAGAGTGTCTACGCTTATGTCACACAGCGCGTGCAC 2484
    |||||||
Db 2425 AGGCGAGAGTGGCTTGTGAGAGTGTCTACGCTTATGTCACACAGCGCGTGCAC 2484
QY 2461 AGGCGAGAGTGGCTTGTGAGAGTGTCTACGCTTATGTCACACAGCGCGTGCAC 2520
    |||||||
Db 2461 AGGCGAGAGTGGCTTGTGAGAGTGTCTACGCTTATGTCACACAGCGCGTGCAC 2520
QY 2485 TCGAGGAGCAATGCTCTACAGTGTGAGAGGATCCGAGAGGCTCATCTCTGCAAGC 2544
    |||||||
Db 2485 TCGAGGAGCAATGCTCTACAGTGTGAGAGGATCCGAGAGGCTCATCTCTGCAAGC 2544
QY 2521 TCGAGGAGCAATGCTCTACAGTGTGAGAGGATCCGAGAGGCTCATCTCTGCAAGC 2580
    |||||||
Db 2521 TCGAGGAGCAATGCTCTACAGTGTGAGAGGATCCGAGAGGCTCATCTCTGCAAGC 2580
QY 2545 TCGTGTGAGAGCTGTGTAGGAGAGATGAGAAACAAGTGTGAGGAGATGAGGGGG 2604
    |||||||
Db 2545 TCGTGTGAGAGCTGTGTAGGAGAGATGAGAAACAAGTGTGAGGAGATGAGGGGG 2604
QY 2581 TCGTGTGAGAGCTGTGTAGGAGAGATGAGAAACAAGTGTGAGGAGATGAGGGGG 2640
    |||||||
Db 2581 TCGTGTGAGAGCTGTGTAGGAGAGATGAGAAACAAGTGTGAGGAGATGAGGGGG 2640
QY 2605 AGGGGCTGCTGCTGCTGTTGGTGGATGATTTCTTTGGTGGAGACCTCAGCTCAGCCAGC 2664
    |||||||
Db 2605 AGGGGCTGCTGCTGCTGTTGGTGGATGATTTCTTTGGTGGAGACCTCAGCTCAGCCAGC 2664
QY 2641 AGGGGCTGCTGCTGCTGTTGGTGGATGATTTCTTTGGTGGAGACCTCAGCTCAGCCAGC 2700
    |||||||
Db 2641 AGGGGCTGCTGCTGCTGTTGGTGGATGATTTCTTTGGTGGAGACCTCAGCTCAGCCAGC 2700
QY 2665 CGAAAACCTTCTCAGAGACCTGTGTCAGAGGTGCTCTGAGATGTGGCTGCGGTGAACT 2724
    |||||||
Db 2665 CGAAAACCTTCTCAGAGACCTGTGTCAGAGGTGCTCTGAGATGTGGCTGCGGTGAACT 2724
QY 2701 CGAAAACCTTCTCAGAGACCTGTGTCAGAGGTGCTCTGAGATGTGGCTGCGGTGAACT 2760
    |||||||
Db 2701 CGAAAACCTTCTCAGAGACCTGTGTCAGAGGTGCTCTGAGATGTGGCTGCGGTGAACT 2760

QY 2725 TCGGAGAGACAGTGTGAACCTTCCCTGTAGAGAGAGAGCCCTGGGTGGACAGCTTTTG 2784
    |||||||
Db 2725 TCGGAGAGACAGTGTGAACCTTCCCTGTAGAGAGAGAGCCCTGGGTGGACAGCTTTTG 2784
QY 2761 TCGGAGAGACAGTGTGAACCTTCCCTGTAGAGAGAGAGCCCTGGGTGGACAGCTTTTG 2820
    |||||||
Db 2761 TCGGAGAGACAGTGTGAACCTTCCCTGTAGAGAGAGAGCCCTGGGTGGACAGCTTTTG 2820
QY 2785 TTCAAGATGCGGCGCCACAGGCTATTTCCCTGTGTGCGGCTGTGTGTGATACCGAGCC 2844
    |||||||
Db 2785 TTCAAGATGCGGCGCCACAGGCTATTTCCCTGTGTGCGGCTGTGTGTGATACCGAGCC 2844
QY 2821 TTCAAGATGCGGCGCCACAGGCTATTTCCCTGTGTGCGGCTGTGTGTGATACCGAGCC 2880
    |||||||
Db 2821 TTCAAGATGCGGCGCCACAGGCTATTTCCCTGTGTGCGGCTGTGTGTGATACCGAGCC 2880
QY 2845 TGGAGGTGACAGAGCACTACTCAGCTATGCGCGGAGCTCTCATGAGAGCACTGCTACCT 2904
    |||||||
Db 2845 TGGAGGTGACAGAGCACTACTCAGCTATGCGCGGAGCTCTCATGAGAGCACTGCTACCT 2904
QY 2881 TGGAGGTGACAGAGCACTACTCAGCTATGCGCGGAGCTCTCATGAGAGCACTGCTACCT 2940
    |||||||
Db 2881 TGGAGGTGACAGAGCACTACTCAGCTATGCGCGGAGCTCTCATGAGAGCACTGCTACCT 2940
QY 2905 TCAACCGGCGCTTCAAGGCTGAGGAGAAACATGCGTGCACAACTCTTGGGGTCTGCGG 2964
    |||||||
Db 2905 TCAACCGGCGCTTCAAGGCTGAGGAGAAACATGCGTGCACAACTCTTGGGGTCTGCGG 2964
QY 2941 TCAACCGGCGCTTCAAGGCTGAGGAGAAACATGCGTGCACAACTCTTGGGGTCTGCGG 3000
    |||||||
Db 2941 TCAACCGGCGCTTCAAGGCTGAGGAGAAACATGCGTGCACAACTCTTGGGGTCTGCGG 3000
QY 2965 TGAAGTGTACACAGCTGTCTTGTGATTTGCAAGSTGAACAGCTCTCAGAGGCTGTGACCA 3024
    |||||||
Db 2965 TGAAGTGTACACAGCTGTCTTGTGATTTGCAAGSTGAACAGCTCTCAGAGGCTGTGACCA 3024
QY 3001 TGAAGTGTACAGAGCTGTCTTGTGATTTGCAAGSTGAACAGCTCTCAGAGGCTGTGACCA 3060
    |||||||
Db 3001 TGAAGTGTACAGAGCTGTCTTGTGATTTGCAAGSTGAACAGCTCTCAGAGGCTGTGACCA 3060
QY 3025 ACATCTACAGATCTCTCTGTGTGAGGCGTACAGGTTTCAAGCATGTGTGTGTGAGCTCC 3084
    |||||||
Db 3025 ACATCTACAGATCTCTCTGTGTGAGGCGTACAGGTTTCAAGCATGTGTGTGTGAGCTCC 3084
QY 3061 ACATCTACAGATCTCTCTGTGTGAGGCGTACAGGTTTCAAGCATGTGTGTGTGAGCTCC 3120
    |||||||
Db 3061 ACATCTACAGATCTCTCTGTGTGAGGCGTACAGGTTTCAAGCATGTGTGTGTGAGCTCC 3120
QY 3085 CATTTTCATCAGCAAGTTTGAAGAAACCCACATTTTCTGCGCGCTCATCTGTACACAG 3144
    |||||||
Db 3085 CATTTTCATCAGCAAGTTTGAAGAAACCCACATTTTCTGCGCGCTCATCTGTACACAG 3144
QY 3121 CATTTTCATCAGCAAGTTTGAAGAAACCCACATTTTCTGCGCGCTCATCTGTACACAG 3180
    |||||||
Db 3121 CATTTTCATCAGCAAGTTTGAAGAAACCCACATTTTCTGCGCGCTCATCTGTACACAG 3180
QY 3145 CTTCCCTCTCTACTCTCATCTCTGAAAGCAAGAACAGCAGAGGATGTGCGTGGGGCCAG 3204
    |||||||
Db 3145 CTTCCCTCTCTACTCTCATCTCTGAAAGCAAGAACAGCAGAGGATGTGCGTGGGGCCAG 3204
QY 3181 CTTCCCTCTCTACTCTCATCTCTGAAAGCAAGAACAGCAGAGGATGTGCGTGGGGCCAG 3240
    |||||||
Db 3181 CTTCCCTCTCTACTCTCATCTCTGAAAGCAAGAACAGCAGAGGATGTGCGTGGGGCCAG 3240
QY 3205 GCGGCGCGCGGCTGTGCGCTTCCGAGGCGGTGAGTGTGCGTGTGCGCACCACCAATCTCTG 3264
    |||||||
Db 3205 GCGGCGCGCGGCTGTGCGCTTCCGAGGCGGTGAGTGTGCGTGTGCGCACCACCAATCTCTG 3264
QY 3241 GCGGCGCGCGGCTGTGCGCTTCCGAGGCGGTGAGTGTGCGTGTGCGCACCACCAATCTCTG 3300
    |||||||
Db 3241 GCGGCGCGCGGCTGTGCGCTTCCGAGGCGGTGAGTGTGCGTGTGCGCACCACCAATCTCTG 3300
QY 3265 TCAAGCTGACGACACGCTGTACCTACCTACGTGACACCTCTGAGGAGTCACTGACAGCC 3324
    |||||||
Db 3265 TCAAGCTGACGACACGCTGTACCTACCTACGTGACACCTCTGAGGAGTCACTGACAGCC 3324
QY 3301 TCAAGCTGACGACACGCTGTACCTACCTACGTGACACCTCTGAGGAGTCACTGACAGCC 3360
    |||||||
Db 3301 TCAAGCTGACGACACGCTGTACCTACCTACGTGACACCTCTGAGGAGTCACTGACAGCC 3360
QY 3325 AGAGCAGAGTGTGAGGAGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3384
    |||||||
Db 3325 AGAGCAGAGTGTGAGGAGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3384
QY 3361 AGAGCAGAGTGTGAGGAGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420
    |||||||
Db 3361 AGAGCAGAGTGTGAGGAGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420
QY 3385 ACCGCGACAGCTGCTCAGACTTCAAGACATCTCTGAGACATGATGAGCCACCGCCACAGC 3444
    |||||||
Db 3385 ACCGCGACAGCTGCTCAGACTTCAAGACATCTCTGAGACATGATGAGCCACCGCCACAGC 3444
QY 3421 ACCGCGACAGCTGCTCAGACTTCAAGACATCTCTGAGACATGATGAGCCACCGCCACAGC 3480
    |||||||
Db 3421 ACCGCGACAGCTGCTCAGACTTCAAGACATCTCTGAGACATGATGAGCCACCGCCACAGC 3480
QY 3445 AGGCGAGAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3504
    |||||||
Db 3445 AGGCGAGAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3504
QY 3481 AGGCGAGAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3540
    |||||||
Db 3481 AGGCGAGAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3540
QY 3505 GCGGCGCCACAGCCAGGCGCCAGCGCTGAGAGTGTGAGGCTGTGAGTGTGAGCGG 3564
    |||||||
Db 3505 GCGGCGCCACAGCCAGGCGCCAGCGCTGAGAGTGTGAGGCTGTGAGTGTGAGCGG 3564
QY 3541 GCGGCGCCACAGCCAGGCGCCAGCGCTGAGAGTGTGAGGCTGTGAGTGTGAGCGG 3600
    |||||||
Db 3541 GCGGCGCCACAGCCAGGCGCCAGCGCTGAGAGTGTGAGGCTGTGAGTGTGAGCGG 3600
QY 3565 AGGCGCTGATGTCCGCTGAAAGCTGAGTGTGCGGCTGAGGAGTGTGAGGAGTGTGAGCC 3624
    |||||||
Db 3565 AGGCGCTGATGTCCGCTGAAAGCTGAGTGTGCGGCTGAGGAGTGTGAGGAGTGTGAGCC 3624
QY 3601 AGGCGCTGATGTCCGCTGAAAGCTGAGTGTGCGGCTGAGGAGTGTGAGGAGTGTGAGCC 3660
    |||||||
Db 3601 AGGCGCTGATGTCCGCTGAAAGCTGAGTGTGCGGCTGAGGAGTGTGAGGAGTGTGAGCC 3660
QY 3625 AAGGCTGAGAGTGTGACAGACACTGCTGCTTCACTTCCCAAGCTGTGAGGCTGTG 3684
    |||||||
Db 3625 AAGGCTGAGAGTGTGACAGACACTGCTGCTTCACTTCCCAAGCTGTGAGGCTGTG 3684
QY 3661 AAGGCTGAGAGTGTGACAGACACTGCTGCTTCACTTCCCAAGCTGTGAGGCTGTG 3720
    |||||||
Db 3661 AAGGCTGAGAGTGTGACAGACACTGCTGCTTCACTTCCCAAGCTGTGAGGCTGTG 3720
QY 3685 CAGCCGAGGCGAGCTTCTCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3744
    |||||||
Db 3685 CAGCCGAGGCGAGCTTCTCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3744
QY 3721 CAGCCGAGGCGAGCTTCTCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3780
    |||||||
Db 3721 CAGCCGAGGCGAGCTTCTCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3780
QY 3745 TCCATCCCAAGATTCGCACTTGTACCCCTGCGCTGCGCTCTTGTGCTTCCACCC 3804
    |||||||
Db 3745 TCCATCCCAAGATTCGCACTTGTACCCCTGCGCTGCGCTCTTGTGCTTCCACCC 3804
QY 3781 TCCATCCCAAGATTCGCACTTGTACCCCTGCGCTGCGCTCTTGTGCTTCCACCC 3840
    |||||||
Db 3781 TCCATCCCAAGATTCGCACTTGTACCCCTGCGCTGCGCTCTTGTGCTTCCACCC 3840
QY 3805 ACCATCAGGTGAGAGACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3864
    |||||||
Db 3805 ACCATCAGGTGAGAGACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3864
```

Db	3841	ACCATCCGAGGTGGAGACCCCTGAGAAGGACCCCTGGAGACTCTGGGAATTTCGACTGACCCAA	3900		
Qy	3865	AGGTGTGCCCCTGTACACAGCGGAGGACCCCTGCACCTGGATGGGGGTCCTGTGGGTCAAA	3924		
Db	3901	AGGTGTGCCCCTGTACACAGCGGAGGACCCCTGCACCTGGATGGGGGTCCTGTGGGTCAAA	3960		
Qy	3925	TTGGGGGAGAGTGGCTGTGGGAGTAAATPACTGAATATATGAGTTTTCATTTTGAAAAA	3984		
Db	3961	TTGGGGGAGAGTGGCTGTGGGAGTAAATPACTGAATATATGAGTTTTCATTTTGAAAAA	4020		
Qy	3985	AAAAAAAAAAAAAAAAAAAAA 4006			
Db	4021	AAAAAAAAAAAAAAAAAAAAA 4042			
RESULT 2					
AAV22428					
ID	AAV22428	standard; cDNA; 4037 BP.			
XX	AAV22428;				
XX	13-AUG-1998	(first entry)			
XX					
DE	Human telomerase reverse transcriptase encoding cDNA refined sequence.				
XX					
KW	Human: telomerase reverse transcriptase; hTERT; TRT; diagnosis;				
XX	prognosis; cell proliferation; cancer; ageing; ribonucleoprotein; ss.				
XX	Homo sapiens.				
XX					
FT	Key	Location/Qualifiers			
FT	CDS	56..3454			
FT	/*tag= a				
FT	/product= "telomerase reverse transcriptase"				
FT	/note= "refined sequence"				
XX					
PN	GB2317891-A.				
PD	08-APR-1998.				
XX					
PF	01-OCT-1997;	97GB-0020890.			
XX					
PR	14-AUG-1997;	97US-0915503.			
PR	01-OCT-1996;	96US-0724643.			
PR	18-APR-1997;	97US-0844419.			
PR	25-APR-1997;	97US-0846017.			
PR	06-MAY-1997;	97US-0851843.			
PR	09-MAY-1997;	97US-0854050.			
PR	14-AUG-1997;	97US-0911312.			
PR	14-AUG-1997;	97US-0912951.			
XX					
PA	(GERO-) GERON CORP.				
PA	(UYTE-) UNIV TECHNOLOGY CORP.				
XX					
PI	Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;				
PI	Morlin GB, Nakamura T, Harley CB;				
XX					
DR	WPI, 1998-171633/16.				
DR	P-PSDB, AAW56113.				
XX					
PT	Pure and recombinant human Telomerase Reverse Transcriptase and its				
PT	variants - are useful in the diagnosis, prognosis and treatment of				
PT	cell proliferation conditions especially cancer and ageing				
XX					
PS	Example 1; Fig 74; 387pp; English.				
CC	The present sequence encodes human telomerase reverse transcriptase				
CC	(hTERT), which is a ribonucleoprotein. The present invention also				
CC	describes the following methods: (A) determining whether a test compound				
CC	is a modulator of hTERT by detecting the change in hTERT recombinant				
CC	protein or polynucleotide, on administration of the compound; (B)				
CC	preparation of recombinant telomerase by contacting a protein				

		CC	preparation of hTERT with a telomerase RNA component; (C) detection of
		CC	the hTERT RNA or protein in a sample by binding a relevant probe to the
		CC	sample and detecting the complex formed or in the case of RNA detection,
		CC	amplifying the product and correlating the presence of complex or
		CC	amplification product with presence of hTERT in the sample; and (D)
		CC	increasing the proliferation of a vertebrate cell by increasing hTERT
		CC	expression; and (E) the use of an agent that causes an increase in cell
		CC	vertebrate cell proliferation to create a medicament that inhibits
		CC	ageing. A protein preparation of hTERT and the polynucleotide encoding
		CC	hTERT can be used in the manufacture of medicaments for inhibiting the
		CC	effect of ageing or cancer. Inhibitors of telomerase activity can be
		CC	used to treat conditions that are associated with high telomerase
		CC	activity. A protein preparation of hTERT can also be used in the new
		CC	methods.
SQ	Sequence 4037 BP; 682 A; 1362 C; 1275 G; 714 T; 4 other;		
	Query Match	99.4%; Score 3981; DB 19; Length 4037;	
	Best Local Similarity	98.9%; Pred. No. 3.2e-147;	
	Matches 3991; Conservative	4; Mismatches 4; Indels 36; Gaps 1	
QY	8 GGAGGCGTCGCCTCCGTGGACGTCGGGAAGCCCTGGGCCCGGACCCTCCGGCATGGCC	67	
DB	1 GAAGCGCTCGTCCTCGTCGCAAGGGGAAGCCCTGGGCCCGGACCCTCCGGCATGGCC	60	
QY	68 GCGCGCTCCCCTGCGCGAGCCGTGGCGCTCCCTGCTGCGCACACTACCGAAGTGCT	127	
DB	61 GCGCGCTCCCCGCTGGCGAGCCGTGGCGCTCCGCTGCGCAGCACTACCGAAGTGCT	120	
QY	128 GCCCGTGGCCAGTTGTGTGCGGCGCTGGGGGCCCCAGGGCTGGCGGCTGGTCAGCGGG	187	
DB	121 GCCCGTGGCCAGTTGTGTGCGGCGCTGGGGGCCCCAGGGCTGGCGGCTGGTCAGCGGG	180	
QY	188 GGACCCGCGCGCTTCCGCGCGCTGGTGCGCCAGTCTGTGTGGTGCTCCCTGGGACGC	247	
DB	181 GGACCCGCGCGCTTCCGCGCGCTGGTGCGCCAGTCTGTGTGGTGCTCCCTGGGACGC	240	
QY	248 ACGGCGCGCCCCCGCGCCCCCTCTTCGCGCAGAAGTGCTCTGCTGAAGAAGCTGTGGC	307	
DB	241 ACGGCGCGCCCCCGCGCCCCCTCTTCGCGCAGAAGTGCTCTGCTGAAGAAGCTGTGGC	300	
QY	308 CGAGAGCTCGAAGAGGCTGTGGAGGCGGGCGGAAGAAGTGCTGGGCTGGCTGGC	367	
DB	301 CGAGAGCTCGAAGAGGCTGTGGAGGCGGGCGGAAGAAGTGCTGGGCTGGCTGGC	360	
QY	368 GCTGTGACGGGGCCCGCGGGGGCCCCCGGAGGCTTTCACACACAGCTGCGCAGCTA	427	
DB	361 GCTGTGACGGGGCCCGCGGGGGCCCCCGGAGGCTTTCACACACAGCTGCGCAGCTA	420	
QY	428 CCTGGCCAAACAGGTGATCCGAGGACAAGCTGGGGGGGAGCGGGGGCTGCTGTGGG	487	
DB	421 CCTGGCCAAACAGGTGATCCGAGGACAAGCTGGGGGGGAGCGGGGGCTGCTGTGGG	480	
QY	488 CCGCGTGGGCGAGACGTGCTGACCTGCTGGACAGCTGCGGCTCTTGTGTGTGT	547	
DB	481 CCGCGTGGGCGAGACGTGCTGACCTGCTGGACAGCTGCGGCTCTTGTGTGTGT	540	
QY	548 GCGTCCCAAGTGGCTTACAGAGTGTGGGGCGCGCGCTGTACACAGTGGGGCTGGCCAC	607	
DB	541 GCGTCCCAAGTGGCTTACAGAGTGTGGGGCGCGCGCTGTGTACACAGTGGGGCTGGCCAC	600	
QY	608 TTAGGCGCGGGCCCCCGCCACAGCTAGTGGACCCGGAAGGCTGTGGATTGGAGAGGGC	667	
DB	601 TTAGGCGCGGGCCCCCGCCACAGCTAGTGGACCCGGAAGGCTGTGGATTGGAGAGGGC	660	
QY	668 CTGGAACCATTAAGTACAGGAGAGCGGGGCTCCCTGGGCTGACAGCCCCGGGTGCGAG	727	
DB	661 CTGGAACCATTAAGTACAGGAGAGCGGGGCTCCCTGGGCTGACAGCCCCGGGTGCGAG	720	
QY	728 GAGGGCGGGGGGAGTGGCCAGGCGGAAGTGTGGCGTTGGCCAAAGAGGCCAGGCGTGGGC	787	
DB	721 GAGGGCGGGGGGAGTGGCCAGGCGGAAGTGTGGCGTTGGCCAAAGAGGCCAGGCGTGGGC	780	

Oy	788	TGCCCCGTAGCCCGAGACGGCACCCTTGGAGAGGGGTCTTGAGGCCCAACCCGGGCAGAC	847
Dd	781	TGCCCGTAGCCGAGAGCCGACGCCCTTTGGAGAGGGGTCTTGAGGCCCAACCCGGGCAGAC	840
Oy	848	GCGTSGAACGAATGAAACCGTGGTTTTTCGTGTGGTGTACACTGGCCACAACCCCGCCAAACAC	907
Dd	841	GCGTSGAACGAATGAAACCGTGGTTTTTCGTGTGGTGTACACTGGCCACAACCCCGCCAAACAC	900
Oy	908	CACCTCTTTTGGAGAGGGGTGGCTGTCTGTGGACAGGGCACATCCGACCATCCGTGGGGCCGCA	967
Dd	901	CACCTCTTTTGGAGAGGGGTGGCTCTTCTGTGGACAGGGCACATCCGACCATCCGTGGGGCCGCA	960
Oy	968	GCACACAGCGGGGGCCCCCATCATCTGCGGGCACACAGTCCCTGGGACAGCGCTGTCC	1027
Dd	961	GCACACAGCGGGGGCCCCCATCAATCTGCGGGCACACAGTCCCTGGGACAGCGCTGTCC	1020
Oy	1028	CCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCCAGGGGCACAAGAGAGCTGGC	1087
Dd	1021	CCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCCAGGGGCACAAGAGAGCTGTGG	1080
Oy	1088	GCCCCTCTTCTACTACACTCTCTGTAGAGGCCACAGCCTACATGGGCGCTCGAGAGCTCTGTGA	1147
Dd	1081	GCCCCTCTTCTACTACACTCTCTGTAGAGGCCACAGCCTACATGGGCGCTCGAGAGCTCTGTGA	1140
Oy	1148	GACCACTTTTCTGTGGGTTCAGAGGCCCTGATGTGACAGAGACATCCCGCAGATTGCCCGCT	1207
Dd	1141	GACCACTTTTCTGTGGGTTCAGAGGCCCTGTGATGTGACAGAGACATCCCGCAGATTGCCCGCT	1200
Oy	1208	GCCCCACGCTTAOTGGCAAATAGCGGGCCCCCTGTTTCTGTGACACTGTGTGGGAACACGCGCA	1267
Dd	1201	GCCCCACGCTTAOTGGCAAATAGCGGGCCCCCTGTTTCTGTGACACTGTGTGGGAACACGCGCA	1260
Oy	1268	GTGCCCCCTACGGGGGTGTCTCCCAAGAAGGACACTGCCCGCTCGAAGCTGGCGGTCAACCCAC	1327
Dd	1261	GTGCCCCCTACGGGGGTGTCTCCCAAGAAGGACACTGCCCGCTCGAAGCTGGCGGTCAACCCAC	1320
Oy	1328	AACCGGTGTGTGTGCGCGGGAGAAAGCCCAAGGAGCTCTGTGTGGGGCCCCCAGAGAGAGA	1387
Dd	1321	AACCGGTGTGTGTGCGCGGGAGAAAGCCCAAGGAGCTCTGTGTGGGGCCCCCAGAGAGAGA	1380
Oy	1388	CACAGAACCCCCGTGCGCTGTGTGTGACAGCTGCTCCGCGACACAGAGAGCCTCTGTGACAGTGTGA	1447
Dd	1381	CACAGAACCCCCGTGCGCTGTGTGTGACAGCTGCTCCGCGACACAGAGAGCCTCTGTGACAGTGTGA	1440
Oy	1448	CGGCTTGTGTGCGGGGCTCCTGTGCGCGGGGTGGTGTGGCCCTCTGTGGGCTCTCAGAGCA	1507
Dd	1441	CGGCTTGTGTGCGGGGCTCCTGTGCGCGGGGTGGTGTGGCCCTCTGTGGGCTCTCAGAGCA	1500
Oy	1508	CACAGAACGCGCGCTTCTCAGAGAAACACCAAGAAAGTTATCTCCCTGTGGGAGACATCCCAA	1567
Dd	1501	CACAGAACGCGCGCTTCTCAGAGAAACACCAAGAAAGTTATCTCCCTGTGGGAGACATCCCAA	1560
Oy	1568	GCTTCTGCTCAGAGAGCTGAGAGTGAAGATGTAGCGTGGGGAATCGCTTGGTGGCGGACG	1627
Dd	1561	GCTTCTGCTCAGAGAGCTGAGAGTGAAGATGTAGCGTGGGGAATCGCTTGGTGGCGGACG	1620
Oy	1628	GAGGCCAAGGGGGTGGTGTGTCCGGCGCCAGAGACACCGTGTGCGTGGAGAGATCCGTGGC	1687
Dd	1621	GAGGCCAAGGGGGTGGTGTGTGTCCGGCGCCAGAGACACCGTGTGCGTGGAGAGATCCGTGGC	1680
Oy	1688	CAGGTCTCTCACTGTGGTGAAGATGTGTAGAGTGTGTGABATGTGTGACGTCTTTCCTTTTA	1747
Dd	1681	CAGGTCTCTCACTGTGCTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1740
Oy	1748	TGTCTACGGAACACACGTTTCAAAAAGAACAGGCTCTTTTCTCTACGGAAGAGTGTCTGGAG	1807
Dd	1741	TGTCTACGGAACACACGTTTCAAAAAGAACAGGCTCTTTTCTCTACGGAAGAGTGTCTGGAG	1800
Oy	1808	CAGTTGTCAAAAGCATTTGAGATCAGACAGCACTTTTGAAGAGGGTTCAGACTGGCGGAGCTGTCT	1867
Dd	1801	CAGTTGTCAAAAGCATTTGAGATAATCAGACAGCACTTTTGAAGAGGGTTCAGACTGGCGGAGCTGTCT	1860
Oy	1868	GGAAACAAAGTCAAGGCAAGCATCTGGGAACCCAGAGCCGCCCTCTGTGAAGTCAACTCTCG	1927

Db	1861	GGAGACAGAGCTAGGACGACCTGGGAAACCCAGGCCCGCCCTTGTCGAGCTCCAGACTCG	1920
Oy	1928	CTTCATCCCCAAAGCCGACGGGGCTGGGGCCGATTGTGAACTATGAGACTACGCTGGGAGAC	1987
Db	1921	CTTCTATCCCAACCTGACGGGGCTGGGGCCATTGTGAACATGAGACTACGCTGGGAGAC	1980
Oy	1988	CAGAACTCTCCGAGAGAAAAAGAGGGCCGAGAGCTCTACCTGAGGGTGAAGGCACTGTT	2047
Db	1981	CAGAACTCTCCGAGAGAAAAAGAGGGCCGAGAGCTCTACCTGAGGGTGAAGGAGCTGTT	2040
Oy	2048	CAGGGCTCTAACTACGAGGGGGGGGGCCGCTCTGAGGCGCTCTCTGCTG	2107
Db	2041	CAGGGCTCTAACTACGAGGGGGGGGGCCGCTCTGAGGCGCTCTCTGCTG	2100
Oy	2108	CCGTGAGATATCCACAGGGGCTTGGGCACCTTGTCTGCTGGTGGCGGCCAGGACCC	2167
Db	2101	CCGTGAGATATCCACAGGGGCTTGGGCACCTTGTCTGCTGGTGGCGGCCAGGACCC	2160
Oy	2168	GGCGGCTGACCTGTA-----CATTCCCCA	2191
Db	2161	GGCGGCTGACCTGTACTTGTTCAGAGCTGGATGTACAGGGGGGCTACGACACACTCCCCCA	2250
Oy	2192	GGACAGGCTACGAGAGGTCATCGCCAGCACTCATCAACCCCGAAGACAGTACGCTGGCG	2251
Db	2221	GGACAGGCTACGAGAGGTCATCGCCAGCACTCATCAACCCCGAAGACAGTACGCTGGCG	2280
Oy	2252	TCGGATGAGCGCTGCTCCAGAAAGGCCGCCATGGGACGTGGACGTCCGAAAGGCTTTCAGAGCCA	2311
Db	2281	TCGGATGAGCGCTGCTCCAGAAAGGCCGCCATGGGACGTGGACGTCCGAAAGGCTTTCAGAGCCA	2340
Oy	2312	GGCTCTACCTTTCAGACAGACCTCCAGGCCGTACATGAGAGATGGTGGTGTACCTCGAGGA	2371
Db	2341	GGCTCTACCTTTCAGACAGACCTCCAGGCCGTACATGAGAGATGGTGGTGTACCTCGAGGA	2400
Oy	2372	GACCAAGCCCGCTAGAGGATGGCGCTCTCATGAGCAAGGTCTCTCCGTAATAGGCCAG	2431
Db	2401	GACCAAGCCCGCTAGAGGATGGCGCTCTCATGAGCAAGGTCTCTCCGTAATAGGCCAG	2460
Oy	2432	CAGTGGCTCTGAGAGCTCTCTCAGGCTTCATGTGCCACACAGCCGTGGGCAATCAGGGG	2491
Db	2461	CAGTGGCTCTGAGAGCTCTCTCAGGCTTCATGTGGCCACACAGCCGTGGGCAATCAGGGG	2520
Oy	2492	CAGTCTACAGTCCAGTSCCAGAGGGATCCCGAGGGCTCCATCTCTCCAGCGTGTCTG	2551
Db	2521	CAGTCTACAGTCCAGTSCCAGAGGGATCCCGAGGGCTCCATCTCTCCAGCGTGTCTG	2580
Oy	2552	CAGCTGTGCTAGGCGACAGAGAAACAAGCTGTTTGGCGGGATTTCGGCGGAGCGGCT	2611
Db	2581	CAGCTGTGCTAGGCGACAGAGAAACAAGCTGTTTGGCGGGATTTCGGCGGAGCGGCT	2640
Oy	2612	GCTCCGTGTTTTGAGAGATTTCTTGTGGTGACACTCACCTCACCCACCGCGAAAC	2671
Db	2641	GCTCCGTGTTTTGAGAGATTTCTTGTGGTGACACTCACCTCACCCACCGCGAAAC	2700
Oy	2672	CTTCTCTAGAACCTGTGTGAGAGTGGAGGTGCCATGATATGGTGTGGTGGAACTTGGGGA	2731
Db	2701	CTTCTCTAGAACCTGTGTGAGAGTGGAGGTGCCATGATATGGTGTGGTGGAACTTGGGGA	2760
Oy	2732	GACAGTGTAACTTCCCTGTAAAGAAAGAGAGCCCTGGGTGGAGAGGCTTGTGTAAAT	2791
Db	2761	GACAGTGTAACTTCCCTGTAAAGAAAGAGAGCCCTGGGTGGAGAGGCTTGTGTAAAT	2820
Oy	2792	GGCGGCCACGAGGCTATTTCCCTGTGTGGGCTGTGCTGTGATATCCCGGACCTGGAGGT	2851
Db	2821	GGCGGCCACGAGGCTATTTCCCTGTGTGGGCTGTGCTGTGATATCCCGGACCTGGAGGT	2880
Oy	2852	GCAGAGGCACTACCACTATGACCCGGACCTCCATCAAGACCAAGTCTCACTTCAACCG	2911
Db	2881	GCAGAGGCACTACCACTATGACCCGGACCTCCATCAAGACCAAGTCTCACTTCAACCG	2940
Oy	2912	CGGCTTCAAGGCTGGAGAAACATGGCTGCAGAACTTTTGGGGTCTTGGCGCTGAAGTG	2971

```

Db 2941 CGGCTTCAAGGCTGGAGGAAACATGCTGCGCAAACTTTGGGGCTTTGGCGGTGAAGTG 3000
QY 2972 TCACAGCCTGTTTCTGATTTGACGTGAACAGCCTCCAGACGGGTGTCACCAACATCTA 3031
Db 3001 TCACAGCCTGTTTCTGATTTGACGTGAACAGCCTCCAGACGGGTGTCACCAACATCTA 3060
QY 3032 CAAGATCCCTCTGCTGACAGCGGTACAGATTTCACGATGTGTGTCAGTCCCATTTTCA 3091
Db 3061 CAAGATCCCTCTGCTGACAGCGGTACAGATTTCACGATGTGTGTCAGTCCCATTTTCA 3120
QY 3092 TCACAGATTGGAAGAAACCCCAATTTTCTGCGGTCTATCTCTGACAGCCCTCCT 3151
Db 3121 TCACAGATTGGAAGAAACCCCAATTTTCTGCGGTCTATCTCTGACAGCCCTCCT 3180
QY 3152 CTGCTACTCCATCTCTGAAGCCAAAGACGACGAGGATGTGCTGGGGGCCAAGGGCGCCG 3211
Db 3181 CTGCTACTCCATCTCTGAAGCCAAAGACGACGAGGATGTGCTGGGGGCCAAGGGCGCCG 3240
QY 3212 CGGGCTCTGCTGCTCCAGAGCCGTGACAGTGGCTGTGCCACCAAGCATTTCTGTCAGCT 3271
Db 3241 CGGGCTCTGCTGCTCCAGAGCCGTGACAGTGGCTGTGCCACCAAGCATTTCTGTCAGCT 3300
QY 3272 GACTCGACACCGGTGCTACACTACGTGCACATCTGGGGTCACTGACAGACGCCAGAGCA 3331
Db 3301 GACTCGACACCGGTGCTACACTACGTGCACATCTGGGGTCACTGACAGACGCCAGAGCA 3360
QY 3332 GCTGAGTGGAAAGCTCCCGGGGAGACGAGCTGACTGCCCTGGAGGCCAGCCAGCCGGC 3391
Db 3361 GCTGAGTGGAAAGCTCCCGGGGAGACGAGCTGACTGCCCTGGAGGCCAGCCAGCCGGC 3420
QY 3392 ACTGCCCTCAGACTTCAAGACCATCTGAGACTGATGGCCACCCAGACCCAGGGCGA 3451
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGAGACTGATGGCCACCCAGACCCAGGGCGA 3480
QY 3452 GAGGAGACACGAGAGCCGTGACGCGCGGCTTACTGCCAGAGGAGGAGGGCGGCC 3511
Db 3481 GAGGAGACACGAGAGCCGTGACGCGCGGCTTACTGCCAGAGGAGGAGGGCGGCC 3540
QY 3512 CACACCCAGGCGCCGACCGGTGGAGTCTGAGGCTGAGTGAAGTGTGGCCGAGGCGTG 3571
Db 3541 CACACCCAGGCGCCGACCGGTGGAGTCTGAGGCTGAGTGAAGTGTGGCCGAGGCGTG 3600
QY 3572 CATGTCCGGCTGAAGCTGAGTGTCCGGCTGAGGCTGAGGAGTGTCCAGCCAGGGCT 3631
Db 3601 CATGTCCGGCTGAAGCTGAGTGTCCGGCTGAGGCTGAGGAGTGTCCAGCCAGGGCT 3660
QY 3632 GAGTGTCCAGACACCTGCGGCTTCTACTTCCACAGGCTGGGGCTCGGCTCCACCCCA 3691
Db 3661 GAGTGTCCAGACACCTGCGGCTTCTACTTCCACAGGCTGGGGCTCGGCTCCACCCCA 3720
QY 3692 GGGCCAGCTTTTCTCACCAGAGACCGCGGCTTCCACTCCACATAGAAATAGTCAATCC 3751
Db 3721 GGGCCAGCTTTTCTCACCAGAGACCGCGGCTTCCACTCCACATAGAAATAGTCAATCC 3780
QY 3752 CCAGATTGGCATTTGTCACCCCTCGCCCTCTTGGCTTTCACCCCAACCATTC 3811
Db 3781 CCAGATTGGCATTTGTCACCCCTCGCCCTCTTGGCTTTCACCCCAACCATTC 3840
QY 3812 AGGTGAGACCTTGAGAAAGACCTGGAGCTCTGGGAATTTGAGAGACCAAGGATG 3871
Db 3841 AGGTGAGACCTTGAGAAAGACCTGGAGCTCTGGGAATTTGAGAGACCAAGGATG 3900
QY 3872 CCTGTACACAGGCGAGGACCTGCACTGATGGAGGGGCTCTGTGGGTCAAAATTTGGGG 3931
Db 3901 CCTGTACACAGGCGAGGACCTGCACTGATGGAGGGGCTCTGTGGGTCAAAATTTGGGG 3960
QY 3932 GAGGTCTGTGGGAGTAAATTAATATATAGATTTTCACTTTTGAAGAAAAA 3991
Db 3961 GAGGTCTGTGGGAGTAAATTAATATATAGATTTTCACTTTTGAAGAAAAA 4020
QY 3992 AAAAAAAAAAAAAA 4006
Db 4021 AAAAAAAAAAAAAA 4035

```

```

RESULT 3
AAV60320
ID AAV60320 standard; cDNA; 4023 BP.
XX
AC AAV60320;
XX
DT 04-DEC-1998 (first entry)
XX
DE Human telomerase gene referred to as hEST2.
XX
KW Catalytic subunit; human; telomerase; telomere maintenance;
XX diagnosis; treatment; cancer; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 59..3458
FT /*lag- a
XX
PN W09837181-A2.
XX
PD 27-AUG-1998.
XX
PF 20-FEB-1998; 98MO-US03404.
XX
PR 30-OCT-1997; 97US-0064322.
PR 20-FEB-1997; 97US-0038750.
PR 20-MAY-1997; 97US-0047151.
PR 01-AUG-1997; 97US-0054549.
PR 14-AUG-1997; 97US-0055762.
XX
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Counter CM, Meyerson M, Weinberg RA;
XX
DR WPI: 1998-495367/42.
XX
DR P-PSDB; AAW71376.
XX
PT New isolated human telomerase catalytic sub-unit gene - used to
PT develop products for increasing or reducing the life span of cells
PT such as cancer cells or transformed cells
XX
PS Claim 5; Fig 5A-B; 96pp; English.
XX
CC The present sequence encodes the catalytic subunit of a human
CC telomerase holoenzyme. Disruption of the telomerase gene alters
CC telomere maintenance. The DNA is essential for telomerase activity,
CC and the protein is physically associated with telomerase and a
CC constituent of active telomerase complex. The products can be used
CC for increasing or reducing the lifespan of cells such as cancer cells
CC or transformed cells. They can also be used in the diagnosis and
CC treatment of malignancies. In addition, cells with a longer lifespan
CC can be transplanted into or grafted onto an individual (e.g. as skin
CC grafts, as systems for delivery of therapeutic proteins, such as hormones
CC and enzymes), to whom they provide therapeutic benefit.
XX
SO Sequence 4023 BP; 668 A; 1363 C; 1277 G; 715 T; 0 other;
Query Match 99.2%; Score 3973.8; DB 19; Length 4023;
Best Local Similarity 99.1%; Pred. No. 6,1e-147;
Matches 3985; Conservative 0; Mismatches 2; Indels 36; Gaps 1;
QY 5 CAGGACGCGTGGTCTCTGCTGCGACAGTGGAAAGCCTTGCCCGGACCCCGCGAT 64
Db 1 CAGGACGCGTGGTCTCTGCTGCGACAGTGGAAAGCCTTGCCCGGACCCCGCGAT 60
QY 65 GCGCGGCGTCCCGCGGCGGAGCCGCGGCTGCTGCTGCGAGCCAGCAGCAGCGAGGT 124
Db 61 GCCGCGGCTCCCGCGGCGGAGCCGCGGCTGCTGCTGCGAGCCAGCAGCGAGGT 120
QY 125 GCTGCCGCTGGCCACGTTGCTGCGGCGCTGGGGCCCAAGGCTGGCGGTGTCAGCG 184

```


Dh	121	GCCTCCGCTGGCCACCTTGTGTCCGGCCCTGGGGCCCCAGGGAGCTGGGGCTGTGTACACG	180
Qy	185	CGGGAGCCGGCGGCTTTCGCGCGCTGTGTGCCAAGTCCCTGGTGTGCTGCCCTGGGA	244
Dh	181	CGGGAGCCCCGGGCTTTCGGGGCGTGGGGCCCAAGTCCGTGTGTGGTCCCTGGGA	240
Qy	245	CGCACGGCGCGCCCGCGCGGCCCTCTCTTCCGACCAAGTGTCTGTGCTTCAAGACATGGT	304
Dh	241	CGCACGGCGCGCCCGCGCGGCCCTCTCTTCCGACCAAGTGTCTGTGCTTCAAGACATGGT	300
Qy	305	GGCCCGAATGCTCAAGAGCTGTGTGAGCGCGGGCCGCGAAGACGTGCTGTGGCTTGAGCTT	364
Dh	301	GGCCCGAATGCTCAAGAGCTGTGTGAGCGCGGGCCGCGAAGACGTGCTGTGGCTTGAGCTT	360
Qy	365	CGCGCTGTGGAGGGGGCCCGGGGGCCCCCGCAGAGCTTTCACCAACAGGTGTGGAG	424
Dh	361	CGCGCTGTGGAGGGGGCCCGGGGGCCCCCGCAGAGCTTTCACCAACAGGTGTGGAG	420
Qy	425	CTACCTGCCCCAACAGCTGTACGACGACGTGCGGGGAGCGGGGCGTGGGGGCTGTGGT	484
Dh	421	CTACCTGCCCCAACAGCTGTACGACGACGTGCGGGGAGCGGGGCGTGGGGGCTGTGGT	480
Qy	485	GGCGCGGTGGGGGAGACGTGTGTGTACGTGTGCGTACGTGTGCGTGTGGCTTGTGGCT	544
Dh	481	GGCGCGGTGGGGGAGACGTGTGTGTACGTGTGCGTGTGCGTGTGCGTGTGGCTTGTGGCT	540
Qy	545	GGTGGCTTCCACGTGTGCTGTACCAAGTGTGGGGCCGCCGTGTACCAAGCTGTGGCGTGC	604
Dh	541	GGTGGCTTCCACGTGTGCTGTACCAAGTGTGGGGCCGCCGTGTACCAAGCTGTGGCGTGC	600
Qy	605	CACCTAGGCCCGGCCCGCCGACCAAGCTAGTGGACCCCGAAGAGTGTGTGGATGGCAAGC	664
Dh	601	CACCTAGGCCCGGCCCGCCGACCAAGCTAGTGGACCCCGAAGAGTGTGTGGATGGCAAGC	660
Qy	665	GGCTGTGAACCATAGCTGACGAGGAGCGCGGGGTCCCTGTGGGCTGTGCACAGCCCGGGTGC	724
Dh	661	GGCTGTGAACCATAGCTGACGAGGAGCGCGGGGTCCCTGTGGGCTGTGCACAGCCCGGGTGC	720
Qy	725	GAGGAGGGGGGGGAGCGAGTGCACCAATGTGCGCTTGTGGCCCAAGAGGCCAGGCGTGG	784
Dh	721	GAGGAGGGGGGGGAGCGAGTGCACCAATGTGCGCTTGTGGCCCAAGAGGCCAGGCGTGG	780
Qy	785	CGCTCCCTGTAGCCCGAGACGCGCCGTGTGGGCGAGGGGTCGTGGGCGCCACCGGGGAG	844
Dh	781	CGCTCCCTGTAGCCCGAGACGCGCCGTGTGGGCGAGGGGTCGTGGGCGCCACCGGGGAG	840
Qy	845	GACGGGTGAGCCAGTGAACCGT	904
Dh	841	GACGGGTGAGCCAGTGAACCGT	900
Qy	905	AAGCAACCTCTTGTGAGGGTGGGCTCTGTGGACAGCGGCACCTCCACCACTCGTGGGGCG	964
Dh	901	AAGCAACCTCTTGTGAGGGTGGGCTCTGTGGACAGCGGCACCTCCACCACTCGTGGGGCG	960
Qy	965	CGAGACACGCGGGGGCCCGCCCATCATGTGGGGGACACAGTGTCCGTGGGACAGCGCTTG	1024
Dh	961	CGAGACACGCGGGGGCCCGCCCATCATGTGGGGGACACAGTGTCCGTGGGACAGCGCTTG	1020
Qy	1025	TGCCCGGGTGTAGCGCGAGACCAAGCACTTCTCTTACTCTCAGGGAGCAAGAGACAGCT	1084
Dh	1021	TGCCCGGGTGTAGCGCGAGACCAAGCACTTCTCTTACTCTCAGGGAGCAAGAGACAGCT	1080
Qy	1085	GGGGCGCTCTCTTCACTACGTCTGTGAGGCCAGCTGTACTGTGGGCTGTGGAGGCTCTGT	1144
Dh	1081	GGGGCGCTCTCTTCACTACGTCTGTGAGGCCAGCTGTACTGTGGGCTGTGGAGGCTCTGT	1140
Qy	1145	GGAGACCACTCTTGTGGGTTCCAGGCGCTGATGTCAGGGACTCCCGGAGGTTTCCCGG	1204
Dh	1141	GGAGACCACTCTTGTGGGTTCCAGGCGCTGATGTCAGGGAGTCCCGGAGGTTTCCCGG	1200
Qy	1205	CGTGGCCCGAGCGCTACTGTGCAAAATGCGGGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGT	1264

[illegible]

QY 2309 CCACGCTCTACCTTGACAGACCTCCAGCCGTACATGACAGAGTTGCTGCTCACCTGA 2368
 DB 2341 CCACGCTCTACCTTGACAGACCTCCAGCCGTACATGACAGAGTTGCTGCTCACCTGA 2400
 QY 2369 GGAGACCAAGCCCGCTGAGGAGTCCGCTCATCGAGCAGAGCTCCCTGTAATGAGC 2428
 DB 2401 GGAGACCAAGCCCGCTGAGGAGTCCGCTCATCGAGCAGAGCTCCCTGTAATGAGC 2460
 QY 2429 CAGCAGTGGCTCTGAGAGTCTTCTAGCTTCATGTCACACAGCCGCTGGGCTCAG 2488
 DB 2461 CAGCAGTGGCTCTGAGAGTCTTCTAGCTTCATGTCACACAGCCGCTGGGCTCAG 2520
 QY 2489 GGGCAAGTCTCTAGTCCAGTCCAGGAGATCCCGCAGGGCTCCATCTCTCCAGCTGCT 2548
 DB 2521 GGGCAAGTCTCTAGTCCAGTCCAGGAGATCCCGCAGGGCTCCATCTCTCCAGCTGCT 2580
 QY 2549 CTGCAAGCTGTGTACAGCGGACATGGAGAACAAAGCTGTTGGGGGATTCGGCGGACGG 2608
 DB 2581 CTGCAAGCTGTGTACAGCGGACATGGAGAACAAAGCTGTTGGGGGATTCGGCGGACGG 2640
 QY 2609 GGTCGCTCTGCGTTGGTGGATGATTTCTGTTGGTACACCTCACCTCACCACGCGAA 2668
 DB 2641 GGTCGCTCTGCGTTGGTGGATGATTTCTGTTGGTACACCTCACCTCACCACGCGAA 2700
 QY 2669 AACCTTCTCAGGACCCCTGCTCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAATTTGGC 2728
 DB 2701 AACCTTCTCAGGACCCCTGCTCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAATTTGGC 2760
 QY 2729 GAAGACAGTGTGTAATTTCCCTGTAGAACAGAGCCCTGGGGTGGCAGGCTTTGTTCA 2788
 DB 2761 GAAGACAGTGTGTAATTTCCCTGTAGAACAGAGCCCTGGGGTGGCAGGCTTTGTTCA 2820
 QY 2789 GATGCCGGCCCAAGGCTATTTCCCTGTTGGGGCTGCTGGTGGATACCGGAGCCCTGGA 2848
 DB 2821 GATGCCGGCCCAAGGCTATTTCCCTGTTGGGGCTGCTGGTGGATACCGGAGCCCTGGA 2880
 QY 2849 GGTGCAAGCAGTACTCTCAGTATGCCCCGAGCCTTCATCAGAGCCAGTCTCACTTCAA 2908
 DB 2881 GGTGCAAGCAGTACTCTCAGTATGCCCCGAGCCTTCATCAGAGCCAGTCTCACTTCAA 2940
 QY 2909 CCGCGGCTTCAAGGCTGGGAGAACATGCTGCGCAAACTCTTTGGGGCTTTGGCGGTGA 2968
 DB 2941 CCGCGGCTTCAAGGCTGGGAGAACATGCTGCGCAAACTCTTTGGGGCTTTGGCGGTGA 3000
 QY 2969 GTGTCAAGCCTGTTCTGGATTTGGAGGTGAACAGCTCCAGAGGCTGGACCAACAT 3028
 DB 3001 GTGTCAAGCCTGTTCTGGATTTGGAGGTGAACAGCTCCAGAGGCTGGACCAACAT 3060
 QY 3029 CTACAAGATCTCTGCTGTCAGGCGTACAGGTTTTCACGATGTGCTCAGCTCCCAT 3088
 DB 3061 CTACAAGATCTCTGCTGTCAGGCGTACAGGTTTTCACGATGTGCTCAGCTCCCAT 3120
 QY 3089 TCATCAGCAAGTTTGAAGAACCCCATTTTCTGCGCGCTCATCTGTACAGCGGCTTC 3148
 DB 3121 TCATCAGCAAGTTTGAAGAACCCCATTTTCTGCGCGCTCATCTGTACAGCGGCTTC 3180
 QY 3149 CCTGTGCTACTCATCTGTAAGACCAAGAACGAGGATGTGGCTGGGGCCCAAGGGCCG 3208
 DB 3181 CCTGTGCTACTCATCTGTAAGACCAAGAACGAGGATGTGGCTGGGGCCCAAGGGCCG 3240
 QY 3209 CGCGCGGCTCTGCTCCGAGGCGTGCAGTGGCTGTGCCACCAAGATTTCTGCTCAA 3268
 DB 3241 CGCGCGGCTCTGCTCCGAGGCGTGCAGTGGCTGTGCCACCAAGATTTCTGCTCAA 3300
 QY 3269 GCTGACTGACACCGTGTACCTACGTGCTCCTGSGGCTCACTCAGACAGCCAGAC 3328
 DB 3301 GCTGACTGACACCGTGTACCTACGTGCTCCTGSGGCTCACTCAGACAGCCAGAC 3360
 QY 3329 GGAGCTGAGTGGAGCTCCGGGAGCAGGCTGACTGCTGGAGGCGCGACCAACC 3388
 DB 3361 GGAGCTGAGTGGAGCTCCGGGAGCAGGCTGACTGCTGGAGGCGCGACCAACC 3420

QY 3389 GGCAGTCCCTAGACTTCAAGACATCTCTGAGTATGGCCACCGCCACAGCCAGGC 3448
 DB 3421 GGCAGTCCCTAGACTTCAAGACATCTCTGAGTATGGCCACCGCCACAGCCAGGC 3480
 QY 3449 CGAGAGCAGACACCAAGCAGCCCTGTACGCCGGGCTCTACGTCACAGGAGGAGGGCG 3508
 DB 3481 CGAGAGCAGACACCAAGCAGCCCTGTACGCCGGGCTCTACGTCACAGGAGGAGGGCG 3540
 QY 3509 GCCACACCCAGGCGCCGACCCCTGGAGTCTGAGGCGCTGAGTGTGTTGGCGAGGC 3568
 DB 3541 GCCACACCCAGGCGCCGACCCCTGGAGTCTGAGGCGCTGAGTGTGTTGGCGAGGC 3600
 QY 3569 CTGCATGTCGCGCTGAAGGCTGAGTCTCGGCTGAGAGCCGTAAGGCTGACGCCAAG 3628
 DB 3601 CTGCATGTCGCGCTGAAGGCTGAGTCTCGGCTGAGAGCCGTAAGGCTGACGCCAAG 3660
 QY 3629 GCTGAGTGTCCAGACACCTGCGGCTTCTACTTCCCAAGAGCTGGCGCTCGGCTCCAGC 3688
 DB 3661 GCTGAGTGTCCAGACACCTGCGGCTTCTACTTCCCAAGAGCTGGCGCTCGGCTCCAGC 3720
 QY 3689 CCAGGCGCAGCTTTTCTCACCAGAGAGCCGCTTCCATCCCAATAGATAGTCA 3748
 DB 3721 CCAGGCGCAGCTTTTCTCACCAGAGAGCCGCTTCCATCCCAATAGATAGTCA 3780
 QY 3749 TCCCCAGATTCGCAATGTTTCAACCCCTGCGCCCTGCTTCCCTTCCACCCACCA 3808
 DB 3781 TCCCCAGATTCGCAATGTTTCAACCCCTGCGCCCTGCTTCCCTTCCACCCACCA 3840
 QY 3809 TCCAGTGTGAGACCTTGAAGAGAGCCCTGGAGCTTGGGAATTTGGATGACCAAGGT 3868
 DB 3841 TCCAGTGTGAGACCTTGAAGAGAGCCCTGGAGCTTGGGAATTTGGATGACCAAGGT 3900
 QY 3869 GTGCCCTGTACACAGGCGAGGAGCCCTGACCTGAGTGGGGTCCCTGTGGTCAATTGG 3928
 DB 3901 GTGCCCTGTACACAGGCGAGGAGCCCTGACCTGAGTGGGGTCCCTGTGGTCAATTGG 3960
 QY 3929 GGGGAGTGTCTGTGGAGTAAATATCTGAATATATGAGTTTTCAGTTTGAAGAAAAA 3988
 DB 3961 GGGGAGTGTCTGTGGAGTAAATATCTGAATATATGAGTTTTCAGTTTGAAGAAAAA 4020
 QY 3989 AAA 3991
 DB 4021 AAA 4023

RESULT 4
 ID ABL53711 standard; cDNA: 4070 BP.
 XX ABL53711;
 AC 17-JUN-2002 (first entry)
 XX
 DT 17-JUN-2002 (first entry)
 XX
 DE Human telomerase catalytic subunit hTERT cDNA.
 XX
 KW hTERT; telomerase; reverse transcriptase; immortalisation; human;
 KW vaccine; enzyme; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200216555-A2.
 PD 28-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-GB03726.
 XX
 PR 17-AUG-2000; 2000GB-0020246.
 PR 17-AUG-2000; 2000US-225734P.
 XX
 PA (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
 XX
 PI Jones CJ, Kipling DG, Wilkinson G, McSharry B, Skinner JW;
 XX

QY	1746	TATGTACAGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGAGAGTGTCTGG	1805
Db	1759	TATGTACAGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGAGAGTGTCTGG	1818
QY	1806	AGCAAGTTGCAAACCATTTGGATATCAGACAGCACTTAAAGAGGTGCAGTGGGGAGCTG	1865
Db	1819	AGCAAGTTGCAAACCATTTGGATATCAGACAGCACTTAAAGAGGTGCAGTGGGGAGCTG	1878
QY	1866	TGCGAAGCAGAGGTCTCAGGACAGCATCGGGAAAGCCAGGCCCGCCCTCTGACGTCAGACTC	1925
Db	1879	TCGGAAGCAGAGGTCTCAGGACAGCATCGGGAAAGCCAGGCCCGCCCTCTGACGTCAGACTC	1938
QY	1926	CGCTTCATCCCCCAAGCCTGACAGGGGCTCCGGCGGATTTGTAAATAGTACTAGTGTGGGA	1985
Db	1939	CGCTTCATCCCCCAAGCCTGACAGGGGCTCCGGCGGATTTGTAAATAGTACTAGTGTGGGA	1998
QY	1986	GCCAGAACGTTCCCGCAGAGAAAAGAGGGCCGAGACGCTCTACCTCGAGGGTGAAGCACTG	2045
Db	1999	GCCAGAACGTTCCCGCAGAGAAAAGAGGGCCGAGACGCTCTACCTCGAGGGTGAAGCACTG	2058
QY	2046	TTTCAGCGTCTCAACTACGAGCGGGCGGGCGCCCGGCTCTGTGGCGCTGTGTGTG	2105
Db	2059	TTTCAGCGTCTCAACTACGAGCGGGCGGGCGCCCGGCTCTGTGGCGCTGTGTGTG	2118
QY	2106	GGCCGCGGACGATATCCAGACAGGGGCTGGGCGACCTTGCTCTGCTGCTGGGGCCAGAC	2165
Db	2119	GGCCGCGGACGATATCCAGACAGGGGCTGGGCGACCTTGCTCTGCTGCTGGGGCCAGAC	2178
QY	2166	CCGCGCGCTGAGCTGTA-----CATGCC	2189
Db	2179	CCGCGCGCTGAGCTGTGTGTCAAGATGTGTACGGGGCGGCTGACAGACCATCC	2238
QY	2190	CAGAGACGGCTCACGAGGATCATCGGCAGATCATCAACCCCAAGAACGTAAGTGTG	2249
Db	2239	CAGAGACGGCTCACGAGGATCATCGGCAGATCATCAACCCCAAGAACGTAAGTGTG	2298
QY	2250	CGTGGATATGCCGCTGTGTCAGAAAGGCCGCGCATGTGGGCAAGTCCGCAAGGCTTCAAGAGC	2309
Db	2299	CGTGGATATGCCGCTGTGTCAGAAAGGCCGCGCATGTGGGCAAGTCCGCAAGGCTTCAAGAGC	2358
QY	2310	CACGTCTCTACTCTTGACAGACCTCCAGCCGTATCTGCAAGTGTGTGCTACCTGCAG	2369
Db	2359	CACGTCTCTACTCTTGACAGACCTCCAGCCGTATCTGCAAGTGTGTGCTACCTGCAG	2418
QY	2370	GAGACACAGCCGCTGAGGGATGTCGTCGTCATCGACAGAGTCTCTCCCTGAATGAGGCC	2429
Db	2419	GAGACACAGCCGCTGAGGGATGTCGTCGTCATCGACAGAGTCTCTCCCTGAATGAGGCC	2478
QY	2430	AGCAGTGGCCTCTTGACAGCTCTTCTCAAGCTTCATGTGCGACACAGCCGTGCGATCAG	2489
Db	2479	AGCAGTGGCCTCTTGACAGCTCTTCTCAAGCTTCATGTGCGACACAGCCGTGCGATCAG	2538
QY	2490	GGCAAGTCTCAACGTTCAGGTCCGAGGGGATTCGCGAGAGGTCCATCTCTCAACGCTGTC	2549
Db	2539	GGCAAGTCTCAACGTTCAGGTCCGAGGGGATTCGCGAGAGGTCCATCTCTCTCAACGCTGTC	2598
QY	2550	TGCAGCCTGTGCTACGCGACGACATGAGAGAACAGCTGTTTGGCGGGATTTCGCGGAGCGG	2609
Db	2599	TGCAGCCTGTGCTACGCGCGACATGAGAGAACAGCTGTTTGGCGGGATTTCGCGGAGCGG	2658
QY	2610	CTGCTCTCGGGTTTGGTGGATGATTTCTTGTGTGTGACACCTACCTACCCAGCGGAA	2669
Db	2659	CTGCTCTCGGGTTTGGTGGATGATTTCTTGTGTGTGACACCTACCTACCCAGCGGAA	2718
QY	2670	ACCTTCTCAAGAGACCCCTGTGAGAGGTGTCCCTGAGATAGGTGTGGTGTGAACCTTGGG	2729
Db	2719	ACCTTCTCAAGAGACCCCTGTGAGAGGTGTCCCTGAGATAGGTGTGGTGTGAACCTTGGG	2778
QY	2730	AAGACAGTGTGAATCTTCCTGTAGAAGACAGAGCCCTGAGGTGCGACGGCTTTTGTTCAG	2789
Db	2779	AAGACAGTGTGAATCTTCCTGTAGAAGACAGAGCCCTGAGGTGCGACGGCTTTTGTTCAG	2838

QY	2790	ATCCGGCCCAACGGCCCTATTCCCTGGTGGGGGCTCTGCTGGATTACCCGGACCCCTGGAG	284.9
Db	2839	ATGCCGGCCCAACGGCCCTATTCCCTGGTGGGGGCTCTGCTGGATTACCCGGACCCCTGGAG	289.9
QY	2850	GTGCAGACGCACTACTCCAGCTATGCGCCGGACCTCCATCAGAACCGAGTCCACTTCAAC	290.9
Db	2899	GTGCAGACGCACTACTCAGCTATGCGCCGGACCTCCATCAGAACCGAGTCCACTTCAAC	295.9
QY	2910	CGCGGCTTCAAGGCTGGGAGGAACATGCGTGCAGAACTCTTTGGGGTCTTTGGCGCTGAAG	296.9
Db	2959	CGCGGCTTCAAGGCTGGGAGGAACATGCGTGCAGAACTCTTTGGGGTCTTTGGCGCTGAAG	301.8
QY	2970	TGTCACAGCCCTGTTTCTGAGATTTCGAGGTAAACGCTCCAGACGCTGTGCACCAATC	302.9
Db	3019	TGTCACAGCCCTGTTTCTGAGATTTCGAGGTAAACGCTCCAGACGCTGTGCACCAATC	307.8
QY	3030	TACAAAGATCCGTCGTCGAGGGCTACAGGTTTCACGCAATGTCGTGAGCTCCATTT	308.9
Db	3079	TACAAAGATCCGTCGTCGAGGGCTACAGGTTTCACGCAATGTCGTGAGCTCCATTT	313.8
QY	3090	CATCAGCAAGTTTGGAGAAACCCACATTTTTCCTGCGGTATCTCTACACGGCTCC	314.9
Db	3139	CATCAGCAAGTTTGGAGAAACCCACATTTTTCCTGCGGTATCTCTACACGGCTCC	319.8
QY	3150	CTCTGCTACTCCATCTGTAAGACCAAGACGAGGATGCTGCTGGGGCCAAAGGGGCC	320.9
Db	3199	CTCTGCTACTCCATCTGTAAGACCAAGACGAGGATGCTGCTGGGGCCAAAGGGGCC	325.8
QY	3210	GCGGGCCCTCTGGCCCTCCGAGGCGGTGTCAATGGCTGTGCCACCAAGCATTTCTGCTCAAG	326.9
Db	3259	GCGGGCCCTCTGGCCCTCCGAGGCGGTGTCAATGGCTGTGCCACCAAGCATTTCTGCTCAAG	331.8
QY	3270	CTGACTGCACACGCTGTCACCTTAAGTGCACCTCTGGGGTCACTCAGACACCCAGACG	332.9
Db	3319	CTGACTGCACACCGTGTACCTTAAGTGCACCTCTGGGGTCACTCAGACACCCAGACG	337.8
QY	3330	CAGCTGACTCGGAAGCTCCCGGGGACAGCGTGACTGACCTGTGAGGCGCGACCAACCCG	338.9
Db	3379	CAGCTGACTCGGAAGCTCCCGGGGACAGCGTGACTGACCTGTGAGGCGCGACCAACCCG	343.8
QY	3390	GCACCTGCCCTCAGACTTCCAGACCATTCCTGTGATGGCCACCGGCCACACGCCAGGCC	344.9
Db	3439	GCACCTGCCCTCAGACTTCCAGACCATTCCTGTGATGGCCACCGGCCACACGCCAGGCC	349.8
QY	3450	GAGAGCAGACACGACGAGCCCTGTCAAGCGCGGCTCTAGCTGCCAGGGAGGGAGGGGGG	350.9
Db	3499	GAGAGCAGACACGACGAGCCCTGTCAAGCGCGGCTCTAGCTGCCAGGGAGGGAGGGGGG	355.8
QY	3510	CCCAACCCAGGCGCCGACCGCTGGAAGTCTGAAGGCTGAGTGAAGTCTTTGGCCGAGGCC	356.9
Db	3559	CCCAACCCAGGCGCCGACCGCTGGAAGTCTGAAGGCTGAGTGAAGTCTTTGGCCGAGGCC	361.8
QY	3570	TGCATGTCGGGCTTAAGGCTGAGTGTCCGGCTTAGGCCCTGAGCGAGTGTCCAGCCAAAGG	362.9
Db	3619	TGCATGTCGGGCTTAAGGCTGAGTGTCCGGCTTAGGCCCTGAGCGAGTGTCCAGCCAAAGG	367.8
QY	3630	CTGAGTGTCCAGACACCTCGCGCTTCAATCCCAAGGCGTGGGCGTCCGGCTCCAGCC	368.9
Db	3679	CTGAGTGTCCAGACACCTCGCGCTTCAATCCCAAGGCGTGGGCGTCCGGCTCCAGCC	373.8
QY	3690	CAGGCGCAGCTTTCCTCACCAGGAGCCGGCTTCCACTCCACCCACATAGAAATAGTCAT	374.9
Db	3739	CAGGCGCAGCTTTCCTCACCAGGAGCCGGCTTCCACTCCACCCACATAGAAATAGTCAT	379.8
QY	3750	CCCCAGATTGGCCATTGTTCACCCCTGCGCTGCGCTCTTTGCTTCCACCCACCAT	380.9
Db	3799	CCCCAGATTGGCCATTGTTCACCCCTGCGCTGCGCTCTTTGCTTCCACCCACCAT	385.8
QY	3810	CCAGGTGAGACCCCTGAGGAAGAACCCGTGGAGGCTGTGGGAATTTGGAGTGAACAAAGTG	386.9
Db	3859	CCAGGTGAGACCCCTGAGGAAGAACCCGTGGAGGCTGTGGGAATTTGGAGTGAACAAAGTG	391.8
QY	3870	TGCCCTGTACACAGGCAAGAACCCCTGACCTGTGATGGGGGTCCCTGTGGGTCAATTTGGG	392.9

[illegible]

QY 1148 GACCATCTTTCGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCCGCT 1207
DB 1141 GACCATCTTTCGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCCGCT 1200
QY 1208 GCCCCAGGCTACTGGCAATATGCGGCCCTGTTTCGAGCTGCTTGGGAACACAGCGCA 1267
DB 1201 GCCCCAGGCTACTGGCAATATGCGGCCCTGTTTCGAGCTGCTTGGGAACACAGCGCA 1260
QY 1268 GTGCCCCAGGCGGTGCTCCAGAGGACTGCCCCGCTGGAGTGGGGTACCCCGAGC 1327
DB 1261 GTGCCCCAGGCGGTGCTCCAGAGGACTGCCCCGCTGGAGTGGGGTACCCCGAGC 1320
QY 1328 AGCCGGTCTGTGCTCCGGGAAAGCCAGAGGCTGTGCGGGGCCCGGAGAGAGAGA 1387
DB 1321 AGCCGGTCTGTGCTCCGGGAAAGCCAGAGGCTGTGCGGGGCCCGGAGAGAGAGA 1380
QY 1388 CACAGACCCCCGCTGCTGTGTGACAGCTCTCCGCCAGCAGACAGCCCTGTGGAGTGA 1447
DB 1381 CACAGACCCCCGCTGCTGTGTGACAGCTCTCCGCCAGCAGACAGCCCTGTGGAGTGA 1440
QY 1448 GGGCTGTGGGGGCTGCTGCGCGGGCTGGTGGCCCCAGGCTCTGGGCTCCAGGCA 1507
DB 1441 GGGCTGTGGGGGCTGCTGCGCGGGCTGGTGGCCCCAGGCTCTGGGCTCCAGGCA 1500
QY 1508 CAAGCAAGCCGCTCTCTCAGGAAACACCAAGAGTTCACTCTCCCTGGGGAAAGCATGCCAA 1567
DB 1501 CAAGCAAGCCGCTCTCTCAGGAAACACCAAGAGTTCACTCTCCCTGGGGAAAGCATGCCAA 1560
QY 1568 GCTCTGCTGCAAGAGCTGACGTGAGATGAGCTGCGGGAGCTGCTTGGCTGCGAG 1627
DB 1561 GCTCTGCTGCAAGAGCTGACGTGAGATGAGCTGCGGGAGCTGCTTGGCTGCGAG 1620
QY 1628 GAGCCAGAGGGGTGGCTGTGTTCCGGCGCAGAGACCGCTGGCTGGAGAGATCTGGC 1687
DB 1621 GAGCCAGAGGGGTGGCTGTGTTCCGGCGCAGAGACCGCTGGCTGGAGAGATCTGGC 1680
QY 1688 CAAGTCTCTGCACTGCTGATGATGTGATGCTGCTGAGCTGCTCAAGTCTTTCTTTA 1747
DB 1681 CAAGTCTCTGCACTGCTGATGATGTGATGCTGCTGAGCTGCTCAAGTCTTTCTTTA 1740
QY 1748 TGTACGGAGACACGTTTCAAAAAGACAGCTCTTTTCTTACCGGGAAGAGTGTGAG 1807
DB 1741 TGTACGGAGACACGTTTCAAAAAGACAGCTCTTTTCTTACCGGGAAGAGTGTGAG 1800
QY 1808 CAAGTCTCAAAAGCATTTGAATCAGACAGCACTTGAAGAGGCTGAGTGGGAGCTGTC 1867
DB 1801 CAAGTCTCAAAAGCATTTGAATCAGACAGCACTTGAAGAGGCTGAGTGGGAGCTGTC 1860
QY 1868 GGAAGCAGAGGTCAGGAGCATCGGGAAGCCAGGCCCGCTGCTGAGCTCCAGACTCGG 1927
DB 1861 GGAAGCAGAGGTCAGGAGCATCGGGAAGCCAGGCCCGCTGCTGAGCTCCAGACTCGG 1920
QY 1928 CTTATCCCAAGGCTGAGGGGCTGCGGGCATTTGTGAACATGACTACGTCGTGGAGC 1987
DB 1921 CTTATCCCAAGGCTGAGGGGCTGCGGGCATTTGTGAACATGACTACGTCGTGGAGC 1980
QY 1988 CAGAAGCTTCCGAGAGAAAGAGGGCGAGCTCTCACTCGAAGGGAAGAGCACTGTT 2047
DB 1981 CAGAAGCTTCCGAGAGAAAGAGGGCGAGCTCTCACTCGAAGGGAAGAGCACTGTT 2040
QY 2048 CAGGCTGCTCAACTAGAGCGGGCGGGCGCCCGGCTCTCTGGGGCTCTGTGCTGGG 2107
DB 2041 CAGGCTGCTCAACTAGAGCGGGCGGGCGCCCGGCTCTCTGGGGCTCTGTGCTGGG 2100
QY 2108 CCTGAGCATATNCAACAGGGGCTGGGCACTTGTGCTGTGGTGGCGGGGCCAGAGACC 2167
DB 2101 CCTGAGCATATNCAACAGGGGCTGGGCACTTGTGCTGTGGTGGCGGGGCCAGAGACC 2160
QY 2168 GCGGCTGAGCTGTA-----CATCCCCA 2191
DB 2161 GCGGCTGAGCTGTACTTTGTCAAGAGTGGATGTGACGGGGCGCTGACGACACCATCCCCA 2220

QY 2192 GGACAGGCTCAAGAGTCAATGACCAGCATCATCAAAACCCAGAAACAGACTGCTGCG 2251
DB 2221 GGACAGGCTCAAGAGTCAATGACCAGCATCATCAAAACCCAGAAACAGACTGCTGCG 2280
QY 2252 TCGGATCCCGTGGTCCAGAAAGCGCCCATATGGGACGTCCGCAAGGCTTCAAGAGCA 2311
DB 2281 TCGGATCCCGTGGTCCAGAAAGCGCCCATATGGGACGTCCGCAAGGCTTCAAGAGCA 2340
QY 2312 GGTCTCACTCAAGAGACCTCCAGCCGTACATGGGAGAGTTCGGGGCTCACTGACAGA 2371
DB 2341 GGTCTCACTCAAGAGACCTCCAGCCGTACATGGGAGAGTTCGGGGCTCACTGACAGA 2400
QY 2372 GACCAAGCCCGTAGAGGATGCGCTGTCATGAGCAGAGCTCTCCCTGAATGAGGCCAG 2431
DB 2401 GACCAAGCCCGTAGAGGATGCGCTGTCATGAGCAGAGCTCTCCCTGAATGAGGCCAG 2460
QY 2432 CAGTGGCTCTTCCAGAGCTTCTCAAGCTTATGTGCAACCAAGCCGCTGCGCATCAGGG 2491
DB 2461 CAGTGGCTCTTCCAGAGCTTCTCAAGCTTATGTGCAACCAAGCCGCTGCGCATCAGGG 2520
QY 2492 CAAGTCTCAAGTCCAGTGCAGGGGATCCGAGGGGCTCAATCCCTGTCACGCTGCTG 2551
DB 2521 CAAGTCTCAAGTCCAGTGCAGGGGATCCGAGGGGCTCAATCCCTGTCACGCTGCTG 2580
QY 2552 CAGCCTGTCTACAGGCGCATGGAACACAGCTGTTTGCAGGGATTCGCGCGAGCGGCT 2611
DB 2581 CAGCCTGTCTACAGGCGCATGGAACACAGCTGTTTGCAGGGATTCGCGCGAGCGGCT 2640
QY 2612 GCTCTGCGTTTGGTGGATGATTTCTTGTGTGACACCTCACTCAACCCAGCGGAAC 2671
DB 2641 GCTCTGCGTTTGGTGGATGATTTCTTGTGTGACACCTCACTCAACCCAGCGGAAC 2700
QY 2672 CTTCTCAGAGACCTGATGCCAGAGTGTCCCTGAGATGCTGCGGTGGAATCTGCGGA 2731
DB 2701 CTTCTCAGAGACCTGATGCCAGAGTGTCCCTGAGATGCTGCGGTGGAATCTGCGGA 2760
QY 2732 GACAGTGTGAATCTTCCGTGTAAGAGACGAGGCCCTGGGTGACAGCTTTTGTACAT 2791
DB 2761 GACAGTGTGAATCTTCCGTGTAAGAGAGAGGCCCTGGGTGACAGCTTTTGTACAT 2820
QY 2792 GCGGCGCCAGGCGCTATCCCTGGTGGGCTGCTGTGTGAATCCCGGACCTGGAGGT 2851
DB 2821 GCGGCGCCAGGCGCTATCCCTGGTGGGCTGCTGTGTGAATCCCGGACCTGGAGGT 2880
QY 2852 GCAGAGCACTACTCCACATATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACG 2911
DB 2881 GCAGAGCACTACTCCACATATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACG 2940
QY 2912 CGGCTTCAAGGCTGGGAGAACATGCTGCAAACTCTTTGGGGCTTGGCGCTGAAGTG 2971
DB 2941 CGGCTTCAAGGCTGGGAGAACATGCTGCAAACTCTTTGGGGCTTGGCGCTGAAGTG 3000
QY 2972 TCACAGGCTGTTTCTGGAATTTGCAAGGTGAACAGCTCCAGAGGGGTGACCAACATTA 3031
DB 3001 TCACAGGCTGTTTCTGGAATTTGCAAGGTGAACAGCTCCAGAGGGGTGACCAACATTA 3060
QY 3032 CAAGATCTCTCTGCTGAGGGGTACAGGTTTACAGCATGTGTGCTGACGCTCCCAATTCA 3091
DB 3061 CAAGATCTCTCTGCTGAGGGGTACAGGTTTACAGCATGTGTGCTGACGCTCCCAATTCA 3120
QY 3092 TCAGCAATTTTGAAGAACCCCACTTTTCTGCGGCTCATCTGTGACAGGCTGCT 3151
DB 3121 TCAGCAATTTTGAAGAACCCCACTTTTCTGCGGCTCATCTGTGACAGGCTGCT 3180
QY 3152 CTGCTACTCACTCAAGTGAAGGCAAGAAAGCAAGGATGTCGCTGGGGGCGCAAGGGGCGCG 3211
DB 3181 CTGCTACTCACTCAAGTGAAGGCAAGAAAGCAAGGATGTCGCTGGGGGCGCAAGGGGCGCG 3240
QY 3212 GGGGCTCTGCTTCCGAGGGCGTGAAGTGGCTGTGCCCAAGCATCTCTGCTCAAGCT 3271
DB 3241 GGGGCTCTGCTTCCGAGGGCGTGAAGTGGCTGTGCCCAAGCATCTCTGCTCAAGCT 3300
QY 3272 GACTGCAACCGTGTCACTTACGTGCCACCTCTTGGGGTCACTCAGAGACGCCAGAGCGCA 3331

QY	548	GGCTCCAGCTGCGCTTACCAAGTGTGGGGGCGCGCTGTACACAGCTGGCGCTGCCAC	607
Dp	541	GGCTCCAGCTGGGCGCTTACCAAGGTGTGGGGGCGCGCGTGTACAGCTGGCGCTGCCAC	600
QY	608	TCAGAGCGGGGGCGCGCCAGCGTGTGGACCCCGAAGGGGTCGGGATCGGAACGGGC	667
Dp	601	TCAGAGCGGGGGCGCGCCAGCGTGTGGACCCCGAAGGGGTCGGGATCGGAACGGGC	660
QY	668	CTGGAACCATAGCGTCAGAGGAGCGCGGGGTCCCTCTGGGCGCTGCAGCGCCGGGTGCGAG	727
Dp	661	CTGGAACCATAGCGTCAGAGGAGCGCGGGGTCCCTCTGGGCGCTGCAGCGCCGGGTGCGAG	720
QY	728	GAGGCGGGGGGCGAGTGGCAGCGCGGTCGTGGGAGGGGTCGTGGGCCACCGGGCAGAGC	787
Dp	721	GAGGCGGGGGGCGAGTGGCAGCGCGGTCGTGGGAGGGGTCGTGGGCCACCGGGCAGAGC	780
QY	788	TGCCCCGTAGCGCGGAGCGAGCGCCGCTTGGGAGGGGTCGTGGGCCACCGGGCAGAGC	847
Dp	781	TGCCCCGTAGCGCGGAGCGAGCGCCGCTTGGGAGGGGTCGTGGGCCACCGGGCAGAGC	840
QY	848	GCGGTGAGCCGAGTGAACCGTGGTTTCTGTGTGGTGTACCTGGCAGAACCCGCGGAAGAAGC	907
Dp	841	GCGGTGAGCCGAGTGAACCGTGGTTTCTGTGTGGTGTACCTGGCAGAACCCGCGGAAGAAGC	900
QY	908	CACCTCTTTGGAGGGTGCCTCTCTTGGCACGCGGCCACTGCCATCCATCCGTGGGCGCGCA	967
Dp	901	CACCTCTTTGGAGGGTGCCTCTCTTGGCACGCGGCCACTGCCATCCATCCGTGGGCGCGCA	960
QY	968	GCACACAGCGGGGCGCCCATTCACATTCGGGGCACACAGCTCCCTGGGACAGCGCTTGGCC	1027
Dp	961	GCACACAGCGGGGCGCCCATTCACATTCGGGGCACACAGCTCCCTGGGACAGCGCTTGGCC	1020
QY	1028	CCCGGTGTACGCGGAGACCAAGCAGCTTCTCTACTCTCAGGCGCAAGAGAGCAGCTGCG	1087
Dp	1021	CCCGGTGTACGCGGAGACCAAGCAGCTTCTCTACTCTCAGGCGCAAGAGAGCAGCTGCG	1080
QY	1088	GCCCTCTCTCTACTAGAGCTCTTGAGGCGCCAGCCTGACTGGCGCTGSGAGGCTGTGGA	1147
Dp	1081	GCCCTCTCTCTACTAGAGCTCTTGAGGCGCCAGCCTGACTGGCGCTGSGAGGCTGTGGA	1140
QY	1148	GACCATCTTCTGGGTCCAGGGCCCGAGATGCGAGGAACTCCCGCAGTTGGCCCGGCT	1207
Dp	1141	GACCATCTTCTGGGTCCAGGGCCCGAGATGCGAGGAACTCCCGCAGTTGGCCCGGCT	1200
QY	1208	GCCCGACGCTACTGGCAATGCGGCCCTGTCTTGTGAGAGCTGTGTGGAAACCAAGCGCA	1267
Dp	1201	GCCCGACGCTACTGGCAATGCGGCCCTGTCTTGTGAGAGCTGTGTGGAAACCAAGCGCA	1260
QY	1268	GTCGCCCTCAGGGGGTGTCTCTCAAGACGCACTGCCGTGCGAGCTGGCGGTACCCAGC	1327
Dp	1261	GTCGCCCTCAGGGGGTGTCTCTCAAGACGCACTGCCGTGCGAGCTGGCGGTACCCAGC	1320
QY	1328	AGCGGAGTGTGTGGCCCGGGAGAAAGCCCAAGGGCTGTGGGGGGCGCCCGAGAGAGAGA	1387
Dp	1321	AGCGGAGTGTGTGGCCCGGGAGAAAGCCCAAGGGCTGTGGGGGGCGCCCGAGAGAGAGA	1380
QY	1388	CACAGACCCCGCTGCGCTGTGTGAGCTGTCCGCGCAGCAGCAGACCCCTG6GAGGTGTA	1447
Dp	1381	CACAGACCCCGCTGCGCTGTGTGAGCTGTCCGCGCAGCAGCAGACCCCTG6GAGGTGTA	1440
QY	1448	CGGCTTGCTGCGGGGCTGCTTGCAGGCGGCTGTGGTCCCGAGCGCTCTGGGGCTCCAGGCA	1507
Dp	1441	CGGCTTGCTGCGGGGCTGCTTGCAGGCGGCTGTGGTCCCGAGCGCTCTGGGGCTCCAGGCA	1500
QY	1508	CAAGCAAGCGCGCTTCTCTAGGAACCAAGAAAGTTCAATCTCCCTGGGGGAAGCATGCCAA	1567
Dp	1501	CAAGCAAGCGCGCTTCTCTAGGAACCAAGAAAGTTCAATCTCCCTGGGGGAAGCATGCCAA	1560
QY	1568	GCTCTGCTGAGAGAGCTGACGTGAAGATGAGCGTGGGAGCTGCGCTTGGCTGGCGAG	1627
Dp	1561	GCTCTGCTGAGAGAGCTGACGTGAAGATGAGCGTGGGAGCTGCGCTTGGCTGGCGAG	1620
QY	1628	GAGCCCAAGGGGTGGCGTGTCTCGGCGCCAGAGCAGCTCTGCGCTGAGAGATCTTGGC	1687

[illegible]


```

Db 2701 CTTCTCAGAGACCCCTGCTCCAGGCTGCCAGTATGCTGCTGCTGCACTTCTGGCA 2760
Oy 2732 GACAGTGTGTAACCTTCTCTAGTAAGACAGAGCCCTGGGTGGCACGGCTTTTTCAGAT 2791
Db 2761 GACAGTGTGTAACCTTCTCTAGTAAGACAGAGCCCTGGGTGGCACGGCTTTTTCAGAT 2820
Oy 2792 GCCGGCCCAAGGCTTATCCCTGCTGGGCTGCTGCTGATATCCGGAACCTTGAGGT 2851
Db 2821 GCCGGCCCAAGGCTTATCCCTGCTGGGCTGCTGCTGATATCCGGAACCTTGAGGT 2880
Oy 2852 GCAGAGGACTACTCCAGCTATGCCCAGGACTTCATCAGAGCCAGTCTCACTTCAACCG 2911
Db 2881 GCAGAGGACTACTCCAGCTATGCCCAGGACTTCATCAGAGCCAGTCTCACTTCAACCG 2940
Oy 2912 CGGCTTCAAGGCTGGAGGAACATGCTGCMAACCTTTGGGGCTTGGGGCTGGAAGTG 2971
Db 2941 CGGCTTCAAGGCTGGAGGAACATGCTGCMAACCTTTGGGGCTTGGGGCTGGAAGTG 3000
Oy 2972 TCACAGGCTGTTTCTGAGATTGAGTGGAACGCTCCAGAGCGGTGGCAACATCTA 3031
Db 3001 TCACAGGCTGTTTCTGAGATTGAGTGGAACGCTCCAGAGCGGTGGCAACATCTA 3060
Oy 3032 CAGATTCCTCTGCTGCAAGCGTTCACGATGTGCTGCAAGCTCCCATTTCA 3091
Db 3061 CAGATTCCTCTGCTGCAAGCGTTCACGATGTGCTGCAAGCTCCCATTTCA 3120
Oy 3092 TCAGCAAGTTTGAAGAACCACCATTTTCTGCGCGCTCATCTCTGACACGGCCCTCCT 3151
Db 3121 TCAGCAAGTTTGAAGAACCACCATTTTCTGCGCGCTCATCTCTGACACGGCCCTCCT 3180
Oy 3152 CTGCTACTCATCTCGAAGCCAGAAACGAGAGGATGCTGCTGGGGGCGCAAGGGCGCGC 3211
Db 3181 CTGCTACTCATCTCGAAGCCAGAAACGAGAGGATGCTGCTGGGGGCGCAAGGGCGCGC 3240
Oy 3212 CGGCGCTCTGCGCTCGAGGCGCGTGCAGTGGCTGCCACCAACATCTCTGCTCAAGT 3271
Db 3241 CGGCGCTCTGCGCTCGAGGCGCGTGCAGTGGCTGCCACCAACATCTCTGCTCAAGT 3300
Oy 3272 GACTCGACACCGGTGCACCTACGTGCACGCTGCGGGGTCACTCAGAGACCCCAAGACGA 3331
Db 3301 GACTCGACACCGGTGCACCTACGTGCACGCTGCGGGGTCACTCAGAGACCCCAAGACGA 3360
Oy 3332 GCTGAGTGGGAAGCTCCCGGGGAGAGAGGCTGACTGCTCCGAGAGCCCGCAACCCGGC 3391
Db 3361 GCTGAGTGGGAAGCTCCCGGGGAGAGAGGCTGACTGCTCCGAGAGCCCGCAACCCGGC 3420
Oy 3392 ACTGCCCTCAGACTTCAGAACCATCTGAGACTGATGAGCCACCCGCCACAGCCAGGCCGA 3451
Db 3421 ACTGCCCTCAGACTTCAGAACCATCTGAGACTGATGAGCCACCCGCCACAGCCAGGCCGA 3480
Oy 3452 GAGCAGACACACGAGCCCTGTACGCGCGGCTCTACGTCCAGGAGGAGGAGGGCGGCGC 3511
Db 3481 GAGCAGACACACGAGCCCTGTACGCGCGGCTCTACGTCCAGGAGGAGGAGGGCGGCGC 3540
Oy 3512 CACAGCCAGGCGCGCAGCGCTGGGAGTCTGAGGCCGAGTAGTGTGGCCGAGGCCCTG 3571
Db 3541 CACAGCCAGGCGCGCAGCGCTGGGAGTCTGAGGCCGAGTAGTGTGGCCGAGGCCCTG 3600
Oy 3572 CATGTCCGGCTAAAGGCTGATGTCGCGGCTGAGGCGCTGAGGAGTGCAGGCCAAAGGGT 3631
Db 3601 CATGTCCGGCTAAAGGCTGATGTCGCGGCTGAGGCGCTGAGGAGTGCAGGCCAAAGGGT 3660
Oy 3632 GAGGTGCAGACACCTGCTCTACCTTCCGACAGAGCTGGGGCTCGGCTCCACCCCA 3691
Db 3661 GAGGTGCAGACACCTGCTCTACCTTCCGACAGAGCTGGGGCTCGGCTCCACCCCA 3720
Oy 3692 GGGCGAGCTTTTCTCAGACAGAGACCGGGTTCACATCCCAATAGAAATATGCAATCC 3751
Db 3721 GGGCGAGCTTTTCTCAGACAGAGACCGGGTTCACATCCCAATAGAAATATGCAATCC 3780
Oy 3752 CAGATTCGCAATTTGTACACCCCTGCGCTGCGCTCTTTTGGCTTCCACCCCAACATCC 3811
Db 3781 CAGATTCGCAATTTGTACACCCCTGCGCTGCGCTCTTTTGGCTTCCACCCCAACATCC 3840

```

```

Oy 3812 AGGTGAGACCCCTGAGAGAACCCCTGGAGCTCTGGGAATTTGAGTACCAAGGTGTG 3871
Db 3841 AGGTGAGACCCCTGAGAGAACCCCTGGAGCTCTGGGAATTTGAGTACCAAGGTGTG 3900
Oy 3872 CCCTGTACACAGGCGAGGACCTGCACCTGATGGGGGTCCCTGTGGGTCAAAATTTGGGG 3931
Db 3901 CCCTGTACACAGGCGAGGACCTGCACCTGATGGGGGTCCCTGTGGGTCAAAATTTGGGG 3960
Oy 3932 GAGGTCTGTGGGAGTAAATATGAAATATGATTTTACGTTTGAAGAAAAA 3986
Db 3961 GAGGTCTGTGGGAGTAAATATGAAATATGATTTTACGTTTGAAGAAAAA 4015

RESULT 7
AAZ00724
ID AAZ00724 standard; DNA; 4015 BP.
XX
AC AAZ00724;
XX
DT 06-OCT-1999 (first entry)
XX
DE Human telomerase catalytic domain DNA.
XX
RW Telomerase; catalytic domain; human; quantitation; tumour cell; melanoma;
KW body fluid; metastases; T-cell lymphoblastoma; chronic myeloid leukemia;
KW acute lymphatic leukemia; melanoma; pulmonary carcinoma; colon cancer;
KW breast cancer; ss.
XX
OS Homo sapiens.
XX
PN DE19804372-A1.
XX
PD 05-AUG-1999.
XX
PF 04-FEB-1998; 98DE-1004372.
XX
PR 04-FEB-1998; 98DE-1004372.
XX
PA (DAHM/) DAHM M W.
XX
PI Dahm MW;
XX
DR WPI; 1999-431408/37.
XX
PT Quantifying tumor cells by amplifying mRNA encoding the catalytic
PT subunit of telomerase
XX
PS Example; Fig 1A-B; 26pp; German.
XX
CC This invention describes a novel method for the quantitation of tumour
CC cells in a body fluid which comprises (1) enrichment or isolation of
CC tumour cells in the sample, (2) amplification of mRNA from these cells
CC that encodes the catalytic subunit of telomerase and (3) quantifying
CC the amount of amplified mRNA. The method is applied to tumour cells
CC derived from (micro)metastases, e.g. associated with a wide range of
CC tumours such as T-cell lymphoblastoma, chronic myeloid or acute
CC lymphatic leukemia, melanoma, pulmonary carcinoma, cancer of colon or
CC breast etc. This sequence encodes a human telomerase protein catalytic
CC domain.
XX
SO Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;

Query Match 99.1%; Score 3959; DB 20; Length 4015;
Best Local Similarity 99.1%; Pred. No. 9.4e-147;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

Oy 8 GCAGCGCTGCTCTGCTGCGCACGTGGGAACCCCTGGCCCGGCAACCCCGGAGTGC 67
Db 1 GCAGCGCTGCTCTGCTGCGCACGTGGGAACCCCTGGCCCGGCAACCCCGGAGTGC 60
Oy 68 GCGCGCTCCCGCTGCGAGCGGTGCGCTCCCTGCTGCGAGCACTACCGGAGTGTCT 127

```


Qy	2252	TCGGATATCCGCTGTGTCAGAAAGGCCGCCATGGGACAGTCCGACAGGCCCTTCAAGAGCCA	23111
Db	2281	TCGGATATCCGCTGTGTCAGAAAGGCCGCCATGGGACAGTCCGACAGGCCCTTCAAGAGCCA	23140
Qy	2312	GCCTCTACCTGTACAGAGACCTCCAGCCGATACATGTGACACTTGTGTGCTGCACCTGTGAGA	23711
Db	2341	GCCTCTACCTGTACAGAGACCTCCAGCCGATACATGTGACACTTGTGTGCTGCACCTGTGAGA	24000
Qy	2372	GACCAAGCCCGCTATGAGATATGCCCTGCTCATGAGACAGACTCTCTCCGTAAATGAGCCAG	24311
Db	2401	GACCAAGCCCGCTATGAGATATGCCCTGCTCATGAGACAGACTCTCTCCGTAAATGAGCCAG	24600
Qy	2432	CAGTATGCCCTTGTGACAGCTTCTCTACGCTTCATGTGTGCCACACAGCGCTGTGCATAGGGG	24911
Db	2461	CAGTATGCCCTTGTGACAGCTTCTCTACGCTTCATGTGTGCCACACAGCGCTGTGCATAGGGG	25200
Qy	2492	CAAGTCTACGTCCAGTATCCAGAGGGATATCCGACAGGCTTCATCTCTCCACGCTGCTCTG	25511
Db	2521	CAAGTCTACGTCCAGTATCCAGAGGGATATCCGACAGGCTTCATCTCTCCACGCTGCTCTG	25800
Qy	2552	CAGCCTGTGCTACGAGCAGATGAGAAACAAGCTGTGTGGCGGATTTCCGCGCGAGACGGCT	26111
Db	2581	CAGCCTGTGCTACGAGCAGATGAGAAACAAGCTGTGTGGCGGATTTCCGCGCGAGACGGCT	26400
Qy	2612	GCCTCCTGCTTTGTGATGATTTCTTTGTGTGTGACACCTCACCTTACCACCGAGGAAAC	26711
Db	2641	GCCTCCTGCTTTGTGATGATTTCTTTGTGTGTGACACCTCACCTTACCACCGAGGAAAC	27000
Qy	2672	CTTTCCTAGAACCTGTGATCCAGAGTATCCCTAGATATGGGTGGTGTGTGTGAATCTGGGAA	27311
Db	2701	CTTTCCTAGAACCTGTGATCCAGAGTATCCCTAGATATGGGTGGTGTGTGTGAATCTGGGAA	27600
Qy	2732	GACATGTGTAACTTCCCTGTAGAAAGACAGGCCCTGTGGTGTGTGTGTGTGTGTGTGACAT	27911
Db	2761	GACATGTGTAACTTCCCTGTAGAAAGACAGGCCCTGTGGTGTGTGTGTGTGTGTGTGACAT	28200
Qy	2792	GGCGGCCACAGGCTATTTCCCTGT	28511
Db	2821	GGCGGCCACAGGCTATTTCCCTGT	28800
Qy	2852	GGAGAGGACTATCTCCAGCTATGCGCGGACCTTCATCAAGACAGTCTTCACCTTCAACCG	29111
Db	2881	GGAGAGGACTATCTCCAGCTATGCGCGGACCTTCATCAAGACAGTCTTCACCTTCAACCG	29400
Qy	2912	CGGCTTCAGGCTGTGGAGAAACATGCTGTGCAAACTCTTTGGGGCTTTTGGGCTGTAGATG	29711
Db	2941	CGGCTTCAGGCTGTGGAGAAACATGCTGTGCAAACTCTTTGGGGCTTTTGGGCTGTAGATG	30000
Qy	2972	TCACAGCCTGTTTTCTGTGATTTGTGACGTGAACAGCTTCCACACAGCTGTCCACACAATCTTA	30311
Db	3001	TCACAGCCTGTTTTCTGTGATTTGTGACGTGAACAGCTTCCACACAGCTGTGTCCACACAATCTTA	30600
Qy	3032	CAGATCTCTCTCTGTGACAGGGGTATGAGTTTACGCAATGTGTCTGTACAGTCCCATTTCA	30911
Db	3061	CAGATCTCTCTCTGTGACAGGGGTATGAGTTTACGCAATGTGTCTGTACAGTCCCATTTCA	31200
Qy	3092	TCAGCAGTTTGTGAGAAACCCCAATTTTCTGTGGGATGTATCTGTGACAGGGCTTCCCT	31511
Db	3121	TCAGCAGTTTGTGAGAAACCCCAATTTTCTGTGGGATGTATCTGTGACAGGGCTTCCCT	31800
Qy	3152	CTGTACATCCATCTTGAAGGCAAGAACGAGGATATGCTGTGGGGGCGCAGAGGGCGCGC	32111
Db	3181	CTGTACATCCATCTTGAAGGCAAGAACGAGGATATGCTGTGGGGGCGCAGAGGGCGCGC	32400
Qy	3212	GGGGCCTCTGCTGTGAGAGCGGTGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	32711
Db	3241	GGGGCCTCTGCTGTGAGAGCGGTGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	33000
Qy	3272	GACTGTGACACCTGTGTACCTTACGTGCACATCTCTGGGGTCACTATGAGACAGCCAGACGCA	33311
Db	3301	GACTGTGACACCTGTGTACCTTACGTGCACATCTCTGGGGTCACTATGAGACAGCCAGACGCA	33600
Qy	3332	GCTGATGTGGAACTCTCCGGGGAGACAGCTGATCTCCTGTGAGAGCGCGAGCCAAACCTGGC	33911

Db	3361	GCTGAGTGGAGACCTCCCGGGGAGCAGACGTGACTGCCCTTGAGAGGCCAGCCAAACCGGC	3420
Oy	3392	ACTGGCCCTGCAAGCTTCATGAACCATCCGCGAATCGTAGTGAGCCACCACCGCCCAACCCAGGCGCA	3451
Db	3421	ACTGCCCCCTGACACTTCGTAAGACCATCTCGACTGATGAGCCACCGCCCAACAGCCGCCA	3480
Oy	3452	GAGCAGACACCAAGCACCCCTGTCAACGCGGGCTCTAGCTGCCAGGGAGGAGGGGCGGC	3511
Db	3481	GAGCAGACACCAAGCACCCCTGTCAACGCGGGCTCTAGCTGCCAGGGAGGAGGGGCGGC	3540
Oy	3512	CACACCCAGGCGCCGACACGCGCTGGAGGCTTGAGGCGCTGAGTGTGTTGGCCAGAGCCCTG	3571
Db	3541	CACACCCAGGCGCCGACACGCGCTGGAGGCTTGAGGCGCTGAGTGTGTTGGCCAGAGCCCTG	3600
Oy	3572	CATTGTCGGGCTGGAAGGCTGAGTGTGCCGGCTGAGGCGCTGAGCGAGTGTCCACGCCAAGGGCT	3631
Db	3601	CATTGTCGGGCTGGAAGGCTGAGTGTGCCGGCTGAGGCGCTGAGCGAGTGTCCACGCCAAGGGCT	3660
Oy	3632	GAGTGTCCAGACACACCTGCGCTTTCACCTTCCCACAGGCTGGCGCTGGGCTCACGCCA	3691
Db	3661	GAGTGTCCAGACACACCTGCGCTTTCACCTTCCCACAGGCTGGCGCTGGGCTCACGCCA	3720
Oy	3692	GGGCGAGTTTTTCTTCACACAGAACCCGGGCTTCCACGCCCAATAGAATAAGTCATCC	3751
Db	3721	GGGCGAGTTTTTCTTCACACAGAACCCGGGCTTCCACGCCCAATAGAATAAGTCATCC	3780
Oy	3752	CCAGATTGGCCATTGTTACGCCCGCGCCGCTGCGCTTGGCTTGCACACCCCAACATCC	3811
Db	3781	CCAGATTGGCCATTGTTACGCCCGCGCCGCTGCGCTTGGCTTGCACACCCCAACATCC	3840
Oy	3812	AGGTGGAGACCCCGAAGAGAACCCGTGGAGGCTGGGAAATTGGAGTAGCAAAAGGTGG	3871
Db	3841	AGGTGGAGACCCCGAAGAGAACCCGTGGAGGCTGGGAAATTGGAGTAGCAAAAGGTGG	3900
Oy	3872	CCCTGTACACAGGCGAGACCCCTGACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG	3931
Db	3901	CCCTGTACACAGGCGAGACCCCTGACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG	3960
Oy	3932	GAGGTGCTGTGGGAGTAAATATCTGAATATATGAGTGTTCAGTTTGAATAAAA 3986	
Db	3961	GAGGTGCTGTGGGAGTAAATATCTGAATATATGAGTGTTCAGTTTGAATAAAA 4015	
<hr/>			
RESULT 8			
AAHA5901			
ID	AAHA5901	standard; DNA; 4015 BP.	
XX	AAHA5901;		
AC	XX		
AC	XX		
DT	06-SEP-2001	(first entry)	
XX	DE		
XX	Human hTERT gene.		
XX	Human: hTERT; telomerase; catalytic subunit; mRNA quantitation; detection; beta-region; diagnosis; cancer; ds.		
KW	Homo sapiens.		
OS			
XX			
Key	Location/Qualifiers		
FT	/tag= a		
FT	/number= 1		
FT	275..1628		
FT	/tag= b		
FT	/number= 2		
FT	1629..1824		
FT	/tag= c		
FT	/number= 3		
FT	1825..2005		
FT	/tag= d		
FT	/number= 4		
FT	2006..2185		
FT	exon		

QY 788 TCCCTTGAAGCGGAGCGAGCGCCGTTGGCAGAGGGTCTCTGGGCCACCCGGGCGAGAC 847
 Db 781 TCCCTTGAAGCGGAGCGAGCGCCGTTGGCAGAGGGTCTCTGGGCCACCCGGGCGAGAC 840
 QY 848 GCGTGGACCGAGTGAACCGGTGTTCTGTGTGTGTACCTGTGCAGAACCGCGGAGAAAGC 907
 Db 841 GCGTGGACCGAGTGAACCGGTGTTCTGTGTGTGTACCTGTGCAGAACCGCGGAGAAAGC 900
 QY 908 CACCTTTTGGAGGTGCGCTCTGTGCAGCGGACACTCCCAACCCATCCGTTGGGCGCCCA 967
 Db 901 CACCTTTTGGAGGTGCGCTCTGTGCAGCGGACACTCCCAACCCATCCGTTGGGCGCCCA 960
 QY 968 GCACACGCGGGGCGCCCATATCCATCCGCGGCCACACGCTCCGGGAGAGCGCTTGTCC 1027
 Db 961 GCACACGCGGGGCGCCCATATCCATCCGCGGCCACACGCTCCGGGAGAGCGCTTGTCC 1020
 QY 1028 CCGGCTGAGCGCGAGAACCAAGCACTTCTCTACTCTCAGCGGAGAGAGAGAGAGCGCG 1087
 Db 1021 CCGGCTGAGCGCGAGAACCAAGCACTTCTCTACTCTCAGCGGAGAGAGAGAGAGCGCG 1080
 QY 1088 GCGCTCTTCTACTACTAGCTCTGTAGGCGCAGCTGTGCGCTCGGAGGCTGTGGA 1147
 Db 1081 GCGCTCTTCTACTACTAGCTCTGTAGGCGCAGCTGTGCGCTCGGAGGCTGTGGA 1140
 QY 1148 GACCACTTTCTGTGGTTCCAGGCGCTGGATGCGAGGACTCCCGAGGTTGCCCGCT 1207
 Db 1141 GACCACTTTCTGTGGTTCCAGGCGCTGGATGCGAGGACTCCCGAGGTTGCCCGCT 1200
 QY 1208 GCGCCAGCGCTACTGCGAAATGCGGCGCCCTGTTCTGTGAGACTGTTGGGAACCAAGCGCA 1267
 Db 1201 GCGCCAGCGCTACTGCGAAATGCGGCGCCCTGTTCTGTGAGACTGTTGGGAACCAAGCGCA 1260
 QY 1268 GTGCCCCCTACGCGGAGTCTCTCTCAAGACGACTGCGCGCTGCGAGTGGCGTCAACCCAGC 1327
 Db 1261 GTGCCCCCTACGCGGAGTCTCTCTCAAGACGACTGCGCGCTGCGAGTGGCGTCAACCCAGC 1320
 QY 1328 AGCCGCTGTCTGTGCGCGGAGAAAGCGCCAGGCGTGTGGCGCGCCCGAGAGAGAGGA 1387
 Db 1321 AGCCGCTGTCTGTGCGCGGAGAAAGCGCCAGGCGTGTGGCGCGCCCGAGAGAGAGGA 1380
 QY 1388 CACAGACCGCGCGCTGTGTGAGCTGTCTCGGCACACAGAGAGCGCTGGCAGGTGA 1447
 Db 1381 CACAGACCGCGCGCTGTGTGAGCTGTCTCGGCACACAGAGAGCGCTGGCAGGTGA 1440
 QY 1448 GCGCTGTGTGCGGCGCTGTGTGCGGCGTGTGTGCGCGCGCTGTGTGCGCGCTGTGTGCGCG 1507
 Db 1441 GCGCTGTGTGCGGCGCTGTGTGCGGCGTGTGTGCGCGCGCTGTGTGCGCGCTGTGTGCGCG 1500
 QY 1508 CACAGACCGCGCTGTGTGAGCTGTCTCGGCACACAGAGAGCTGTGTGCGCGCGCTGTGTGCGCG 1567
 Db 1501 CACAGACCGCGCTGTGTGAGCTGTCTCGGCACACAGAGAGCTGTGTGCGCGCGCTGTGTGCGCG 1560
 QY 1568 GCTCTGCTGAGAGACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1627
 Db 1561 GCTCTGCTGAGAGACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
 QY 1628 GAGCCCAAGGGTGTGCGTGTGTCTCGGCGCAGAGACAGCTCTGCGTGAGAGAGATCTGGC 1687
 Db 1621 GAGCCCAAGGGTGTGCGTGTGTCTCGGCGCAGAGACAGCTCTGCGTGAGAGAGATCTGGC 1680
 QY 1688 CAACTTCTGAGAGCTGTGTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1747
 Db 1681 CAACTTCTGAGAGCTGTGTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740
 QY 1748 TGTCAAGAGAGACAGCTTTCACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1807
 Db 1741 TGTCAAGAGAGACAGCTTTCACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
 QY 1808 CAACTTGAAG 1867
 Db 1801 CAACTTGAAG 1860

QY 1868 GGAAGCAGAGAGTGAAG 1927
 Db 1861 GGAAGCAGAGAGTGAAG 1920
 QY 1928 CTTCTATCCCAAG 1987
 Db 1921 CTTCTATCCCAAG 1980
 QY 1988 CAGAACTTCCAG 2047
 Db 1981 CAGAACTTCCAG 2040
 QY 2048 CAGAGTCTCAATCAAG 2107
 Db 2041 CAGAGTCTCAATCAAG 2100
 QY 2108 CCGTGAAGATTCACAG 2167
 Db 2101 CCGTGAAGATTCACAG 2160
 QY 2168 GCGGCTGAGCTGTGTA-----CATCCGCA 2191
 Db 2161 GCGGCTGAGCTGTGTA-----CATCCGCA 2220
 QY 2192 GGAAGGCTCAG 2251
 Db 2221 GGAAGGCTCAG 2280
 QY 2252 TCGGTATGCGGTGTGTCAG 2311
 Db 2281 TCGGTATGCGGTGTGTCAG 2340
 QY 2312 CGTCTTACCTTACAG 2371
 Db 2341 CGTCTTACCTTACAG 2400
 QY 2372 GACAGAGCGCGCTGAG 2431
 Db 2401 GACAGAGCGCGCTGAG 2460
 QY 2433 CAGTGGGCTCTTGTGAG 2491
 Db 2461 CAGTGGGCTCTTGTGAG 2520
 QY 2492 CAACTTACAGTCAAG 2551
 Db 2521 CAACTTACAGTCAAG 2580
 QY 2552 CAGCCTGTCTACGCGAG 2611
 Db 2581 CAGCCTGTCTACGCGAG 2640
 QY 2612 GCTCTGCTGT 2671
 Db 2641 GCTCTGCTGT 2700
 QY 2672 CTTCTCTAG 2731
 Db 2701 CTTCTCTAG 2760
 QY 2733 GACAGTGTGAATCTTCCGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2791
 Db 2761 GACAGTGTGAATCTTCCGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
 QY 2792 GCGGCGCCAG 2851
 Db 2821 GCGGCGCCAG 2880
 QY 2852 GCAAGAGAGATCTCAG 2911
 Db 2881 GCAAGAGAGATCTCAG 2940
 QY 2912 CCGCTTCAAGGCTGAG 2971

|||||
Db 2941 CGGCTTCAAGGCTGGAGAACATGCGCAACTTTTGGGGCTTGGCGCTGAAGTG 3000
QY 2972 TCACAGCCTGTTTGGATTTGAGGTGAACAGCTCCAGAGCGGTGTCACACATCTA 3031
Db 3001 TCACAGCCTGTTTGGATTTGAGGTGAACAGCTCCAGAGCGGTGTCACACATCTA 3060
QY 3032 CAAGATCTCTGCTGAGGCGTACAGGTTCACGATGTGTGTCAGTCCCATTTTCA 3091
Db 3061 CAAGATCTCTGCTGAGGCGTACAGGTTCACGATGTGTGTCAGTCCCATTTTCA 3120
QY 3092 TCAGCAAGTTTGAAGAACCACATTTTCTGCGGCTCATCTCTGACAGGCTCCCT 3151
Db 3121 TCAGCAAGTTTGAAGAACCACATTTTCTGCGGCTCATCTCTGACAGGCTCCCT 3180
QY 3152 CTGCTACTCCATCCGAAAGCCAAAGACGAGGATGTGCTGGGGGGCCAAAGGGCGCCG 3211
Db 3181 CTGCTACTCCATCCGAAAGCCAAAGACGAGGATGTGCTGGGGGGCCAAAGGGCGCCG 3240
QY 3212 CGGCGCTCTGCTCCGAGGCGTGCAGTGTGCTGCCAAGCATTCCTGCTCAAGCT 3271
Db 3241 CGGCGCTCTGCTCCGAGGCGTGCAGTGTGCTGCCAAGCATTCCTGCTCAAGCT 3300
QY 3272 GACTCGACACCGTGTACCTACCTACCTGCTGCGGTCTCTGACAGACGCCAGCGCA 3331
Db 3301 GACTCGACACCGTGTACCTACCTACCTGCTGCGGTCTCTGACAGACGCCAGCGCA 3360
QY 3332 GCTGAGTGGAAAGTCCCGGGGAGAGAGCTGACTGAGGCGGCGGAGCCAGCCGCGC 3391
Db 3361 GCTGAGTGGAAAGTCCCGGGGAGAGAGCTGACTGAGGCGGCGGAGCCAGCCGCGC 3420
QY 3392 ACTGCGCTCAGACTTCAAGACATCTGAGTGTGAGTGGCCACCGCCACAGCCAGCGCA 3451
Db 3421 ACTGCGCTCAGACTTCAAGACATCTGAGTGTGAGTGGCCACCGCCACAGCCAGCGCA 3480
QY 3452 GAGCAGACACAGACAGCCCTTCAAGCGCGGCTCTAGCTCCAGAGAGAGAGGGCGCC 3511
Db 3481 GAGCAGACACAGACAGCCCTTCAAGCGCGGCTCTAGCTCCAGAGAGAGAGGGCGCC 3540
QY 3512 CACACCCAGGCGCGCAGCTGAGGAGTGTGAGGCTGAGTGTGAGGAGGCTG 3571
Db 3541 CACACCCAGGCGCGCAGCTGAGGAGTGTGAGGCTGAGTGTGAGGAGGCTG 3600
QY 3572 CATGTCCGCTGAAAGCTGAGTGTCCGCTGAGGCTGAGGAGTGTCCAGCCAAAGGCT 3631
Db 3601 CATGTCCGCTGAAAGCTGAGTGTCCGCTGAGGCTGAGGAGTGTCCAGCCAAAGGCT 3660
QY 3632 GAGTGTCCAGACACCTGCGCTTCACTTCCACAGGCGGCGTGGCTCCACCCCA 3691
Db 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCACAGGCGGCGTGGCTCCACCCCA 3720
QY 3692 GGGCGAGCTTTTCTCAGACAGAGCGCGCTTCCACTCCCAATAGAAATAGTCCATCC 3751
Db 3721 GGGCGAGCTTTTCTCAGACAGAGCGCGCTTCCACTCCCAATAGAAATAGTCCATCC 3780
QY 3752 CCAATTTGCCATTTGTACCCCTGCGCTCCCTTTCCTTTCACACCCCAATCC 3811
Db 3781 CCAATTTGCCATTTGTACCCCTGCGCTCCCTTTCCTTTCACACCCCAATCC 3840
QY 3812 AGGTGGAGACCTGAGAAAGACCCCTGGGAGCTGGGAAATTTGGAGTACCAAGGTGTG 3871
Db 3841 AGGTGGAGACCTGAGAAAGACCCCTGGGAGCTGGGAAATTTGGAGTACCAAGGTGTG 3900
QY 3872 CCCTGTACACAGGAGAGACCTGACCTGAGTGGGGTCCCTGTGGTCAAAATTTGGGG 3931
Db 3901 CCCTGTACACAGGAGAGACCTGACCTGAGTGGGGTCCCTGTGGTCAAAATTTGGGG 3960
QY 3932 GAGGTGCTGTGGAGTAAATAGTAATATATAGTGTTCAGTTTGAATTTGAAAAA 3986
Db 3961 GAGGTGCTGTGGAGTAAATAGTAATATATAGTGTTCAGTTTGAATTTGAAAAA 4015

ABA97534
ID ABA97534 standard; DNA; 4015 BP.
XX
AC ABA97534;
XX
DT 05-APR-2002 (first entry)
XX
DE Cancer cell discrimination method related human DNA.
XX
KW Human; telomerase; enzyme; cancer cell discrimination; gene;
KW reverse transcriptase; ds.
XX
OS Homo sapiens.
PN JP2001309791-A.
XX
PD 06-NOV-2001.
XX
PE 02-MAY-2000; 2000JP-0138250.
PR 02-MAY-2000; 2000JP-0138250.
XX
PA (KANE/) KANEUCHI H.
PA (KAMI/) KAMIMORI M.
DR WPI; 2002-134853/18.
XX
PT Discrimination of a cancer cell in a sample tissue, comprises
PT determining the expression level of a reverse transcriptase component
PT of telomerase using a hybridization assay -
XX
PS Claim 2; Page 9-10; 16pp; Japanese.
XX
CC The present invention relates to a method for the discrimination of a
CC cancer cell in a sample tissue, which involves determining the expression
CC level of a reverse transcriptase component of telomerase in a cell
CC constituting the sample tissue by an in situ hybridization of the mRNA of
CC the enzyme, and judging a cell showing a higher expression level than
CC that of the reverse transcriptase component of telomerase in a normal
CC cell to be a cancer cell. The present sequence is a human DNA used in the
CC exemplification of the invention.
XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;
Query Match 99.1%; Score 3969; DB 24; Length 4015;
Best Local Similarity 99.1%; Pred. No. 9.4e-147;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;
QY 8 GCAGCGCTGCTCTGCTGCGCAGGTGGAGAGCCCTGGCCCCCGGCACACCCCGGATGCC 67
Db 1 GCAGCGCTGCTCTGCTGCGCAGGTGGAGAGCCCTGGCCCCCGGCACACCCCGGATGCC 60
QY 68 GCGGCGTCCCGCTGCGAGCGCGTGGCGCTCTGCTGCGAGCACTACCGGAGTGTCT 127
Db 61 GCGGCGTCCCGCTGCGAGCGCGTGGCGCTCTGCTGCGAGCACTACCGGAGTGTCT 120
QY 128 GCGGCTGCGACAGTTGTGTCGCGCGCTGGGGCCCGAGGCTGGCGGTGTGTCAGCGGG 187
Db 121 GCGGCTGCGACAGTTGTGTCGCGCGCTGGGGCCCGAGGCTGGCGGTGTGTCAGCGGG 180
QY 188 GCAGCCGCGGCTTTCGCGCGCGCTGGTGGCCCAATGCTGCTGTGCTGCTGGAGCC 247
Db 181 GCAGCCGCGGCTTTCGCGCGCGCTGGTGGCCCAATGCTGCTGTGCTGCTGGAGCC 240
QY 248 ACGGCGCGCCCCCGCGCGCGCTCTTCCGCGAGTGTCTGCTGGAAGAGTGTGGC 307
Db 241 ACGGCGCGCCCCCGCGCGCGCTCTTCCGCGAGTGTCTGCTGGAAGAGTGTGGC 300
QY 308 CCGAGTGTGCGAGAGCTGTGCGAGCGCGGCGGAAGAACGTGCTGCGCTTGGCTTGC 367
Db 301 CCGAGTGTGCGAGAGCTGTGCGAGCGCGGCGGAAGAACGTGCTGCGCTTGGCTTGC 360
QY 368 CCTGCTGAGCGGGGCGCGCGCGGCGCGCGCGCGCGAGGCTTTCACACAGAGCTGCGAGCTA 427

```

Db 361 GCTGCTGAGAGGGGCCCCGGGGGGCCCCCGGAGGCTTTCACACACAGCTGCGCAGCTA 420
Oy 428 CCTGCCCAACACAGCTGACCGACGACTGCGGGGAGACGGGGGCGTGGGGCTGCTGCTGGC 487
Db 421 CCTGCCCAACACAGCTGACCGACGACTGCGGGGAGACGGGGGCGTGGGGCTGCTGCTGGC 480
Oy 488 CCGGCTGGGGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
Db 481 CCGGCTGGGGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Oy 548 GGGTCCCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607
Db 541 GGGTCCCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Oy 608 TCAAGCCCCGGGGCCCCCGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667
Db 601 TCAAGCCCCGGGGCCCCCGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Oy 668 CTGGAACCATAGCTGACGAGGAGCGCGGGGTCCCTGCGGCTGCCAGCCCGGGGTGCGAG 727
Db 661 CTGGAACCATAGCTGACGAGGAGCGCGGGGTCCCTGCGGCTGCCAGCCCGGGGTGCGAG 720
Oy 728 GAGGCGCGGGGAGCTGCCAGCCGAAAGTGTGCGTTGCCAAGAGGCCCAAGGCGTGGCGC 787
Db 721 GAGGCGCGGGGAGCTGCCAGCCGAAAGTGTGCGTTGCCAAGAGGCCCAAGGCGTGGCGC 780
Oy 788 TGCCCCCTGAGCCGAGCGGAGCGCCGCTTGGGCGAGGGGTCTTGGGCCACCCCGGGGAGAGAC 847
Db 781 TGCCCCCTGAGCCGAGCGGAGCGCCGCTTGGGCGAGGGGTCTTGGGCCACCCCGGGGAGAGAC 840
Oy 848 GCGTGGACCGAGTGAACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
Db 841 GCGTGGACCGAGTGAACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Oy 908 CAGCTCTTTGAGGGGGGTGCTCTGTGGCAGGGGCACTGCCACCCATCCGCGGGGGCGGCA 967
Db 901 CAGCTCTTTGAGGGGGGTGCTCTGTGGCAGGGGCACTGCCACCCATCCGCGGGGGCGGCA 960
Oy 968 GCACACAGGGGGGCCCCCATGCAATGGGGGCGACAGCTCCCTGGGACACGCTGTGCC 1027
Db 961 GCACACAGGGGGGCCCCCATGCAATGGGGGCGACAGCTCCCTGGGACACGCTGTGCC 1020
Oy 1028 CCGGCTGTACGCGGAGACCAAGCACTTCTCTACTCTCTGAGGCGCAAGAGAGCAAGTGTGCG 1087
Db 1021 CCGGCTGTACGCGGAGACCAAGCACTTCTCTACTCTCTGAGGCGCAAGAGAGCAAGTGTGCG 1080
Oy 1088 GCCCTCTCTACTACTAGCTCTGTAGGCGCCAGCTGACTGCGCGCTCGAGAGCTGTGGA 1147
Db 1081 GCCCTCTCTACTACTAGCTCTGTAGGCGCCAGCTGACTGCGCGCTCGAGAGCTGTGGA 1140
Oy 1148 GACCATCTTTGAGGGGTCCAGAGCGCACTGCGCGCGAGCTGCGCGAGTGTGCGCGCT 1207
Db 1141 GACCATCTTTGAGGGGTCCAGAGCGCACTGCGCGCGAGCTGCGCGAGTGTGCGCGCT 1200
Oy 1208 GCCCAGACGCTACTGCAAAATGCGGCCCTGTTTGTGAGTGTGCTGGGAACACAGCGCA 1267
Db 1201 GCCCAGACGCTACTGCAAAATGCGGCCCTGTTTGTGAGTGTGCTGGGAACACAGCGCA 1260
Oy 1268 GTGCCCCCTTACGGGGGTCTCTCAAGAGCGCACTGCGCGCGAGCTGCGCGAGTGTGCGCGAG 1327
Db 1261 GTGCCCCCTTACGGGGGTCTCTCAAGAGCGCACTGCGCGCGAGCTGCGCGAGTGTGCGCGAG 1320
Oy 1328 AGCGGGGTGTGTGCGCGGGAGAAAGCCCGAGGCTGTGTGGCGCGCCCGAGAGAGAGA 1387
Db 1321 AGCGGGGTGTGTGCGCGGGAGAAAGCCCGAGGCTGTGTGGCGCGCCCGAGAGAGAGA 1380
Oy 1388 CACAGACCCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1447
Db 1381 CACAGACCCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
Oy 1448 CGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1507

```

```

Db 1441 CGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Oy 1508 CAACGAGACGCCCTTCTCTCAGAGAAACACAGAAAGTGTATCTCTCTGCGGAGACATGCCAA 1567
Db 1501 CAACGAGACGCCCTTCTCTCAGAGAAACACAGAAAGTGTATCTCTCTGCGGAGACATGCCAA 1560
Oy 1568 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1627
Db 1561 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
Oy 1628 GAGCCAGAGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1687
Db 1621 GAGCCAGAGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
Oy 1688 CAAGTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1747
Db 1681 CAAGTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
Oy 1748 TGTACGAGAGACCATGTTTCAAAAAGAACAGGCTGTTTCTACCGGAGAGTGTCTGGAG 1807
Db 1741 TGTACGAGAGACCATGTTTCAAAAAGAACAGGCTGTTTCTACCGGAGAGTGTCTGGAG 1800
Oy 1808 CAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGACGTGCGGGAGCTGTG 1867
Db 1801 CAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGACGTGCGGGAGCTGTG 1860
Oy 1868 GGAAGCAGAGGTCAAGGCAAGCATGCGGGAAGCCAGGCGCCGCTGCTGCTGCTGCTGCTGCTGCTG 1927
Db 1861 GGAAGCAGAGGTCAAGGCAAGCATGCGGGAAGCCAGGCGCCGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Oy 1928 CTTTCATCCCAAGCCCTGAGGGGCTGCGGGCGGATGTGAACATGAGACAGTGTGTGGAGC 1987
Db 1921 CTTTCATCCCAAGCCCTGAGGGGCTGCGGGCGGATGTGAACATGAGACAGTGTGTGGAGC 1980
Oy 1988 CAGAACCTTCCGCAAGAAAAAGAGGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2047
Db 1981 CAGAACCTTCCGCAAGAAAAAGAGGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
Oy 2048 CAGGCTGCTCAACTGCAAGCGGGCGGGGCGCCCGGCTCTGTGGCGGCTGTGTGTGTGTGTGTGT 2107
Db 2041 CAGGCTGCTCAACTGCAAGCGGGCGGGGCGCCCGGCTCTGTGGCGGCTGTGTGTGTGTGTGTGTGT 2100
Oy 2108 CTGAGACATATCCACAGAGGCTGCGGCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2167
Db 2101 CTGAGACATATATCCACAGAGGCTGCGGCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
Oy 2168 GCGCCTGAGCTGTA-----CATCCCCA 2191
Db 2161 GCGCCTGAGCTGTA-----CATCCCCA 2220
Oy 2192 GGAACAGGCTCAGGAGGTCAATCGCGCAGCATATCAAAACCCAGAACAGTGTGTGTGTGTGTGTGTGT 2251
Db 2221 GGAACAGGCTCAGGAGGTCAATCGCGCAGCATATCAAAACCCAGAACAGTGTGTGTGTGTGTGTGTGT 2280
Oy 2252 TCGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2311
Db 2281 TCGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
Oy 2312 GGTCTTACTTGAAGAGCTCCAGCGCTGATGCAATGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2371
Db 2341 GGTCTTACTTGAAGAGCTCCAGCGCTGATGCAATGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
Oy 2372 GACCAAGCCGCTGAGAGGATGCGCTGTGATGCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2431
Db 2401 GACCAAGCCGCTGAGAGGATGCGCTGTGATGCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2460
Oy 2432 CAGTGGCTCTTGTGAGCTGTTCTTCTTACGCTTTCATGTGCCACACGCGTGGGATCAGGGG 2491
Db 2461 CAGTGGCTCTTGTGAGCTGTTCTTCTTACGCTTTCATGTGCCACACGCGTGGGATCAGGGG 2520
Oy 2492 CAAGTCTTACGTCCAGTGTCCAGGAGATCCCGAGGGCTCCATCTCTTCCACAGCTGTCTGTG 2551
Db 2521 CAAGTCTTACGTCCAGTGTCCAGGAGATCCCGAGGGCTCCATCTCTTCCACAGCTGTCTGTG 2580

```


QY 2552 CAGCTTGCTACGCGGACATGAGAAACAAAGCTGTTTCGGGGATTCGGCGGAGCGGCT 2611
 |||||||
 Db 2581 CAGCTTGCTACGCGGACATGAGAAACAAAGCTGTTTCGGGGATTCGGCGGAGCGGCT 2640
 |||||||
 QY 2612 GCTCCTGGCTTGGTGGATGATTTCTGTGTGACACACTCACTCAACCCACGCGAAAC 2671
 |||||||
 Db 2641 GCTCCTGGCTTGGTGGATGATTTCTGTGTGACACACTCACTCAACCCACGCGAAAC 2700
 |||||||
 QY 2672 CTTCCTAGAGACCTTGCTGAGTGTCCCTGAGTATGCTGCGTGGTGAATTCGCGAA 2731
 |||||||
 Db 2701 CTTCCTAGAGACCTTGCTGAGTGTCCCTGAGTATGCTGCGTGGTGAATTCGCGAA 2760
 |||||||
 QY 2732 GACAGTGTGAATCTCCCTGTAGAAGAGAGCCCTGGGTGGACGCGCTTTTGTACAT 2791
 |||||||
 Db 2761 GACAGTGTGAATCTCCCTGTAGAAGAGAGCCCTGGGTGGACGCGCTTTTGTACAT 2820
 |||||||
 QY 2792 GCGGCGCAGAGGCTATTTCCCTGGTGGGCTGCTGCTGATATCCCGGACCTGGAGT 2851
 |||||||
 Db 2821 GCGGCGCAGAGGCTATTTCCCTGGTGGGCTGCTGCTGATATCCCGGACCTGGAGT 2880
 |||||||
 QY 2852 GCAGAGGAGACTACTCAGCTATGCGCGACCTCCATCAGAGCCAGTCACTTCAACCG 2911
 |||||||
 Db 2881 GCAGAGGAGACTACTCAGCTATGCGCGACCTCCATCAGAGCCAGTCACTTCAACCG 2940
 |||||||
 QY 2912 CGGCTCAAGGCTGGGAGAAACATGCGTCCGAACTCTTGGGGTCTTGGCGTGAAGT 2971
 |||||||
 Db 2941 CGGCTCAAGGCTGGGAGAAACATGCGTCCGAACTCTTGGGGTCTTGGCGTGAAGT 3000
 |||||||
 QY 2972 TCACAGCCTGTTCTGATTTGAGGTGAACAGGCTCCAGAGGTTGACACCAATCTA 3031
 |||||||
 Db 3001 TCACAGCCTGTTCTGATTTGAGGTGAACAGGCTCCAGAGGTTGACACCAATCTA 3060
 |||||||
 QY 3032 CAAGATCCTCTGCTGAGGCGTACAGGTTTCACGATGTTGCTGAGCTCCCATTTCA 3091
 |||||||
 Db 3061 CAAGATCCTCTGCTGAGGCGTACAGGTTTCACGATGTTGCTGAGCTCCCATTTCA 3120
 |||||||
 QY 3092 TCAGCAAGTTTGAAGAAACCCACATTTTCTGCGGCTCATCTCTACAGGCTCCCT 3151
 |||||||
 Db 3121 TCAGCAAGTTTGAAGAAACCCACATTTTCTGCGGCTCATCTCTACAGGCTCCCT 3180
 |||||||
 QY 3152 CTGCTACTCCATCCTGTAAGAACCAAGAGGATGCTGCTGGGGGCCAAGGGCGCGC 3211
 |||||||
 Db 3181 CTGCTACTCCATCCTGTAAGAACCAAGAGGATGCTGCTGGGGGCCAAGGGCGCGC 3240
 |||||||
 QY 3212 CGGCGCTCTGCTCGAGGCGCTGAGTGGCTGTGCCACCAAGCATTTCTGCTAAGCT 3271
 |||||||
 Db 3241 CGGCGCTCTGCTCGAGGCGCTGAGTGGCTGTGCCACCAAGCATTTCTGCTAAGCT 3300
 |||||||
 QY 3272 GACTCGACACGCTGTACCTACCTACGTGCCACTCTGGGTCACTAGAGACAGCCAGCGCA 3331
 |||||||
 Db 3301 GACTCGACACGCTGTACCTACCTACGTGCCACTCTGGGTCACTAGAGACAGCCAGCGCA 3360
 |||||||
 QY 3332 GCTGAGTCGAAAGCTCCCGGGAGAGAGCTGAGTGGCTGGAGGCGCAGCAACCGGCG 3391
 |||||||
 Db 3361 GCTGAGTCGAAAGCTCCCGGGAGAGAGCTGAGTGGCTGGAGGCGCAGCAACCGGCG 3420
 |||||||
 QY 3392 ACTGCGCTGAGCTTAAGACCATCTGACTATGGCCACCGCCACAGCCAGCGCGA 3451
 |||||||
 Db 3421 ACTGCGCTGAGCTTAAGACCATCTGACTATGGCCACCGCCACAGCCAGCGCGA 3480
 |||||||
 QY 3452 GAGCAACACACAGAGCCCTGTACAGCGCGGCTCTACGTTCCAGAGGAGGAGGGCGGC 3511
 |||||||
 Db 3481 GAGCAACACACAGAGCCCTGTACAGCGCGGCTCTACGTTCCAGAGGAGGAGGGCGGC 3540
 |||||||
 QY 3512 CACACCCAGAGCCGAGCGCTGGAGTCTGAGGCTGAGAGTGTGTTGGCCAGAGCGCTG 3571
 |||||||
 Db 3541 CACACCCAGAGCCGAGCGCTGGAGTCTGAGGCTGAGAGTGTGTTGGCCAGAGCGCTG 3600
 |||||||
 QY 3572 CATGTCGGGCTGAAGGCTGAGTCCGGCTGAGGCTGAGCGAGTCCAGCCAAAGGCT 3631
 |||||||
 Db 3601 CATGTCGGGCTGAAGGCTGAGTCCGGCTGAGGCTGAGCGAGTCCAGCCAAAGGCT 3660
 |||||||

QY 3632 GAGTGTCCAGACACACTGCGCTTCACTTCCCCACAGGCTGGCGCTGCTCCACCCA 3691
 |||||||
 Db 3661 GAGTGTCCAGACACACTGCGCTTCACTTCCCCACAGGCTGGCGCTGCTCCACCCA 3720
 |||||||
 QY 3692 GGGCCAGCTTTTCTCACCAGAGAGCGGCTTCCACTCCACATAGGAATGTCATCC 3751
 |||||||
 Db 3721 GGGCCAGCTTTTCTCACCAGAGAGCGGCTTCCACTCCACATAGGAATGTCATCC 3780
 |||||||
 QY 3752 CCAGATTGGCATTTGTCACCCCTGCGCCCTCCCTTGGCCCTTCCACCCCGACATCC 3811
 |||||||
 Db 3781 CCAGATTGGCATTTGTCACCCCTGCGCCCTCCCTTGGCCCTTCCACCCCGACATCC 3840
 |||||||
 QY 3812 AGGTGAGACCCCTGAGAGACCCCTGGAGCTCTGGAAATTTGAGTGAACCAAGGTGTG 3871
 |||||||
 Db 3841 AGGTGAGACCCCTGAGAGACCCCTGGAGCTCTGGAAATTTGAGTGAACCAAGGTGTG 3900
 |||||||
 QY 3872 CCCGTACACAGGCGAGGACCTTGACCTGATGGGGTCCCTGTGGTCAATTTGGGGG 3931
 |||||||
 Db 3901 CCCGTACACAGGCGAGGACCTTGACCTGATGGGGTCCCTGTGGTCAATTTGGGGG 3960
 |||||||
 QY 3932 GAGGCTGCTGGGAGTAAATATGATATATGATTTTTCAGTTTGAAGAAAAA 3986
 |||||||
 Db 3961 GAGGCTGCTGGGAGTAAATATGATATATGATTTTTCAGTTTGAAGAAAAA 4015
 |||||||

RESULT 10
 AA208150
 ID AA208150 standard; cDNA; 4015 BP.
 XX

AC AA208150;
 DT 17-JAN-2000 (first entry)
 XX

DE Human telomerase reverse transcriptase cDNA.
 XX

KW Human telomerase reverse transcriptase; hTERT; telomerase; hEST2;
 KW catalytic protein component; cell proliferative capacity;
 KW cell immortality; neoplastic phenotype; diagnostic application;
 KW prognostic application; telomerase related condition; cancer;
 KW therapeutic agent; telomerase expression; telomerase activity; ds.
 XX

OS Homo sapiens.
 XX

FH Key Location/Qualifiers
 FT 56..3454
 FT /*tag- a
 FT /product- "Human telomerase reverse transcriptase"
 FT /transl_except- (pos:1877..1879, aa:Gln)
 XX

PN W0950279-A1.
 XX

PD 07-OCT-1999.
 XX

PE 31-MAR-1999; 99MD-US07160.
 XX

PR 31-MAR-1998; 9805-0052919.
 XX

PA (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX

PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morlin GB, Harley CB;
 PI Andrews WH;
 DR WPI: 1999-610834/52.
 DR P-PSDB; AAY28881.
 XX

PT Antisense polynucleotides for human telomerase reverse transcriptase
 PS used for diagnosing or treating cancer.
 XX

Claim 1: Fig 1: 31pp; English.
 CC

The present sequence encodes for human telomerase reverse transcriptase
 (hTERT). This is the catalytic protein component of telomerase and is also
 CC


```

Db 3427 CCTGAGATTTCAGACATCTCGAGCTATGGCCACCCGCCACAGCCAGCCAGAGCA 3486
QY 3457 GACACACAGACAGCCCTTCACGCGCGGCTCTACGTCCAGAGGAGGAGGCGCCACAC 3516
Db 3487 GACACACAGACAGCCCTTCACGCGCGGCTCTACGTCCAGAGGAGGAGGCGCCACAC 3546
QY 3517 CCAGGCGCGGAGCGCTGAGGAGCTGAGGAGCTGAGTGTGTTGGCCAGGCTGATGT 3576
Db 3547 CCAGGCGCGGAGCGCTGAGGAGCTGAGGAGCTGAGTGTGTTGGCCAGGCTGATGT 3606
QY 3577 CCGGCTGAAGGCTGAGTGTGCGGCTGAGGAGCTGAGGAGTGTCCAGGAGGCTGAGT 3636
Db 3607 CCGGCTGAAGGCTGAGTGTGCGGCTGAGGAGCTGAGGAGTGTCCAGGAGGCTGAGT 3666
QY 3637 TCCAGACAGCTGCGCTTCCTCCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3696
Db 3667 TCCAGACAGCTGCGCTTCCTCCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3726
QY 3697 AGCTTTCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3756
Db 3727 AGCTTTCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3786
QY 3757 TTGCGCATGTTCACCCCTGCGCCCTGCTTCCATCCACCCAGCAGTCCAGT 3816
Db 3787 TTGCGCATGTTCACCCCTGCGCCCTGCTTCCATCCACCCAGCAGTCCAGT 3846
QY 3817 GAGACCTGAGAGAGACCTGAGGAGCTTGGAATTTGAGTACCAAGGAGTGCCTG 3876
Db 3847 GAGACCTGAGAGAGACCTGAGGAGCTTGGAATTTGAGTACCAAGGAGTGCCTG 3906
QY 3877 TACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3936
Db 3907 TACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3966
QY 3937 GCTGTGGAGTAATAATATGATATATGATTTTTCAGTTTGAATAAAAAAAAAA 3996
Db 3967 GCTGTGGAGTAATAATATGATATATGATTTTTCAGTTTGAATAAAAAAAAAA 4026
QY 3997 A 3997
Db 4027 A 4027

RESULT 12
AAA29388
ID AAA29388 standard; cDNA: 4027 BP.
AC AAA29388;
XX
DT 12-SEP-2000 (first entry)
DE hEST2, a human telomerase catalytic subunit homologue cDNA.
XX
KW hEST2: telomerase; catalytic subunit; reverse transcriptase; life-span;
retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
KM proliferation; immortal; tumour therapy; macular degeneration; activator;
KN INK4; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 57..3455
FT /tag= a
FT /product= human_telomerase_catalytic_subunit
XX
PN WO20031238-A2.
XX
PD 02-JUN-2000.
XX
PE 24-NOV-1999; 99MO-US27907.
XX
PR 25-NOV-1998; 98US-0109891.

```

```

PR 17-FEB-1999; 99US-0120549.
XX
PA (GENE-) GENETICA INC.
XX
PI Hannon GJ, Beach DH;
XX
DR WPI: 2000-400055/34.
XX
P-PSDB: AAY96566.
XX
PT New method for increasing the proliferative capacity of cell lines
PT comprises administering agents reversibly activating telomerase
PT activity and reversibly inactivating Rb/INK4 and/or p53 pathways useful
PT in treating age related diseases
XX
PS Claim 14, Page 112-116; 123pp; English.
XX
CC This cDNA, designated hEST2, is a human telomerase catalytic subunit
CC homologue of yeast EST2p and Euplores p123. hEST2 is a member of the
CC reverse transcriptase family of enzymes.
CC The invention concerns methods and reagents for extending the life-span,
CC e.g. the number of mitotic divisions, of a cell. The method relies on
CC activation of a telomerase activity and inhibition of one or both of a
CC retinoblastoma (Rb)/INK4 pathway or a p53 pathway. Phosphorylation of Rb
CC by cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the
CC division cycle. Binding of INK4 family members, e.g. the tumour
CC suppressor p16INK4a, inhibits kinase activity and results in growth
CC arrest. Rb inactivators can selectively and reversibly inactivate an
CC Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2
CC is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor
CC and can also be used in the methods. Other molecules which can be used
CC include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which
CC differs from at one or more of residues K22, R24, H95 and/or D97.
CC Additional constructs include a papilloma virus E7 protein, or other
CC viral oncoprotein in which bypasses Rb and/or p53. Antisense constructs of
CC the Rb and p16INK4 genes may also be used. The methods are useful for
CC increasing the proliferative capacity of cells. The cells are
CC subsequently of use in pharmaceutical and cosmetic preparations used to
CC treat conditions related to (premature) ageing, e.g. macular degeneration
CC and arteriosclerosis. The cells can also be used to replace tumour cell
CC lines in vitro and for studies on biochemical and physiological aspects
CC of growth and differentiation. Long lived (immortal) cells could also be
CC of use in the production of normal or genetically engineered
CC biotechnology products.
XX
SQ Sequence 4027 BP; 674 A; 1361 C; 1277 G; 715 T; 0 other;
XX
Query Match 99.0%; Score 3967; DB 21; Length 4027;
Best Local Similarity 99.0%; Pred. No. 1,le-146;
Matches 3980; Conservative 0; Mismatches 5; Indels 36; Gaps 1;
QY 13 GCTGCTCTGCTGCGACGTGGAGAGCCCTGAGCCCGGACACCCCGCATGCGCGG 72
Db 7 GCGTGTCTCTGCTGCGACGTGGAGAGCCCTGAGCCCGGACACCCCGCATGCGCGG 66
QY 73 CTCCTCCCTGCGAGCCGTGCGCTCCTGCTGCGGACGACCTACCGGAGAGTGTCCGC 132
Db 67 CTCCTCCCTGCGAGCCGTGCGCTCCTGCTGCGGACGACCTACCGGAGAGTGTCCGC 126
QY 133 TGGCAGATTCGTGCGGCGCCTTGAGGCGCCAGGCGTGGAGCTGTGTCAGCGGAGACC 192
Db 127 TGGCAGATTCGTGCGGCGCCTTGAGGCGCCAGGCGTGGAGCTGTGTCAGCGGAGACC 186
QY 133 CCGGAGCTTTCGCGCGGCTGAGTGGCCAGTGCCTGTGCTGCTGCTGCGAGCGAGCG 252
Db 187 CCGGAGCTTTCGCGCGGCTGAGTGGCCAGTGCCTGTGCTGCTGCTGCGAGCGAGCG 246
QY 253 CGCGCGCGCGCGCGCGCTGCTGCGGAGGCTGCTGCGTGAAGAGCTGTGGCGGAG 312
Db 247 CGCGCGCGCGCGCGCGCTGCTGCGGAGGCTGCTGCGTGAAGAGCTGTGGCGGAG 306
QY 313 TGTGTCAGAGGCTGTGCGAGGCGGCGGAGGAGCTGTGCTGCTGCTGCTGCTGCTG 372
Db 307 TGTGTCAGAGGCTGTGCGAGGCGGCGGAGGAGCTGTGCTGCTGCTGCTGCTGCTG 366

```

QY 373 TGGAGGGGGCCCCGGGGGGCCCCCGAGGCTTACACACAGGCTGGGACGTAACCTGC 432
DB 367 TGGAGGGGGCCCCGGGGGGCCCCCGAGGCTTACACACAGGCTGGGACGTAACCTGC 426
QY 433 CCAACAGGTTGACCGACGCTGCGGGGGAGAGGGGGCTGGGGGCTGGTGGTGGCGCG 492
DB 427 CCAACAGGTTGACCGACGCTGCGGGGGAGAGGGGGCTGGGGGCTGGTGGTGGCGCG 486
QY 493 TGGGCGAGAGCTGCTGTTTACCTGCTGGGACGCTGGCGGCTCTTTTGTGGTGGCTC 552
DB 487 TGGGCGAGAGCTGCTGTTTACCTGCTGGGACGCTGGCGGCTCTTTTGTGGTGGCTC 546
QY 553 CCACCTGCGGCTTACAGGTTGGGGGCGCGGCTGTACACACTGCGGCTGCACCTAGG 612
DB 547 CCACCTGCGGCTTACAGGTTGGGGGCGCGGCTGTACACACTGCGGCTGCACCTAGG 606
QY 613 CCGGGCCCCCGCCACACGCTAGTGGACCCGAAAGGCTGTGGATGGCAACGGGCTTGA 672
DB 607 CCGGGCCCCCGCCACACGCTAGTGGACCCGAAAGGCTGTGGATGGCAACGGGCTTGA 666
QY 673 ACCTATGCGTACAGGAGCGCGGGGTCCCCCTGGGCTGTGCCAGCCCGGGGTGCGAGAGG 732
DB 667 ACCTATGCGTACAGGAGGCGCGGGGTCCCCCTGGGCTGTGCCAGCCCGGGGTGCGAGAGG 726
QY 733 GCGGGGCGAGTGCAGCGGAGTGTGCGGTTGCCAAGAGGCGCGGCTGGCGCTGGCC 792
DB 727 GCGGGGCGAGTGCAGCGGAGTGTGCGGTTGCCAAGAGGCGCGGCTGGCGCTGGCC 786
QY 793 CTGAGCCGGAAGCGGCGCGGTTGGGCGAGGGTCTTGGGCGCCACCGGGCGAGAGCGGTG 852
DB 787 CTGAGCCGGAAGCGGCGCGGTTGGGCGAGGGTCTTGGGCGCCACCGGGCGAGAGCGGTG 846
QY 853 GACGAGGTGACCGGTTCTGT 912
DB 847 GACGAGGTGACCGGTTCTGT 906
QY 913 CTTTGGAGGGTGCCTCTGTGGACGCGGCACTCCACCCATCCGTGGGCGCGGCGAGCAC 972
DB 907 CTTTGGAGGGTGCCTCTGTGGACGCGGCACTCCACCCATCCGTGGGCGCGGCGAGCAC 966
QY 973 ACGGGGGCCCCCATCCACATCGCGGCGACAGCTCCCTGGGACAGCGCTTGTCCCCGG 1032
DB 967 ACGGGGGCCCCCATCCACATCGCGGCGACAGCTCCCTGGGACAGCGCTTGTCCCCGG 1026
QY 1033 TGTACGCGGAGACCAAGCACTTCTCTACTCTAGGCGAGCAAGAGAGTGGGCGCT 1092
DB 1027 TGTACGCGGAGACCAAGCACTTCTCTACTCTAGGCGAGCAAGAGAGTGGGCGCT 1086
QY 1093 CTTTCTACTAGCTCTCTGTAGGCGCCAGACCTGACTGGCGCTGGAGGCTGTGAGACCA 1152
DB 1087 CTTTCTACTAGCTCTCTGTAGGCGCCAGACCTGACTGGCGCTGGAGGCTGTGAGACCA 1146
QY 1153 TCTTTTGGGGTTCCAGGCGCCGATGCGAGGAGTCCCCGAGGTGGCGGCTGCCCC 1212
DB 1147 TCTTTTGGGGTTCCAGGCGCCGATGCGAGGAGTCCCCGAGGTGGCGGCTGCCCC 1206
QY 1213 AGCGCTACTGGCAATGCGGCGCTGTGTTCGTGAGCTGCTGGGAACACGCGAGTGGC 1272
DB 1207 AGCGCTACTGGCAATGCGGCGCTGTGTTCGTGAGCTGCTGGGAACACGCGAGTGGC 1266
QY 1273 CTTAGGGGGTCTCTCTAAGAGCACTGCGGCTGCGAGCTGGGGTCAACCCAGAGCG 1332
DB 1267 CTTAGGGGGTCTCTCTAAGAGCACTGCGGCTGCGAGCTGGGGTCAACCCAGAGCG 1326
QY 1333 GTGTCTGTGCGGGGAGAAAGCCCAAGGCTGTGTGGGGGCGCGGAGAGAGAGACAG 1392
DB 1327 GTGTCTGTGCGGGGAGAAAGCCCAAGGCTGTGTGGGGGCGCGGAGAGAGAGACAG 1386
QY 1393 ACCCCGCGGCTGTGTGAGCTGTGCGGCGAGACAGAGGCGCGGTGGAGGTGACGCT 1452
DB 1387 ACCCCGCGGCTGTGTGAGCTGTGCGGCGAGACAGAGGCGCGGTGGAGGTGACGCT 1446

QY 1453 TCGTGGGGCGCTGCGCTGCGCGGCTGTGTGTCGCCAGGCGCTGTGGGCTTCAGGACACAAG 1512
DB 1447 TCGTGGGGCGCTGCGCTGCGCGGCTGTGTGTCGCCAGGCGCTGTGGGCTTCAGGACACAAG 1506
QY 1513 AACGCGGCTTCTCAGAGAACACCAAGAGTTCATCTCCCTGGGAGAGCATGCCAAGCTCT 1572
DB 1507 AACGCGGCTTCTCAGAGAACACCAAGAGTTCATCTCCCTGGGAGAGCATGCCAAGCTCT 1566
QY 1573 CCGTGCAGAGGACGACGTTGAGAGTGAAGCCGCGGGGAGTGGCGTGGTGGCGAGAGCC 1632
DB 1567 CCGTGCAGAGGACGACGTTGAGAGTGAAGCCGCGGGGAGTGGCGTGGTGGCGAGAGCC 1626
QY 1633 CAGGGGTTGGCTGTGTTCCGCGCCAGAGACCGCTGTGCGTGAAGAGATCTTGGCCAACT 1692
DB 1627 CAGGGGTTGGCTGTGTTCCGCGCCAGAGACCGCTGTGCGTGAAGAGATCTTGGCCAACT 1686
QY 1693 TCTTGCACCTGCTATGATGATGTGTACGTCGTGAGCTGCTAGGTTCTTTTATGTCA 1752
DB 1687 TCTTGCACCTGCTATGATGATGTGTACGTCGTGAGCTGCTAGGTTCTTTTATGTCA 1746
QY 1753 CGGAGACCACTTCAAAAGAACAGGCGCTTTTCTACCGGAGAGTGTGAGCAAGT 1812
DB 1747 CGGAGACCACTTCAAAAGAACAGGCGCTTTTCTACCGGAGAGTGTGAGCAAGT 1806
QY 1813 TGCAAAGCATTTGATCAGACGACACTTGAAGAGGTTGACACTCGGGAGCTGTGGAAG 1872
DB 1807 TGCAAAGCATTTGATCAGACGACACTTGAAGAGGTTGACACTCGGGAGCTGTGGAAG 1866
QY 1873 CAGAGGTCAGGACGATCGGGAAGCCAGGCGCGCTGTACGTCCAGACTCCGCTTCA 1932
DB 1867 CAGAGGTCAGGACGATCGGGAAGCCAGGCGCGCTGTACGTCCAGACTCCGCTTCA 1926
QY 1933 TCCCAAGCGCTGAGGGGCTGGGCGGATTTGAACATGAGTACGTCGTGGAGCCAGAA 1992
DB 1927 TCCCAAGCGCTGAGGGGCTGGGCGGATTTGAACATGAGTACGTCGTGGAGCCAGAA 1986
QY 1993 CGTTCGCGAGAAAGAGAGGCGGAGGCTCTACCTCGAGGGTGAAGGCACTGTTCAGCG 2052
DB 1987 CGTTCGCGAGAAAGAGAGGCGGAGGCTCTACCTCGAGGGTGAAGGCACTGTTCAGCG 2046
QY 2053 TGTCTACCTAGGACGCGGCGGCGCGCGCGCTGTGTGGGCGCTGTGTGGGCGCGG 2112
DB 2047 TGTCTACCTAGGACGCGGCGGCGCGCGCGCTGTGTGGGCGCTGTGTGGGCGCGG 2106
QY 2113 ACGATATCCAGAGGCGCTGGGCGACCTTCTGTGCTGCTGGGCGCGGAGACCGCGCG 2172
DB 2107 ACGATATCCAGAGGCGCTGGGCGACCTTCTGTGCTGCTGGGCGCGGAGACCGCGCG 2166
QY 2173 CTGAGCTGTA-----CATCCCCAGAGCA 2196
DB 2167 CTGAGCTGTA-----CATCCCCAGAGCA 2226
QY 2197 GCGTCAGGAGGATCGCGCGAGCATCATCAACCCAGAAACAGTACGCTGGCGGT 2256
DB 2227 GCGTCAGGAGGATCGCGCGAGCATCATCAACCCAGAAACAGTACGCTGGCGGT 2286
QY 2257 ATGCGCTGTGTCAGAAAGCCCGCATGGGCGAGTCCGCAAGGCGCTTCAAGAGCAAGCTT 2316
DB 2287 ATGCGCTGTGTCAGAAAGCCCGCATGGGCGAGTCCGCAAGGCGCTTCAAGAGCAAGCTT 2346
QY 2317 CTACCTTGACAGACCTCCAGCGGCTACATGCGACAGTGTGGCTACCTGCGAGAGACCA 2376
DB 2347 CTACCTTGACAGACCTCCAGCGGCTACATGCGACAGTGTGGCTACCTGCGAGAGACCA 2406
QY 2377 GCGCGGTGAGGGATGCGGTCTCATCGAGCGAGCTCTCCCTGAATGAGGCGAGAGTG 2436
DB 2407 GCGCGGTGAGGGATGCGGTCTCATCGAGCGAGCTCTCCCTGAATGAGGCGAGAGTG 2466
QY 2437 GCGCTTTCGAGGCTTCTCTACGCTTCAATGTGCGACACAGCGCTGCGATCAGGGGCAAGT 2496
DB 2467 GCGCTTTCGAGGCTTCTCTACGCTTCAATGTGCGACACAGCGCTGCGATCAGGGGCAAGT 2526
QY 2497 CCTAGCTCAGTGCAGGGGATCCCGGCGAGGCTCCATCTCTCCACAGCTGTGTGCAAGCC 2556

```

Db 2527 CTTACCTTCAGTGGCCAGGGATCCCGAGGGCTCCATCTCTCTCCAGCTCTCTCTACCC 2586
Qy 2557 TGTGCTAAGGGGACATGAGAACAAACCTGTTTGGCGGGATTTCGGCGGACGGGCTGCTCC 2616
Db 2587 TGTGCTAAGGGGACATGAGAACAAACCTGTTTGGCGGGATTTCGGCGGACGGGCTGCTCC 2646
Qy 2617 TGTGCTAAGGGGACATGAGAACAAACCTGTTTGGCGGGATTTCGGCGGACGGGCTGCTCC 2676
Db 2647 TGTGCTAAGGGGACATGAGAACAAACCTGTTTGGCGGGATTTCGGCGGACGGGCTGCTCC 2706
Qy 2677 TCAGAGACCTGCTCGAGAGTGTCCCTGAGTATGCTGCTGCTGATGACTTTCGGAAGACAG 2736
Db 2707 TCAGAGACCTGCTCGAGAGTGTCCCTGAGTATGCTGCTGCTGATGACTTTCGGAAGACAG 2766
Qy 2737 TGTGTAATCTCCTGTAGAAAGACGAGGCCCTGGTGGACGGCTTTTGTTCAGATGCCGG 2796
Db 2767 TGTGTAATCTCCTGTAGAAAGACGAGGCCCTGGTGGACGGCTTTTGTTCAGATGCCGG 2826
Qy 2797 CCCAGGGCTATTCCTCCCTGGTGGCGCTGCTGCTGATACCCGGACCTGGAGGTGCAGA 2856
Db 2827 CCCAGGGCTATTCCTCCCTGGTGGCGCTGCTGCTGATACCCGGACCTGGAGGTGCAGA 2886
Qy 2857 GCGACTACCTCAGCATGATGCCGAGACCTGCATGAGAGCCAGTCTCACCCTTCAACCGGGCT 2916
Db 2887 GCGACTACCTCAGCATGATGCCGAGACCTGCATGAGAGCCAGTCTCACCCTTCAACCGGGCT 2946
Qy 2917 TCAAGGCTGGGAGAGACATGCTGTCGAACCTGTTGGGGTCTTGGCGCTGAAGTGTCA 2976
Db 2947 TCAAGGCTGGGAGAGACATGCTGTCGAACCTGTTGGGGTCTTGGCGCTGAAGTGTCA 3006
Qy 2977 GCGTGTCTGGATTTGAGGTGACGACAGCCCTCAGACGGTGTGACCAACATCTACAGA 3036
Db 3007 GCGTGTCTGGATTTGAGGTGACGACAGCCCTCAGACGGTGTGACCAACATCTACAGA 3066
Qy 3037 TCTCTGCTGAGAGCCGTACAGAGTTTCACGATGTGTCTCAGCTCCATTCATCAGC 3096
Db 3067 TCTCTGCTGAGAGCCGTACAGAGTTTCACGATGTGTCTCAGCTCCATTCATCAGC 3126
Qy 3097 AAGTTGGAAGAACCCACATTTTTCCTCGCGCTATCTGACAGCGCTCCCTCTCT 3156
Db 3127 AAGTTGGAAGAACCCACATTTTTCCTCGCGCTATCTGACAGCGCTCCCTCTCT 3186
Qy 3157 ACTCCATCTCTGAAGCCCAAGACGACGAGATGCTGCTGGGGCCCAAGGGCGCGCGGCC 3216
Db 3187 ACTCCATCTCTGAAGCCCAAGACGACGAGATGCTGCTGGGGCCCAAGGGCGCGCGGCC 3246
Qy 3217 CTCTGCTCTCGAGAGCCGTGACGAGTGTGCTGACCAAGATCTCTGACAGCTGACTC 3276
Db 3247 CTCTGCTCTCGAGAGCCGTGACGAGTGTGCTGACCAAGATCTCTGACAGCTGACTC 3306
Qy 3277 GACACCGTGTCACTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3336
Db 3307 GACACCGTGTCACTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3366
Qy 3337 GTGCGAAGCTCCCGGGGACGACGCTGACTGCTGCTGAGGCGCGCCACCCGCGACTGC 3396
Db 3367 GTGCGAAGCTCCCGGGGACGACGCTGACTGCTGAGGCGCGCCACCCGCGACTGC 3426
Qy 3397 CCTCAGACTTCAAGACCATCTGCTGACTGATGCGCACCGGCCACAGCGCGAGAGCA 3456
Db 3427 CCTCAGACTTCAAGACCATCTGCTGACTGATGCGCACCGGCCACAGCGCGAGAGCA 3486
Qy 3457 GACACCGAGAGCCCTGTACAGCCGGGCTTACGCTCCAGGGAGGAGGGCGGCCACAC 3516
Db 3487 GACACCGAGAGCCCTGTACAGCCGGGCTTACGCTCCAGGGAGGAGGGCGGCCACAC 3546
Qy 3517 CCAGGCCCCGACCGGTGGAGTCTGAGAGCTGAGTGTGTTGGCGGAGGGCTCATGT 3576
Db 3547 CCAGGCCCCGACCGGTGGAGTCTGAGAGCTGAGTGTGTTGGCGGAGGGCTCATGT 3606
Qy 3577 CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGACGAGTGTCCAGCAAGGCTGATG 3636

```

```

Db 3607 CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAGGCTGATG 3666
Qy 3637 TCCACAGACCTGCGCGTCTTCACTTCCCCACAGAGCTGGGCTGCGCTCACCACAGGCTC 3696
Db 3667 TCCACAGACCTGCGCGTCTTCACTTCCCCACAGAGCTGGGCTGCGCTCACCACAGGCTC 3726
Qy 3697 ACCTTTCCTCACCAGAGCCCGGCTTCCACTCCCAACATAGAAATAGTCCATCCAG 3756
Db 3727 ACCTTTCCTCACCAGAGCCCGGCTTCCACTCCCAACATAGAAATAGTCCATCCAG 3786
Qy 3757 TTCGCCATTGTTCAACCCCTGCGCTGCTGCTTTCCTTCCACCCCAACCATCAGT 3816
Db 3787 TTCGCCATTGTTCAACCCCTGCGCTGCTGCTTTCCTTCCACCCCAACCATCAGT 3846
Qy 3817 GAGACCTGAGAGAGACCTGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTGCCCTG 3876
Db 3847 GAGACCTGAGAGAGACCTGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTGCCCTG 3906
Qy 3877 TACACAGCGAGACCCCTGACCTGATGAGGGTCCCTGAGGTCAAAATGGGGAGGT 3936
Db 3907 TACACAGCGAGACCCCTGACCTGATGAGGGTCCCTGAGGTCAAAATGGGGAGGT 3966
Qy 3937 GCTGTGGAGTAAATATGAAATATATGATTTTTCAGTTTGAAGAAAAA 3996
Db 3967 GCTGTGGAGTAAATATGAAATATATGATTTTTCAGTTTGAAGAAAAA 4026
Qy 3997 A 3997
Db 4027 A 4027

RESULT 13
AA18254
ID AA18254 standard; DNA; 3664 BP.
XX
XX AA18254;
XX
XX 26-JUL-1999 (first entry)
XX
XX Human telomerase coding sequence.
XX
XX
XX Telomerase: human; cancer; diagnosis; melanoma; skin cancer; leukemia;
XX neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
XX smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
XX stem cell differentiation; organ regeneration; organ differentiation; ss.
XX
XX Homo sapiens.
XX
XX WO9901560-A1.
XX
XX 14-JAN-1999.
XX
XX 01-JUL-1998; 98WO-US13835.
XX
XX 09-SEP-1997; 97US-0058287.
XX
XX 01-JUL-1997; 97US-0051410.
XX
XX 21-JUL-1997; 97US-0053018.
XX
XX 04-AUG-1997; 97US-0053329.
XX
XX (CAMP-) CAMBIA BIOSYSTEMS LLC.
XX
XX Bowtell D, Kilian A;
XX
XX WPI: 1999-106060/09.
XX
XX P-PSDB: AAY00627.
XX
XX
XX New isolated vertebrate telomerase genes - used to develop products
XX for treating cancers or for organ regeneration, nerve cell or brain
XX cell growth following injury or bone marrow transplantation
XX
XX Claim 3; Fig 1; 134pp; English.
XX

```



```
Db 1861 |CTCGGCTTATCCCAAGCTGACGGGCTGGGCGGATTTGAAACATGACACTGCTGCG 1920
Oy 1983 |GGAGCCAGAAAGCTTCCGAGAGAAAGAGGCGGAGCGCTCTACCTCGAGGGTGAAGGCA 2042
Db 1921 |GGAGCCAGAAAGCTTCCGAGAGAAAGAGGCGGAGCGCTCTACCTCGAGGGTGAAGGCA 1980
Oy 2043 |CTGTTACGGGTGCTCACTACGAGAGGGGCGGCGCGGCGGCGCTCTGAGGCGGCTCTGTG 2102
Db 1981 |CTGTTACGGGTGCTCACTACGAGAGGGGCGGCGCGGCGGCGCTCTGAGGCGGCTCTGTG 2040
Oy 2103 |CTGGGGCTGAGAGATATCCACAGGGGCTGGGCGACCTTGCTGCTGCTGCTGCGGGCCAG 2162
Db 2041 |CTGGGCTGAGAGATATCCACAGGGGCTGGGCGACCTTGCTGCTGCTGCTGCGGGCCAG 2100
Oy 2163 |GACCGGCGGCGCTGAGCTGTACTTTGTCAAGGTGAGATGTGAGGGGCGGCTACGACACATC 2186
Db 2101 |GACCGGCGGCGCTGAGCTGTACTTTGTCAAGGTGAGATGTGAGGGGCGGCTACGACACATC 2160
Oy 2187 |CCCCAGAGACAGGCTCAGAGAGGTGATGCGGAGATCATAAACCCGAGAACAGCTACTG 2246
Db 2161 |CCCCAGAGACAGGCTCAGAGAGGTGATGCGGAGATCATAAACCCGAGAACAGCTACTG 2220
Oy 2247 |GTGCGTGTGATATGCGGTGCTCAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 2306
Db 2221 |GTGCGTGTGATATGCGGTGCTCAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 2280
Oy 2307 |AGCCAGCTGTCTACCTTGACAGACCTTCGACGCTGACGAGCTGACGAGTTCGTTGCGCTC 2366
Db 2281 |AGCCAGCTGTCTACCTTGACAGACCTTCGACGCTGACGAGCTGACGAGTTCGTTGCGCTC 2340
Oy 2367 |CAGAGACAGGCGGCGGCTGAGGAGATGCGGTGCTATGAGAGAGAGCTCTCTCTGAAATG 2426
Db 2341 |CAGAGACAGGCGGCGGCTGAGGAGATGCGGTGCTATGAGAGAGAGCTCTCTCTGAAATG 2400
Oy 2427 |GCCAGAGAGTGGGCTTTGAGAGCTTCTCTACGCTTCATGTCGACACAGCGCGGCGGCG 2486
Db 2401 |GCCAGAGAGTGGGCTTTGAGAGCTTCTCTACGCTTCATGTCGACACAGCGCGGCGGCG 2460
Oy 2487 |AGGGGCAAGTCCAGTGCAGTGCAGAGGAGATCCGAGGGGCTCCATCTCTCTCAGAGCTG 2546
Db 2461 |AGGGGCAAGTCCAGTGCAGTGCAGAGGAGATCCGAGGGGCTCCATCTCTCTCAGAGCTG 2520
Oy 2547 |CTCTGAGGCTGTGTAGGAGGAGATGAGAGAAAGAGCTTTGGGGGAGATTCGGGGGAG 2606
Db 2521 |CTCTGAGGCTGTGTAGGAGGAGATGAGAGAAAGAGCTTTGGGGGAGATTCGGGGGAG 2580
Oy 2607 |GGGCTGTCTCTGCTGTTGGTGGATGATTTTGTGGTGGTGAACCTCACTCACTCACTCA 2666
Db 2581 |GGGCTGTCTCTGCTGTTGGTGGATGATTTTGTGGTGGTGAACCTCACTCACTCACTCA 2640
Oy 2667 |AAAACCTTCTCAGAACCTCTGTCGAGGTGTCCTGAGATAGGCTGCTGCTGGAACCTTG 2726
Db 2641 |AAAACCTTCTCAGAACCTCTGTCGAGGTGTCCTGAGATAGGCTGCTGCTGGAACCTTG 2700
Oy 2727 |CGGAAGACAGTGTGTAACCTCTGTAAGAGAGAGGCGCTGGGTGGACAGGCTTTTGT 2786
Db 2701 |CGGAAGACAGTGTGTAACCTCTGTAAGAGAGAGGCGCTGGGTGGACAGGCTTTTGT 2760
Oy 2787 |CAGATGCGGCGGCGGAGGCTATTCCTGCTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTG 2846
Db 2761 |CAGATGCGGCGGCGGAGGCTATTCCTGCTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTG 2820
Oy 2847 |GAGGTGAGAGAGGACTACTCAGCTATGCGGAGGCTCATCAGAGGCACTGCTACCTTC 2906
Db 2821 |GAGGTGAGAGAGGACTACTCAGCTATGCGGAGGCTCATCAGAGGCACTGCTACCTTC 2880
Oy 2907 |AACGGGAGGCTTAAGGCTGGGAGAGACATGCTGCAAACTTTTGGGGCTTGGGGCTG 2966
Db 2881 |AACGGGAGGCTTAAGGCTGGGAGAGACATGCTGCAAACTTTTGGGGCTTGGGGCTG 2940
Oy 2967 |AAGTGTACAGGCTGTTCTGATTTGACAGTGAACAGCTCCAGAGGCTGCAACAC 3026
Db 2941 |AAGTGTACAGGCTGTTCTGATTTGACAGTGAACAGCTCCAGAGGCTGCAACAC 3000
Oy 3027 |ATCTACAGATCTCTCTGCTGACAGGCTGACAGGCTTTCACGATGTGTCTGACAGTCCCA 3086
Db 3001 |ATCTACAGATCTCTCTGCTGACAGGCTGACAGGCTTTCACGATGTGTCTGACAGTCCCA 3060
Oy 3087 |TTTTCATCAGCAAGTTTGGAAAGAACCCACATTTTTCCTGCGCTCATCTCTGACAGGCC 3146
Db 3061 |TTTTCATCAGCAAGTTTGGAAAGAACCCACATTTTTCCTGCGCTCATCTCTGACAGGCC 3120
Oy 3147 |TTCCTGTCTACTCATCTCAGAAAGCAGAAAGCAGAGATGTGCTGGGGGCGCAAGGCC 3206
Db 3121 |TTCCTGTCTACTCATCTCAGAAAGCAGAAAGCAGAGATGTGCTGGGGGCGCAAGGCC 3180
Oy 3207 |GGGCGGAGGCGCTGCGGCTGCGAGGCGGCTGAGTGGGCTGAGTGGGCGCAACATTCCTG 3266
Db 3181 |GGGCGGAGGCGCTGCGGCTGCGAGGCGGCTGAGTGGGCTGAGTGGGCGCAACATTCCTG 3240
Oy 3267 |AAGCTGACAGCAAGCGGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3326
Db 3241 |AAGCTGACAGCAAGCGGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
Oy 3327 |AGCAGCTGATGCTGGAAGCTCCGGGGAGACGCTGACCTGCTGAGGCGCGCAAGCCAAC 3386
Db 3301 |AGCAGCTGATGCTGGAAGCTCCGGGGAGACGCTGACCTGCTGAGGCGCGCAAGCCAAC 3360
Oy 3387 |CCGGCACTGCTCAGACTTCAAGACATCTGAGACTGATGGCACCCCGCCACAGCCAG 3446
Db 3361 |CCGGCACTGCTCAGACTTCAAGACATCTGAGACTGATGGCACCCCGCCACAGCCAG 3420
Oy 3447 |GCCGAGAGAGACACACAGACAGCCCTGTCAGGCGGCGCTACCTGCTCAGAGAGAGAGGG 3506
Db 3421 |GCCGAGAGAGACACACAGACAGCCCTGTCAGGCGGCGCTACCTGCTCAGAGAGAGAGGG 3480
Oy 3507 |CGGCGCACACCCAGGCGCGGACCGCTGGGAGTCTGAGGCGCTGAGTGTGTTGGCGAG 3566
Db 3481 |CGGCGCACACCCAGGCGCGGACCGCTGGGAGTCTGAGGCGCTGAGTGTGTTGGCGAG 3540
Oy 3567 |GCTGTGATGTGCTGCTGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3626
Db 3541 |GCTGTGATGTGCTGCTGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3600
Oy 3627 |GGGCTGAGTGTGCTGAGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3686
Db 3601 |GGGCTGAGTGTGCTGAGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3660
Oy 3687 |CCCCAGGCGAGCTTTTCTCTCAGAGAGGCGGCTTCACTCCCACTAGAGATGATGTC 3746
Db 3661 |CCCCAGGCGAGCTTTTCTCTCAGAGAGGCGGCTTCACTCCCACTAGAGATGATGTC 3720
Oy 3747 |CATCCAGATTTGCAATTTGTCACCTTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3806
Db 3721 |CATCCAGATTTGCAATTTGTCACCTTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3780
Oy 3807 |CATCCAGTGTGAGACCTCTGAGAAAGACCTCTGAGACTCTGTGGAAATTTGGAGTGAACA 3866
Db 3781 |CATCCAGTGTGAGACCTCTGAGAAAGACCTCTGAGACTCTGTGGAAATTTGGAGTGAACA 3840
Oy 3867 |GTGTGCCCTGTACACAGGCGAGACCTCTGACCTGAGATGAGGGGCTCCCTGTGGGTAAAT 3926
Db 3841 |GTGTGCCCTGTACACAGGCGAGACCTCTGACCTGAGATGAGGGGCTCCCTGTGGGTAAAT 3900
Oy 3927 |GGGGGAGGTGCTGTGGAGATTAATATGATATAGATTTTGTAGTTTGAAGAAAAA 3986
Db 3901 |GGGGGAGGTGCTGTGGAGATTAATATGATATAGATTTTGTAGTTTGAAGAAAAA 3960
Oy 3987 |AAAA 3990
Db 3961 |AAAA 3964
RESULT 14
AAIX8269
```

ID	AAI18269 standard; DNA; 3918 BP.
XX	
AC	AAI18269;
XX	
DT	26-JUL-1999 (first entry)
XX	
DE	Telomerase coding sequence lacking motif A.
XX	
KW	Telomerase: human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KX	neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
RW	stem muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KV	smooth cell differentiation; organ regeneration; organ differentiation; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	MO9901560-A1.
XX	
PD	14-JAN-1999.
XX	
PF	01-JUL-1998; 98WO-US13835.
XX	
PR	09-SEP-1997; 97US-0058287.
XX	
.PR	01-JUL-1997; 97US-0051410.
XX	
PR	21-JUL-1997; 97US-0053018.
XX	
PR	21-JUL-1997; 97US-0053328.
XX	
PR	04-AUG-1997; 97US-0054642.
XX	
PA	(CAMP-) CAMBIA BIOSYSTEMS LLC.
XX	
PI	Bowtell D, Killian A;
XX	
DR	WPI; 1999-106060/09.
XX	
DR	P-PSDB; AAU00641.
XX	
PT	New isolated vertebrate telomerase genes - used to develop products
PT	for treating cancers or for organ regeneration, nerve cell or brain
XX	
XX	cell growth following injury or bone marrow transplantation
XX	
PS	Claim 4; Fig 11n-o; 134pp; English.
XX	
CC	This sequence encodes a truncated human telomerase of the
CC	invention. Primers that amplify the telomerase coding sequence can be
CC	used in a method for diagnosing cancer in a patient. The telomerase can
CC	be used for detection, diagnosis and drug screening. Inhibitors of
CC	telomerase activity can be used to treat cancers such as melanomas,
CC	other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
CC	leukemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
CC	or skin growths. Enhancers of telomerase may be used to stimulate stem
CC	cell proliferation and differentiation (expansion of haematopoietic stem
CC	cells could be administered in the bone marrow transplant context). As
CC	well, many tissues have stem cells. Proliferation of these cells may be
CC	useful in wound healing, hair growth, treatment of disease such as
CC	Wilm's tumour, organ regeneration or differentiation after injury or
CC	diseases, nerve cell or brain cell growth following injury.
CC	Note: The 3' end of this sequence can be replaced by the sequence
CC	shown in AAI18282.
XX	
XX	
SQ	Sequence 3918 BP; 645 A; 1326 C; 1244 G; 703 T; 0 other;
XX	
.	* Query Match 97.6%; Score 3910; DB 20; Length 3918;
XX	Best Local Similarity 99.9%; Pred. No. 1.8e-14;
XX	Matches 3913; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY	63 ATGCGGGCGGCCTTTCGCGAGCCGAGCCGTCTCTGCGCACCACTACGCCGAG 122
Dd	
Db	1 ATGCGCGCGGCTCCCGCGCGGACCGCGCTCTCTCTGCGCACCACTACGCCGAG 60
OY	123 GTGCTGCGCGCTTGACACTGTTCTGGGGGCGCTGGGGCCCCAGAGGCTGGGGTGTGAC 182
Dd	
Db	61 GTGCTGCGCGCTTGACACTGTTCTGGGGGCGCTGGGGCCCCAGAGGCTGGGGTGTGAC 120
OY	183 CGCGGGGACCCGCGGCTTTCCGCGCGCTGTGTGGGCCAATGCTGTGTGCGTCCCTGG 242

Db	121	CGCGGGAGACCCGGGCGCTTTCGCGCGCTGCTG6CCAGTGCCTG6TGTGCGTGCCTTGG	180
QY	243	GAGCGACGCGCCGCCGCCGCCGCCCTTCCTTCGCGCAGGTGCTCGCTGGAAGAGCTG	302
Db	181	GACGAGAGGCGCGCCCGCCGCCGCCCTTCCTTCGCGCAGGTGCTCGCTGAAGAGCTG	240
QY	303	GTCGCGCGAGTGTCTGACGAGAGGCTGTGCGAGCGCGGCGCGAANAAGTGTGCTTGGCG	362
Db	241	GTCGCGCGAGTGTCTGACGAGAGGCTGTGCGAGCGCGGCGCGAANAAGTGTGCTTGGCG	300
QY	363	TTTCGCGGCTGTGAGCGGGGGCGCGGGGGGGCCCCCGGAGGCTTCACACACAGCTGCGC	422
Db	301	TTTCGCGGCTGTGAGCGGGGGCGCGGGGGGGCCCCCGGAGGCTTCACACACAGCTGCGC	360
QY	423	AGCTACCTGCCCCAACACAGGTTGACCGACCTGCGGGGGAGCGGGGCGTGGGGGCTGTG	482
Db	361	AGCTACCTGCCCCAACACAGGTTGACCGACCTGCGGGGGAGCGGGGCGTGGGGGCTGTG	420
QY	483	CTGCGCGCGCTGTGGCGCGACGACGTGTGTTCACCTCTGTGGCAGCTGTGGCGCTCTTGTG	542
Db	421	CTGCGCGCGCTGTGGCGCGACGACGTGTGTTCACCTCTGTGGCAGCTGTGGCGCTCTTGTG	480
QY	543	CTGGGGGCTCCACCTGCGCTACGAGGTGTGGGGGCGCGCGTGTACAGCTGCGGCGCT	602
Db	481	CTGGGGGCTCCACCTGCGCTACGAGGTGTGGGGGCGCGCGTGTACAGCTGCGGCGCT	540
QY	603	GCCACTACAGGCGCGCGCGCGCCACACAGCTAGTGAAGCCCCGGAAGCGTCTGGATGCGAA	662
Db	541	GCCACTACAGGCGCGCGCGCGCCACACAGCTAGTGAAGCCCCGGAAGCGTCTGGATGCGAA	600
QY	663	CGGGCTGTGAACCATATACGCTGAGGAGGCGCGGGGTCCCCGTGGCGCTGTCCAGCCCCGGT	722
Db	601	CGGGCTGTGAACCATATACGCTGAGGAGGCGCGGGGTCCCCGTGGCGCTGTCCAGCCCCGGT	660
QY	723	GCGAGGAGGGCGGGGGGCGACGTGCGACGCGCAAGTCTGCGGTGCCAAGAGGGCGCAGGGT	782
Db	661	GCGAGGAGGGCGGGGGGCGACGTGCGACGCGCAAGTCTGCGGTGCCAAGAGGGCGCAGGGT	720
QY	783	GCGCGTGGCCCTGAGCCGCGAGCGGAGCGCCCGTGTGGGCGAGGGGTCTGTTGGGCCACCGCGGC	842
Db	721	GCGCGTGGCCCTGAGCCGCGAGCGGAGCGCCCGTGTGGGCGAGGGGTCTGTTGGGCCACCGCGGC	780
QY	843	AGGACGCGTGGACCGGAGTGAACCGTGGTTCGTGTGTGTGTCTACCTGTCCAGACC CGCGAA	902
Db	781	AGGACGCGTGGACCGGAGTGAACCGTGGTTCGTGTGTGTGTCTACCTGTCCAGACC CGCGAA	840
QY	903	GAAAGCACTCTTTGAGAGGGTGGGCTGTGCGACGCGGCACCTCCACACCATCGTGGGC	962
Db	841	GAAAGCACTCTTTGAGAGGGTGGGCTGTGCGACGCGGCACCTCCACACCATCGTGGGC	900
QY	963	CGCGAGACACACGCGGGGCGCCCATCATCATCGCGGCGCACAGTCCCTTGAGGACGCGCT	1022
Db	901	CGCGAGACACACGCGGGGCGCCCATCATCATCGCGGCGCACAGTCCCTTGAGGACGCGCT	960
QY	1023	TGTCCCCCGGTGACGCGCGAGACCAAGACATTCCTCTCTACTCTCTCAGGCGACAAAGSAGAG	1082
Db	961	TGTCCCCCGGTGACGCGCGAGACCAAGACATTCCTCTCTACTCTCTCAGGCGACAAAGSAGAG	1020
QY	1083	CTGGGGGCGCTCTTCTCTACCTACGCTCTCTGAGGCCAGCGCTGACTGTGGGCTGTGGAGGCTG	1142
Db	1021	CTGGGGGCGCTCTTCTCTACCTACGCTCTCTGAGGCCAGCGCTGACTGTGGGCTGTGGAGGCTG	1080
QY	1143	GTCGAGACCATCTTTCGGGGTTCCAGGCGCTGGATGTCAGAGGACACCTCCCGAGGTTGGCC	1202
Db	1081	GTCGAGACCATCTTTCGGGGTTCCAGGCGCTGGATGTCAGAGGACACCTCCCGAGGTTGGCC	1140
QY	1203	CGCGTGGCCCCAGGCGCTACTGTGCAAAATGTGGGCGCCCTGTTTCTGTGAAGCTGTGTTGGAAACAC	1262
Db	1141	CGCGTGGCCCCAGGCGCTACTGTGCAAAATGTGGGCGCCCTGTTTCTGTGAAGCTGTGTTGGAAACAC	1200
QY	1263	CGCGAGTCCCCCTACGGGGGTGCTCTCAGAGCGACCTGCCCGCTGTGAGCTGTGGTCAAC	1322

```
Db 1201 GCGCAGATGCCCCCTACGGGGTGTCTCTCAAGAGGCACTGCCCGCTGGAGCTCGGGTCAAC 1260
Qy 1323 CCAGCAGCCGGGTGTCTGTGCCCCGGGAGAGCCCCAGGGCTGTGTGGCGGCCCCCGAGAG 1382
Db 1261 CCAGCAGCCGGGTGTCTGTGCCCCGGGAGAGCCCCAGGGCTGTGTGGCGGCCCCCGAGAG 1320
Qy 1383 GAGGACACAGAGCCCCGGTGGCTGGTGCAGAGCTGCTCCGGCAGACAGCAGCCCCCTGGGAG 1442
Db 1321 GAGGACACAGAGCCCCGGTGGCTGGTGCAGAGCTGCTCCGGCAGACAGCAGCCCCCTGGGAG 1380
Qy 1443 GTGTAGGGCTTGTGTGGGGGCTGTGGCGGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 1502
Db 1381 GTGTAGGGCTTGTGTGGGGGCTGTGGCGGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 1440
Qy 1503 AGGCAACAGAGAGCCCGCTTCTCTCAGAGAACACAAAGATTCACTCTCCCTGGGGAGCAT 1562
Db 1441 AGGCAACAGAGAGCCCGCTTCTCTCAGAGAACACAAAGATTCACTCTCCCTGGGGAGCAT 1500
Qy 1563 GCCAAGCTCTGCTGACAGAGCTGACGTGGAAATGAGCGTGGGGAAGTGGCTTGGCTG 1622
Db 1501 GCCAAGCTCTGCTGACAGAGCTGACGTGGAAATGAGCGTGGGGAAGTGGCTTGGCTG 1560
Qy 1623 CCGAGAGAGCCCAAGGCGTTGGCTGTGTTCCGGCCGAGAGCAGCCGTGTGCTGAGAGATTC 1682
Db 1561 CCGAGAGAGCCCAAGGCGTTGGCTGTGTTCCGGCCGAGAGCAGCCGTGTGCTGAGAGATTC 1620
Qy 1683 CTGGCAAGATTCTGCACTGGCTGATGATGTGTACGTCGTGAGCTGCTCAGGTCTTTC 1742
Db 1621 CTGGCAAGATTCTGCACTGGCTGATGATGTGTACGTCGTGAGCTGCTCAGGTCTTTC 1680
Qy 1743 TTTTATGTACAGAGAGACACGTTTCAAAAAGAGAGGCTTTTTCATACAGGAGAGTGTTC 1802
Db 1681 TTTTATGTACAGAGAGACACGTTTCAAAAAGAGAGGCTTTTTCATACAGGAGAGTGTTC 1740
Qy 1803 TGGAGCAAGTTGCAAAACATTTGGAATCAGACAGCACTTGAAGAGGCTGAGAGTGGGGAG 1862
Db 1741 TGGAGCAAGTTGCAAAACATTTGGAATCAGACAGCACTTGAAGAGGCTGAGAGTGGGGAG 1800
Qy 1863 CTGTGGAAGACAGAGGTCAAGGACATCGGGAAGCCAGGCCCTGCTGACGTCCAGA 1922
Db 1801 CTGTGGAAGACAGAGGTCAAGGACATCGGGAAGCCAGGCCCTGCTGACGTCCAGA 1860
Qy 1923 CTCCGCTTATCCCCAAGCCTGACGGGGCTGGCGCGATTTGTGAACATGACATGACTGTG 1982
Db 1861 CTCCGCTTATCCCCAAGCCTGACGGGGCTGGCGCGATTTGTGAACATGACATGACTGTG 1920
Qy 1983 GGAGCCAGACGTTCCGACAGAGAAAGAGAGGCCGACGCTCACTCAGCTCGAGGTTGAAGCA 2042
Db 1921 GGAGCCAGACGTTCCGACAGAGAAAGAGAGGCCGACGCTCACTCAGCTCGAGGTTGAAGCA 1980
Qy 2043 CTGTTCAGCTGTCTCACTACGAGCGGGCGCGGCCGCCGCTCTGTGGCGCTCTGTG 2102
Db 1981 CTGTTCAGCTGTCTCACTACGAGCGGGCGCGGCCGCCGCTCTGTGGCGCTCTGTG 2040
Qy 2103 CTGGGCTTGAAGATATTCACAGAGGCTGGCGCACCTTCTGCTGAGTGTGGGGCCAG 2162
Db 2041 CTGGGCTTGAAGATATTCACAGAGGCTGGCGCACCTTCTGCTGAGTGTGGGGCCAG 2100
Qy 2163 GACCCGCGCGCTGAGCTGTACATCCCCCAGAGCAGGCTCAAGAGGCTATTCGACAGATC 2222
Db 2101 GACCCGCGCGCTGAGCTGTACATCCCCCAGAGCAGGCTCAAGAGGCTATTCGACAGATC 2160
Qy 2223 ATCAAAACCCCAAGACAGTACTGCTGGGCTGAGTATGCGGTTGCAAGAGCCGCCAT 2282
Db 2161 ATCAAAACCCCAAGACAGTACTGCTGGGCTGAGTATGCGGTTGCAAGAGCCGCCAT 2220
Qy 2283 GGGCAGTCCGCAAGGCCCTTCAAGAGCCAGCTCTCTACCTTGACAGACTCCAGCCGTAC 2342
Db 2221 GGGCAGTCCGCAAGGCCCTTCAAGAGCCAGCTCTCTACCTTGACAGACTCCAGCCGTAC 2280
Qy 2343 ATGCGACAGATTGTGGTCACTGTCAGAGAGACAGCCGCTGAGGGATCGCTGTCTATC 2402
Db 2281 ATGCGACAGATTGTGGTCACTGTCAGAGAGACAGCCGCTGAGGGATCGCTGTCTATC 2340
```

```
Qy 2403 GAGCAGAGCTCTCTCCCTGAATGAGGCGACAGTAGTGCCCTTGTGAGCTTCTTACGCTTC 2462
Db 2341 GAGCAGAGCTCTCTCCCTGAATGAGGCGACAGTAGTGCCCTTGTGAGCTTCTTACGCTTC 2400
Qy 2463 ATGTGCGACACAGCCCGTGGGCGCATGAGGGGCAAGTCCAGTGCAGTGGCAGGGATCCG 2522
Db 2401 ATGTGCGACACAGCCCGTGGGCGCATGAGGGGCAAGTCCAGTGCAGTGGCAGGGATCCG 2460
Qy 2523 GAGGGCTCAATCTCTCTCAGAGCTGCTGTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2582
Db 2461 CAGGGCTCATCTCTCTCAGAGCTGCTGTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520
Qy 2583 CTGTTCGGGGGATTTGGGGGAGCGGGCTGCTCTGCTGCTTGGTGGATTTCTTGTG 2642
Db 2521 CTGTTCGGGGGATTTGGGGGAGCGGGCTGCTCTGCTGCTTGGTGGATTTCTTGTG 2580
Qy 2643 GTGACACCTCACTCAACCCAGCGCAAAACCTTCCCTCAGAGACCTGTCCGAGGTCCCT 2702
Db 2581 GTGACACCTCACTCAACCCAGCGCAAAACCTTCCCTCAGAGACCTGTCCGAGGTCCCT 2640
Qy 2703 GAGTATGCTCCGTGTGTAACCTTGGGAAGACAGTGTGTAACCTTCTGTAGAAGACAG 2762
Db 2641 GAGTATGCTCCGTGTGTAACCTTGGGAAGACAGTGTGTAACCTTCTGTAGAAGACAG 2700
Qy 2763 GCCCTGGGTGGACAGGCTTTTGTTCAGATGCCGGCCACAGGCTATTCCCTGGTGGCG 2822
Db 2701 GCCCTGGGTGGACAGGCTTTTGTTCAGATGCCGGCCACAGGCTATTCCCTGGTGGCG 2760
Qy 2823 CTGCTGTGATATCCCGGACCCCTGAGAGGTGACAGGAGTACTACAGCTATATGCCGAGC 2882
Db 2761 CTGCTGTGATATCCCGGACCCCTGAGAGGTGACAGGAGTACTACAGCTATATGCCGAGC 2820
Qy 2883 TCCATCAGAGAGTCTCACTCACTTCAACCGCGCTTCAAGGCTGGAGAGAAATCTGTCG 2942
Db 2821 TCCATCAGAGAGTCTCACTCACTTCAACCGCGCTTCAAGGCTGGAGAGAAATCTGTCG 2880
Qy 2943 AAACCTTTGGGGCTTTGGGGCTGAAGTGTCAAGCTGTTTGTGATTTGCAAGTAAAC 3002
Db 2881 AAACCTTTGGGGCTTTGGGGCTGAAGTGTCAAGCTGTTTGTGATTTGCAAGTAAAC 2940
Qy 3003 ACCCTCAGAGGCTGTGACACAACTTCAAGATCTCTGCTGAGGCTTACAGTTT 3062
Db 2941 ACCCTCAGAGGCTGTGACACAACTTCAAGATCTCTGCTGAGGCTTACAGTTT 3000
Qy 3063 CAGGATGTGTGTGACAGTCCCATTTTCATCAGCAAGTTTGAAGAACCCCAATTTTC 3122
Db 3001 CAGGATGTGTGTGACAGTCCCATTTTCATCAGCAAGTTTGAAGAACCCCAATTTTC 3060
Qy 3123 CTGGCGTCACTCTCTGACAGAGGCTCTCCTGTACTTCAATCCTGTAAGCCAAAGACGA 3182
Db 3061 CTGGCGTCACTCTCTGACAGAGGCTCTCCTGTACTTCAATCCTGTAAGCCAAAGACGA 3120
Qy 3183 GGGATGTGCTGGGGGACCAAGGGCGCCCGGGCCCTGTGCCCTCGAGAGCCGTCAAGTGG 3242
Db 3121 GGGATGTGCTGGGGGACCAAGGGCGCCCGGGCCCTGTGCCCTCGAGAGCCGTCAAGTGG 3180
Qy 3243 CTGTGCGACCAAGATTTCTGCTCAAGCTGACTGACACCGTGTACACCTGACAGTGCATC 3302
Db 3181 CTGTGCGACCAAGATTTCTGCTCAAGCTGACTGACACCGTGTACACCTGACAGTGCATC 3240
Qy 3303 CTGGGGCTACTCAGAGAGACCGCAGAGCGAGCTGAGTGGAGAGTCCCGGGGACAGAGCTG 3362
Db 3241 CTGGGGCTACTCAGAGAGACCGCAGAGCGAGCTGAGTGGAGAGTCCCGGGGACAGAGCTG 3300
Qy 3363 ACTGGCTTGAAGGCCGAGCAGCAACCCGAGCTGCTCAGACTTCAAGACATCTGTGGAC 3422
Db 3301 ACTGGCTTGAAGGCCGAGCAGCAACCCGAGCTGCTCAGACTTCAAGACATCTGTGGAC 3360
Qy 3423 TGATGGCACCCCGCCACAGAGGCGAGAGCAGACACACAGAGGAGGAGGAGGAGGAGGAG 3482
Db 3361 TGATGGCACCCCGCCACAGAGGCGAGAGCAGACACACAGAGGAGGAGGAGGAGGAGGAG 3420
```


[illegible]

Dp	2821	TCATTCAGAGCCAGCTCTCACCTTCAACCGGGGTTCAAGGCTGGAGGAACTAGTGTCG	2880
Qy	2943	AAACTCTTTGGGGCTCTGGGGCTGAAAGTGCACAGCTCTTTCTGGATTTGCAGGTGAC	3002
Dp	2881	AAACTCTTTGGGGCTCTGGGGCTGAAAGTGCACAGCTCTTTCTGGATTTGCAGGTGAC	2940
Qy	3003	AGCCCTCAGAGGGGTGCACCAACATCTAGAGATCTCTCTCGCAGGCGTACAGGTTT	3062
Dp	2941	AGCTCCAGAGGGGTGCACCAACATCTAGAGATCTCTCTCTCGAGCGTACAGGTTT	3000
Qy	3063	CACGCATGTGTGTGACGCTCCCATTTTCATCAGCAATTTGGAGAACCCCAATTTTC	3122
Dp	3001	CACGCATGTGTGTGACGCTCCCATTTTCATCAGCAATTTGGAGAACCCCAATTTTC	3060
Qy	3123	CTGGCGCATCTCTGACAGGGGCTCCCTGTACTCTCATCTTAAAGCCAAAGACGA	3182
Dp	3061	CTGGCGCATCTCTGACAGGGGCTCCCTGTACTCTCATCTTAAAGCCAAAGACGA	3120
Qy	3183	GGGATGTGCTGGGGGGCCAGAGGGGCGCGGCGCTCTCCCTCCGAGAGCGTGCAGTG	3242
Dp	3121	GGGATGTGCTGGGGGGCCAGAGGGGCGCGGCGCTCTCCCTCCGAGAGCGTGCAGTG	3180
Qy	3243	CTGTGCCACCAAGCATTTCTGTCTCAAGCTGACACCGTGTCACTTACGTGCACTC	3302
Dp	3181	CTGTGCCACCAAGCATTTCTGTCTCAAGCTGACACCGTGTCACTTACGTGCACTC	3240
Qy	3303	CTGGGGGTACACAGAGAGCCGACAGCGAGCTGAGTGGGAACCTCCGGGGACGACGCTG	3362
Dp	3241	CTGGGGGTACACAGAGAGCCGACAGCGAGCTGAGTGGGAACCTCCGGGGACGACGCTG	3300
Qy	3363	ACTGCGCTGGAGGCCGACCAACCCGGCATGCTCCTGACTTCAGACTTAAGACATCTGTGAC	3422
Dp	3301	ACTGCGCTGGAGGCCGACCAACCCGGCATGCTCCTGACTTCAGACTTAAGACATCTGTGAC	3360
Qy	3423	TGATGGGACACCGGCGCCACAGCCGAGAGGAGAGACACACAGCCCTGTGACAGCGGG	3482
Dp	3361	TGATGGGACACCGGCGCCACAGCCGAGAGGAGAGACACACAGCCCTGTGACAGCGGG	3420
Qy	3483	CTTACAGTCCAGGAGGAGGGGCGGCCACACCCAGGCCCGCACGCTGGGAGTGTGA	3542
Dp	3421	CTTACAGTCCAGGAGGAGGGGCGGCCACACCCAGGCCCGCACGCTGGGAGTGTGA	3480
Qy	3543	GGCGTAGTGTGTTTTGGGCCGAGGGCTGCAATGTCCGGGTGAAGGCTAGTGTCCGGCTG	3602
Dp	3481	GGCGTAGTGTGTTTTGGGCCGAGGGCTGCAATGTCCGGGTGAAGGCTAGTGTCCGGCTG	3540
Qy	3603	AGGCGTACGAGGAGTGTCCACCAAGAGGCTGAGTGTCCACACACCTGCGTTCACATTC	3662
Dp	3541	AGGCGTACGAGGAGTGTCCACCAAGAGGCTGAGTGTCCACACACCTGCGTTCACATTC	3600
Qy	3663	CCCAACAGGCTGCGGCTGCGCTCCACCCCAAGGGCCAGCTTTTCTTCACAGAGCCCGGCT	3722
Dp	3601	CCCAACAGGCTGCGGCTGCGCTCCACCCCAAGGGCCAGCTTTTCTTCACAGAGCCCGGCT	3660
Qy	3723	TCCACTCCCCACATAGGAATAGTCCATGCCAGATTGCGCATTTTCACCCCTGGCCCTG	3782
Dp	3661	TCCACTCCCCACATAGGAATAGTCCATGCCAGATTGCGCATTTGTCACCCCTGGCCCTG	3720
Qy	3783	CCCTCCTTTGCTTCCACCCCAACCATCCAGGTGAGAGCCCTGAGAGAGACCTGGGAGC	3842
Dp	3721	CCCTCCTTTGCTTCCACCCCAACCATCCAGGTGAGAGCCCTGAGAGAGACCTGGGAGC	3780
Qy	3843	TCTGGGAATTTGAGATGACCAAAAGGTGTCCCTGTACACAGGCGAGGACCTGTGACCTGG	3902
Dp	3781	TCTGGGAATTTGAGATGACCAAAAGGTGTCCCTGTACACAGGCGAGGACCTGTGACCTGG	3840
Qy	3903	ATGAGGGTCCCTGTGGGTCAAAATTTGGGGGAGGTCGTGGAGATGAAATACTGAATATA	3962
Dp	3841	ATGAGGGTCCCTGTGGGTCAAAATTTGGGGGAGGTCGTGGAGATGAAATACTGAATATA	3900
Qy	3963	TGAGTTTTTACGTTTTGA 3980	

Db 3901 TGAGTTTTCAGTTTGA 3918

Search completed: April 16, 2003, 20:04:39

Job time : 841 secs

g

Qy	2425	AGGCAGAGAGGCGCTTTCACAGCTCTTCCTCAGTCCGTTTCATGTGCCACACAGCGCGTGGCA	2448
Db	2461	AGGCAGAGAGGCGCTTTCAGAGCTCTTCACGCTCTTCACGTCTCATGTGCCACACAGCGCGTGGCA	2520
Qy	2485	TCAGGGGCAAGCTCTACAGTCTCCAGTCCAGGGAGATCCGGGAGGGCTCATCTCTCCAGCG	2544
Db	2521	TCAGGGGCAAGCTCTACAGTCTCCAGTCCAGTCCAGGGAGATCCGGGAGGGCTCATCTCTCCAGCG	2580
Qy	2545	TGCTCTGACAGCTGTGTCTACGCGGACATGAGAGAACAGCTGTTTGGCGGGGATTTGGCGGG	2604
Db	2581	TGCTCTGACAGCTGTGTCTACGCGGACATGAGAGAACAGCTGTTTGGCGGGGATTTGGCGGGG	2640
Qy	2605	ACGGGCTGTCTGTGCTTGGTGGTGAATTTCTGTGTGTGACACCTCAGCTCAGCCAGC	2664
Db	2641	ACGGGCTGTCTGTGCTTGGTGGTGAATTTCTGTGTGTGACACCTCAGCTCAGCCAGC	2700
Qy	2665	CGAAGAACCTTCCACAGAGACCTCGGTCCGAGGTGTCCCTGGATATGGCTGTGCTGTGTAACT	2724
Db	2701	CGAAGAACCTTCCACAGAGACCTCGGTCCGAGGTGTCCCTGGATATGGCTGTGCTGTGTAACT	2760
Qy	2725	TGCGGAGAGACAGTGGTGAACCTCCCTGTGTGAAGAGAGAGGCCCTGGGTGGGACGGGCTTTTG	2788
Db	2761	TGCGGAGAGACAGTGGTGAACCTCCCTGTGTGAAGAGAGAGGCCCTGGGTGGGACGGGCTTTTG	2820
Qy	2785	TTTCAGATGTGGCGCCACAGGCTATTCCTCGTGGGCGCTGTCTGGATATCCCGGACCC	2844
Db	2821	TTTCAGATGTGGCGCCACAGGCTATTCCTCGTGGGCGCTGTCTGGATATCCCGGACCC	2880
Qy	2845	TGGAGGTGCAGAGCGACACTACCTCAGCTATGTCCCGGACCTCCATCAGACGAGTCCAGCT	2904
Db	2881	TGGAGGTGCAGAGCGACACTACCTCAGCTATGTCCCGGACCTCCATCAGACGAGTCCAGCT	2940
Qy	2905	TCACACCGGGGCTTCAAGAGCTGGGAGAGACATGCTGTCCGAACCTTTTGGGGTCTTGTGGCG	2964
Db	2941	TCACACCGGGGCTTCAAGAGCTGGGAGAGACATGCTGTCCGAACCTTTTGGGGTCTTGTGGCG	3000
Qy	2965	TGAAATGTCAACACCGTGTTTTGAGTTTCAGAGTGAACACACCTCCAGAGCGGTGTGCACCA	3024
Db	3001	TGAAATGTCAACACCGTGTTTTGAGTTTCAGAGTGAACACACCTCCAGAGCGGTGTGCACCA	3060
Qy	3025	ACATGTACAGAGATCTCCGCTGGTGGAGGCGTACAGGTTTACAGCATGTGTGTGTGACATCC	3084
Db	3061	ACATGTACAGAGATCTCCGCTGGTGGAGGCGTACAGGTTTACAGCATGTGTGTGTGACATCC	3120
Qy	3085	CATTTCATCAGCAAGTTTGTGAAGAACCCACATTTTCTCCGCGCATCTGTGTACACGG	3144
Db	3121	CATTTCATCAGCAAGTTTGTGAAGAACCCACATTTTCTCCGCGCATCTGTGTACACGG	3180
Qy	3145	CCTCCCTCTGTACTACTCATCTTGAAAGCCAGAGACGAGGAGATGTGCTGGGGGGCAAG	3204
Db	3181	CCTCCCTCTGTACTACTCATCTTGAAAGCCAGAGACGAGGAGATGTGCTGGGGGGGGCAAG	3240
Qy	3205	GGCGCGCGCGGCTCTGTGCCCTCCAGAGCGGTGCAATGGCTGTGTCCACACCAATCTCTGCG	3264
Db	3241	GGCGCGCGCGGCTCTGTGCCCTCCAGAGCGGTGCAATGGCTGTGTCCACACCAATCTCTGCG	3300
Qy	3265	TCAGAGCTGACTGCAGACCGGTATCCAGTACGTGCACATCTCTGGGGGTCTACTGTAGGACAGCC	3324
Db	3301	TCAGAGCTGACTGCAGACCGGTATCCAGTACGTGCACATCTCTGGGGGTCTACTGTAGGACAGCC	3360
Qy	3325	ACAGCAGCTGAGTGTGGAGAGTCCCGGGGAGAGAGCTGATGTGCTCGGAGGGCGGACGCCA	3384
Db	3361	ACAGCAGCTGAGTGTGGAGAGTCCCGGGGAGAGAGCTGATGTGCTCGGAGGGCGGACGCCA	3420
Qy	3385	ACCGGCGACGTGCGCTACAGCTTTCAGAACCATCTGTGTGACATGTGGCCACCGCCGACAGCC	3444
Db	3421	ACCGGCGACGTGCGCTACAGCTTTCAGAACCATCTGTGTGACATGTGGCCACCGCCGACAGCC	3480
Qy	3445	AGCGCTGAGACAGACACCAAGCAGCTGTACAGCGCGGGCTCTACGTCCAGAGAGGAGAG	3504
Db	3481	AGCGCTGAGACAGACACCAAGCAGCTGTACAGCGCGGGCTCTACGTCCAGAGAGGAGAG	3540

```

QY 3505 GGGGGCCACACACCAGAGCCGCCACACCCCTGTGGAGTCTTAGAGCCCTGAGTAAAGTTTGGCCG 3564
Db 3541 GGGGGCCACACACCAGAGCCGCCACACCCCTGTGGAGTCTTAGAGCCCTGAGTAAAGTTTGGCCG 3500
QY 3565 AGGCGTCATGTCCGGCTGAAGAGCTGAGTGTCCGGCTGAGCCCTGAGCTGTCACGCTC 3524
Db 3601 AGGCGTCATGTCCGGCTGAAGAGCTGAGTGTCCGGCTGAGCCCTGAGCTGTCACGCTC 3560
QY 3625 AAGGGCTGAGTGTCCAGAGACACCTGGCGTTCACCTCCCGACAGCTGGCGCTGGGCTC 3684
Db 3661 AAGGGCTGAGTGTCCAGAGACACCTGGCGTTCACCTCCCGACAGCTGGCGCTGGGCTC 3720
QY 3685 CACCCCGAGGGCCAGCTTTTCTCTACACAGAGAGCCGGCTCCACATCCGACATTAAGAAATG 3744
Db 3721 CACCCCGAGGGCCAGCTTTTCTCTACACAGAGAGCCGGCTTCACATCCGACATTAAGAAATG 3780
QY 3745 TCCATCCCGAGATTTGCCATTTGTACCCCTGGCCCTGCTTTTGGCTTCCACCCG 3804
Db 3781 TCCATCCCGAGATTTGCCATTTGTACCCCTGGCCCTGCTTTTGGCTTCCACCCG 3840
QY 3805 ACCATCCAGGTGGAGACACCTTGAGAGAGCCCTGGAGACTCTGGGAATTTGGAGTGCACAA 3864
Db 3841 ACCATCCAGGTGGAGACACCTTGAGAGAGCCCTGGAGACTCTGGGAATTTGGAGTGCACAA 3900
QY 3865 AGGTGTGCTCCTGTACACAGGGGAGAGACCTGTGACCTGATGAGGGGTCCCTGTGGGTCAAA 3924
Db 3901 AGGTGTGCTCCTGTACACAGGGGAGAGACCTGTGACCTGATGAGGGGTCCCTGTGGGTCAAA 3960
QY 3925 TTGGGGGAGAGTCTGTGGAGTAAATCTGAATATATGATTTTTAGTTTGAAGAAA 3984
Db 3961 TTGGGGGAGAGTCTGTGGAGTAAATCTGAATATATGATTTTTAGTTTGAAGAAA 4020
QY 3985 AAAAAAAAAAAAAAAAAAAAAA 4006
Db 4021 AAAAAAAAAAAAAAAAAAAAAA 4042

RESULT 2
US-09/721-456-343
Sequence 343, Application US/09721456
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-Nov-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997

```



```
Db 721 ||||| 780
Qy 788 TGGCCCTGAGCCGAGGAGGAGCCGCTTGGAGAGGGTCTGGGCCACCCGGGAGGAC 847
Db 781 TGGCCCTGAGCCGAGGAGGAGCCGCTTGGAGAGGGTCTGGGCCACCCGGGAGGAC 840
Qy 848 GCGTGGACCGAGTACCGCTGTTCTGTGTGTGTACCTGTCCAGACCCCGGAGAGAGC 907
Db 841 GCGTGGACCGAGTACCGCTGTTCTGTGTGTGTACCTGTCCAGACCCCGGAGAGAGC 900
Qy 908 CACCTCTTGGAGGGTGTGCTCTGTGACGGGACACTCCACCCATCCGCTGGGCGCA 967
Db 901 CACCTCTTGGAGGGTGTGCTCTGTGACGGGACACTCCACCCATCCGCTGGGCGCA 960
Qy 968 GCACGACGGGGGCCCCCATCTCAGTCGGGGCACAGCTCCCTGGGAGAGGCTTGTGC 1027
Db 961 GCACGACGGGGGCCCCCATCTCAGTCGGGGCACAGCTCCCTGGGAGAGGCTTGTGC 1020
Qy 1028 CCGGGTGTACGGGACGACGACCTCTGACCTCTCAGGGGACAGAGGAGGAGGAGGAGC 1087
Db 1021 CCGGGTGTACGGGACGACGACCTCTGACCTCTCAGGGGAGAGGAGGAGGAGGAGC 1080
Qy 1088 GCGCTCTTCTACTGACCTCTGTAGGCCACGCTGACCTGTGGCTGAGGCTGTGGA 1147
Db 1081 GCGCTCTTCTACTGACCTCTGTAGGCCACGCTGACCTGTGGCTGAGGCTGTGGA 1140
Qy 1148 GACCATCTTCTGGGTTCAGGCCCTGATGTCAGGAGATCCCGGAGGTTGCCCGCT 1207
Db 1141 GACCATCTTCTGGGTTCAGGCCCTGATGTCAGGAGATCCCGGAGGTTGCCCGCT 1200
Qy 1208 GCGCCAGGCTACTGAGCAATGCGGCCCTGTTCTGTGAGACTGTTGGAGACAGCGCA 1267
Db 1201 GCGCCAGGCTACTGAGCAATGCGGCCCTGTTCTGTGAGACTGTTGGAGACAGCGCA 1260
Qy 1268 GTGCCCTTACGGGGTGTCTCTCAAGACGACACTGCCGCTGCGAGCTGCGTACCCAGC 1327
Db 1261 GTGCCCTTACGGGGTGTCTCTCAAGACGACACTGCCGCTGCGAGCTGCGTACCCAGC 1320
Qy 1328 AGCCGGTGTGTGTGCCCGGGAGAGGCCGAGGAGCTGTGTGGAGCCCGGAGAGAGGA 1387
Db 1321 AGCCGGTGTGTGTGCCCGGGAGAGGCCGAGGAGCTGTGTGGAGCCCGGAGAGAGGA 1380
Qy 1388 CACAGACCCCGGTGCTGTGTGACGCTGTCCGCGAGACAGCGCCCTGTGACAGTGA 1447
Db 1381 CACAGACCCCGGTGCTGTGTGACGCTGTCCGCGAGACAGCGCCCTGTGACAGTGA 1440
Qy 1448 CCGCTTGTGGGGGCTGTGCTGTGCGCGGCTGTGCTCCGAGGCTGTGGGGCTCCAGGA 1507
Db 1441 CCGCTTGTGGGGGCTGTGCTGTGCGCGGCTGTGCTCCGAGGCTGTGGGGCTCCAGGA 1500
Qy 1508 CAGCAGAGCGCGCTTCTCTAGAGAACCAAGAGTTCATCTCCCTGGGAGAGATGCCAA 1567
Db 1501 CAGCAGAGCGCGCTTCTCTAGAGAACCAAGAGTTCATCTCCCTGGGAGAGATGCCAA 1560
Qy 1568 GCTCTGCTGTGAGAGCTGTGAGTGAAGTGTGCGTGGGAGCTGCGTGGCTGCGAG 1627
Db 1561 GCTCTGCTGTGAGAGCTGTGAGTGAAGTGTGCGTGGGAGCTGCGTGGCTGCGAG 1620
Qy 1628 GAGCCAGGGGTGTGTGTCCGCGCAGAGACCGCTGTCCGTGAGAGATCTTGGC 1687
Db 1621 GAGCCAGGGGTGTGTGTCCGCGCAGAGACCGCTGTCCGTGAGAGATCTTGGC 1680
Qy 1688 CAACTTCTGTGACGTGTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1747
Db 1681 CAACTTCTGTGACGTGTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740
Qy 1748 TGTCAAGGAGACAGGTTCAAAAGAACAGGCTCTTTTTCACCGGAAAGTGTGGAG 1807
Db 1741 TGTCAAGGAGACAGGTTCAAAAGAACAGGCTCTTTTTCACCGGCAAGTGTGGAG 1800
Qy 1808 CAACTTGTCAAGGACATGTGATGTGACAGACATTAAGAGGCTCAGCTCGGAGACTGC 1867
Db 1801 CAACTTGTCAAGGACATGTGATGTGACAGACATTAAGAGGCTCAGCTCGGAGACTGC 1860
Qy 1868 GGAAGCAGAGGTATGAGCAGCATCGGAAAGCCAGGCCGCTGTGTGTGTGTGTGTGTGT 1927
Db 1861 GGAAGCAGAGGTATGAGCAGCATCGGAAAGCCAGGCCGCTGTGTGTGTGTGTGTGTGT 1920
Qy 1928 CTTCATCCCAAGCTGTGAGGGGCTGCGGCCGATGTGTGAACATGTGACTGTGTGTGTGT 1987
Db 1921 CTTCATCCCAAGCTGTGAGGGGCTGCGGCCGATGTGTGAACATGTGACTGTGTGTGT 1980
Qy 1988 CAGAACGTTCCGAGAGAAAGAGGAGCCGACGCTCTACCTGTGAGAGGAGCAGTGT 2047
Db 1981 CAGAACGTTCCGAGAGAAAGAGGAGCCGACGCTCTACCTGTGAGAGGAGCAGTGT 2040
Qy 2048 CAGGCTGTCTAAGTACAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 2107
Db 2041 CAGGCTGTCTAAGTACAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 2100
Qy 2108 CCGTGTGATGTATCCAGAGGGGCTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2167
Db 2101 CCGTGTGATGTATCCAGAGGGGCTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
Qy 2168 GCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2191
Db 2161 GCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2190
Qy 2192 GGAAGGCTCAGAGAGGTATCGCAGCATCATCAAAACCCAGAACACTGTGTGTGTGT 2251
Db 2221 GGAAGGCTCAGAGAGGTATCGCAGCATCATCAAAACCCAGAACACTGTGTGTGTGT 2280
Qy 2252 TCGGTATCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2311
Db 2281 TCGGTATCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340
Qy 2312 GCTCTCTACTGTGACAGACTCTCAGCCGTATCATGACAGTGTGTGTGTGTGTGTGTGT 2371
Db 2341 GCTCTCTACTGTGACAGACTCTCAGCCGTATCATGACAGTGTGTGTGTGTGTGTGTGT 2400
Qy 2372 GACGAGCCCGCTGTGAGGATGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2431
Db 2401 GACGAGCCCGCTGTGAGGATGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2460
Qy 2432 CAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2491
Db 2461 CAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2520
Qy 2492 CAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2551
Db 2521 CAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2580
Qy 2552 CAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2611
Db 2581 CAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640
Qy 2612 GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2671
Db 2641 GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2700
Qy 2672 CTTCCTGTGAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2731
Db 2701 CTTCCTGTGAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2760
Qy 2732 GACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2791
Db 2761 GACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2820
Qy 2792 GCGGCGCCAGGCGCTATTCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2851
Db 2821 GCGGCGCCAGGCGCTATTCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2880
Qy 2852 GAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2911
Db 2881 GAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2940
```



```
QY 668 CTGGAACCATAGCCTCAGGAGGAGCGGGGTCCCTCGGCTTCCAGCCCGGGTGGAG 727
    |||
Db 661 CTGGAACCATAGCCTCAGGAGGAGCGGGGTCCCTCGGCTTCCAGCCCGGGTGGAG 720
QY 728 GAGGCGCGGGGAGTGTCCAGCCGAAAGTCTGCGCTTGGCCCAAGAGCCAGGCGTGGCG 787
    |||
Db 721 GAGGCGCGGGGAGTGTCCAGCCGAAAGTCTGCGCTTGGCCCAAGAGCCAGGCGTGGCG 780
QY 788 TGCCTCTAGCCGAGGAGGAGCGCCGTTGGGAGGGGTCTTGGGCCCAAGCCGGGAGAG 847
    |||
Db 781 TGCCTCTAGCCGAGGAGGAGCGCCGTTGGGAGGGGTCTTGGGCCCAAGCCGGGAGAG 840
QY 848 GCGTGGACCGATGACCGCTGATTTCTGATGTGTACCTGCGAAGCCGGCGAAAGAG 907
    |||
Db 841 GCGTGGACCGATGACCGCTGATTTCTGATGTGTACCTGCGAAGCCGGCGAAAGAG 900
QY 908 CACCTCTTTGAGAGGTGCGCTCTCTGAGACGGGCACTCCCAAGCCGCGTGGGCGGCA 967
    |||
Db 901 CACCTCTTTGAGAGGTGCGCTCTCTGAGACGGGCACTCCCAAGCCGCGTGGGCGGCA 960
QY 968 GACACAGCGGGGCCCCCATCCACATCGCGGCACACACGTCCCTGGGAGACGCTTGTCC 1027
    |||
Db 961 GACACAGCGGGGCCCCCATCCACATCGCGGCACACACGTCCCTGGGAGACGCTTGTCC 1020
QY 1028 CCCGCTGACCGCGAGACCAAGCACTTCTCTACTCTCTGAGCGGACAGAGAGAGCTGGC 1087
    |||
Db 1021 CCCGCTGACCGCGAGACCAAGCACTTCTCTACTCTCTGAGCGGACAGAGAGAGCTGGC 1080
QY 1088 GCCCTCTCTCTACTCTCTGAGCGGACAGCTGACAGCGGCTCGGAGGCTGTGGA 1147
    |||
Db 1081 GCCCTCTCTCTACTCTCTGAGCGGACAGCTGACAGCGGCTCGGAGGCTGTGGA 1140
QY 1148 GACCATCTTTTGTGGTTCAGAGGCGCTTGTATGACAGGAGCTCCCGAGAGTTGCCCGCT 1207
    |||
Db 1141 GACCATCTTTTGTGGTTCAGAGGCGCTTGTATGACAGGAGCTCCCGAGAGTTGCCCGCT 1200
QY 1208 GCCCAGGCGTACTGAGCAATGAGGCGCCCTGTTTCTGGAAGCTCTTGGGAAACAAGGCA 1267
    |||
Db 1201 GCCCAGGCGTACTGAGCAATGAGGCGCCCTGTTTCTGGAAGCTCTTGGGAAACAAGGCA 1260
QY 1268 GTGCCCTTACGAGGGTGTCTCTCAAGACGACGTGCGGCTGAGAGTGGGCTACCCAGC 1327
    |||
Db 1261 GTGCCCTTACGAGGGTGTCTCTCAAGACGACGTGCGGCTGAGAGTGGGCTACCCAGC 1320
QY 1328 AGCCGGTGTGTGTCGCCGGGAGAAAGCCAGAGGCTGTGTGGCGGCCCGGAGAGAGAGA 1387
    |||
Db 1321 AGCCGGTGTGTGTCGCCGGGAGAAAGCCAGAGGCTGTGTGGCGGCCCGGAGAGAGAGA 1380
QY 1388 CACACAGCCCGTGGCTGTGTGAGTGTCCGACAGCAGCAGCCTCCGAGAGTGTGA 1447
    |||
Db 1381 CACACAGCCCGTGGCTGTGTGAGTGTCCGACAGCAGCAGCCTCCGAGAGTGTGA 1440
QY 1448 CGGCTTGTGTGGGCGTGTGCGCGGAGTGTGCTCCCAAGGCTTGGGGCTTCAGAGCA 1507
    |||
Db 1441 CGGCTTGTGTGGGCGTGTGCGCGGAGTGTGCTCCCAAGGCTTGGGGCTTCAGAGCA 1500
QY 1508 CAACGAAAGCCGCTTCTCTAGAAACCAACAAAGTTCATCTCCCTGGGAAACATGCAAA 1567
    |||
Db 1501 CAACGAAAGCCGCTTCTCTAGAAACCAACAAAGTTCATCTCCCTGGGAAACATGCAAA 1560
QY 1568 GCTCTCGTGTGAGAGTGTGACGTGAAGATGAGGTGCGGGAATGTGCGTGTGGCTGGAG 1627
    |||
Db 1561 GCTCTCGTGTGAGAGTGTGACGTGAAGATGAGGTGCGGGAATGTGCGTGTGGCTGGAG 1620
QY 1628 GAGCCAGAGGGTGTGGTGTTCGCGCGGACAGACAGCAGTCTTGGGAGAGATCTGGC 1687
    |||
Db 1621 GAGCCAGAGGGTGTGGTGTTCGCGCGGACAGACAGCAGTCTTGGGAGAGATCTGGC 1680
QY 1688 CAAATTCTGTGACTGTGTATGATGTGTACGTGTGAGCTGTCAAGTCTTCTTTTAA 1747
    |||
Db 1681 CAAATTCTGTGACTGTGTATGATGTGTACGTGTGAGCTGTCAAGTCTTCTTTTAA 1740

QY 1748 TGTACGAGAGACCACTTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAGAGTGTGGAG 1807
    |||
Db 1741 TGTACGAGAGACCACTTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAGAGTGTGGAG 1800
QY 1808 CAAATTCAAAAGCATTTGAAATGACAGCACTTTGAAGAGGTGTGAGTGTGGAGTGTG 1867
    |||
Db 1801 CAAATTCAAAAGCATTTGAAATGACAGCACTTTGAAGAGGTGTGAGTGTGGAGTGTG 1860
QY 1868 GAAAGCAGAGGTGAGCAGCATCGGGAAGCCAGGCGCCCTGTGTGAGTGTGAGCTGGC 1927
    |||
Db 1861 GAAAGCAGAGGTGAGCAGCATCGGGAAGCCAGGCGCCCTGTGTGAGTGTGAGCTGGC 1920
QY 1928 CTTCATCCCAAGCCTGAGAGGCTGCGGCGGATTTGTGAACATGACATGCTGTGGAGAC 1987
    |||
Db 1921 CTTCATCCCAAGCCTGAGAGGCTGCGGCGGATTTGTGAACATGACATGCTGTGGAGAC 1980
QY 1988 CAGAAAGTTCGAGAGAAAGAGGCGCGAGCGCTGACCTGAGAGGTGAAGGCACTGTT 2047
    |||
Db 1981 CAGAAAGTTCGAGAGAAAGAGGCGCGAGCGCTGACCTGAGAGGTGAAGGCACTGTT 2040
QY 2048 CAGGCTGTCAACTAGAGAGCGGCGCGGCGCCCGGCTCTGTGGCGCTTGTGTGGG 2107
    |||
Db 2041 CAGGCTGTCAACTAGAGAGCGGCGCGGCGCGGCGCCCGGCTCTGTGTGGG 2100
QY 2108 CCTGAGCATATCCACAGGGCGTGGGACCTTGTGTGTGTGTGGGCGCCAGAGACC 2167
    |||
Db 2101 CCTGAGCATATCCACAGGGCGTGGGACCTTGTGTGTGTGTGGGCGCCAGAGACC 2160
QY 2168 GCCGCTGAGCTGTGA-----CATCCCGCA 2191
    |||
Db 2161 GCCGCTGAGCTGTGAATTTGTCAAGTGAATGTGACGGGCGGTCAGACACATCCCGCA 2220
QY 2192 GGACAGAGCTCAGGAGGTGATGCGCAGATCATCAAAACCCAGAACAGTACTGTGGG 2251
    |||
Db 2221 GGACAGAGCTCAGGAGGTGATGCGCAGATCATCAAAACCCAGAACAGTACTGTGGG 2280
QY 2252 TCGGTATGCGGTGTCCAGAAAGCGCGCCATGTGGCAAGTGTCCAGAGGCTTCAAGAGCA 2311
    |||
Db 2281 TCGGTATGCGGTGTCCAGAAAGCGCGCCATGTGGCAAGTGTCCAGAGGCTTCAAGAGCA 2340
QY 2312 GGTCTTACTGTGACAGACCTTCCAGCGGTACATGCGACAGTGTGTGGTCACTGCGAGGA 2371
    |||
Db 2341 GGTCTTACTGTGACAGACCTTCCAGCGGTACATGCGACAGTGTGTGGTCACTGCGAGGA 2400
QY 2372 GACACAGCGCGGTGAGGAGTGTGTGTATGAGAGAGTGTGTCTCTGAAATGAGCGAG 2431
    |||
Db 2401 GACACAGCGCGGTGAGGAGTGTGTGTATGAGAGAGTGTGTCTCTGAAATGAGCGAG 2460
QY 2432 CAGTGGCTTGTGACGTCTTCTACGCTTCAATGTGTGACACAGCGCTGTGGCATGAGGG 2491
    |||
Db 2461 CAGTGGCTTGTGACGTCTTCTACGCTTCAATGTGTGACACAGCGCGTGTGGCATGAGGG 2520
QY 2492 CAAGTCTTACGTCCAGTGTCCAGAGGATCCGACAGGCTCATCTCTCAAGCTGTCTG 2551
    |||
Db 2521 CAAGTCTTACGTCCAGTGTCCAGAGGATCCGACAGGCTCATCTCTCAAGCTGTCTG 2580
QY 2552 CAGCCTGTGTACGAGGAGCATGGAACAGAGTGTGTGGGGATTTGGCGAGAGGCT 2611
    |||
Db 2581 CAGCCTGTGTACGAGGAGCATGGAACAGAGTGTGTGGGGATTTGGCGAGAGGCT 2640
QY 2612 GCTCTGTGTTTGGTGGATGATTTCTTGTGGTGAACACTCACTCAACGAGGAAAC 2671
    |||
Db 2641 GCTCTGTGTTTGGTGGATGATTTCTTGTGGTGAACACTCACTCAACGAGGAAAC 2700
QY 2672 CTTCCTCAGAGACCTGTGTGCGAGTGTCCGTGATGTGAGTGTGCGGTGGAACCTGGGAA 2731
    |||
Db 2701 CTTCCTCAGAGACCTGTGTGCGAGTGTCCGTGATGTGAGTGTGCGGTGGAACCTGGGAA 2760
QY 2732 GACAGTGTGTAACCTTCCGTGTGAAGAGAGAGCGCTGGGTGACAGGCTTTGTTCAGAT 2791
    |||
Db 2761 GACAGTGTGTAACCTTCCGTGTGAAGAGAGAGCGCTGGGTGACAGGCTTTGTTCAGAT 2820
QY 2792 GCCGCGCACAGGCTATTCCCTGTGTGGGCTGTGCTGTGATPACCGGACCTGTGAGGT 2851
    |||
```


Db 2821 GCGGCCCCACGCTATTCCTGCTGGGCTCTGCTGATACCCGAGCCCTGGAGGT 2880
Qy 2852 GCAGAGCACTACTACACTTATGCCCCGAGCTCCATGAGAGCACTGCTACCTTCAACG 2911
Db 2881 GCAGAGCACTACTACACTTATGCCCCGAGCTCCATGAGAGCACTGCTACCTTCAACG 2940
Qy 2912 CGGCTTCAAGGCTGGAGGAACATGCTGCAAACTTTTGGGGTCTTGGGCTGAAAGT 2971
Db 2941 CGGCTTCAAGGCTGGAGGAACATGCTGCAAACTTTTGGGGTCTTGGGCTGAAAGT 3000
Qy 2972 TCACAGCTGTTTCTGATTTGCAAGGTGACAGCTCCAGAGCTGTGCTACCAACATCTA 3031
Db 3001 TCACAGCTGTTTCTGATTTGCAAGGTGACAGCTCCAGAGCTGTGCTACCAACATCTA 3060
Qy 3032 CAAGATCTCTGCTGCAAGGCTACAGGTTTACGCAATGTGTGGGCTGCTCCATTTC 3091
Db 3061 CAAGATCTCTGCTGCAAGGCTACAGGTTTACGCAATGTGTGGGCTGCTCCATTTC 3120
Qy 3092 TCACAGATTTGGAAGAACCCACATTTTCTGCGGCTCATCTCTGACAGGCTCCCT 3151
Db 3121 TCACAGATTTGGAAGAACCCACATTTTCTGCGGCTCATCTCTGACAGGCTCCCT 3180
Qy 3152 CTGCTACTCTCTGAAAGCAAGAGCAAGGATGCTGCTGGGGGCCAAAGGCGCCG 3211
Db 3181 CTGCTACTCTCTGAAAGCAAGAGCAAGGATGCTGCTGGGGGCCAAAGGCGCCG 3240
Qy 3212 CGGCTTCTGCTGCTGCGAGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3271
Db 3241 CGGCTTCTGCTGCTGCGAGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
Qy 3272 GACTGACACCGTGTACCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3331
Db 3301 GACTGACACCGTGTACCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
Qy 3332 GCTGAGTGGAGAGTCCCGGGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3391
Db 3361 GCTGAGTGGAGAGTCCCGGGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
Qy 3392 ACTGCTCTGAGCTTCAAGACATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3451
Db 3421 ACTGCTCTGAGCTTCAAGACATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
Qy 3452 GAGAGAGACACAGAGAGCTTCAAGAGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAG 3511
Db 3481 GAGAGAGACACAGAGAGCTTCAAGAGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAG 3540
Qy 3512 CACACCCAGAGAGAGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAG 3571
Db 3541 CACACCCAGAGAGAGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAG 3600
Qy 3572 CATGCTCGGCTGAAAGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAG 3631
Db 3601 CATGCTCGGCTGAAAGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAG 3660
Qy 3632 GAGTGTGCTGAGAGAGCTGCTTCACTTCCACAGAGCTGAGTGTGCTGAGTGTGCTGAG 3691
Db 3661 GAGTGTGCTGAGAGAGCTGCTTCACTTCCACAGAGCTGAGTGTGCTGAGTGTGCTGAG 3720
Qy 3692 GGGGCACTTCTTCTCAACAGAGAGCTGCTTCACTTCCACAGAGCTGAGTGTGCTGAG 3751
Db 3721 GGGGCACTTCTTCTCAACAGAGAGCTGCTTCACTTCCACAGAGCTGAGTGTGCTGAG 3780
Qy 3752 CCAGATTCGCAATGTTTCAACCCCTGCGCCCTGCTTCTTCTTCTTCTTCTTCTTCTT 3811
Db 3781 CCAGATTCGCAATGTTTCAACCCCTGCGCCCTGCTTCTTCTTCTTCTTCTTCTTCTT 3840
Qy 3812 AGGTGGAGAGCTTCAAGAGAGCTTGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3871
Db 3841 AGGTGGAGAGCTTCAAGAGAGCTTGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3900
Qy 3872 CCCTGTACACAGAGAGAGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 3931

Db 3901 CCCTGTACACAG 3960
Qy 3932 GAGGTGTGTGTGGAGTAATAATATATATATATATATATATATATATATATATATATAT 3986
Db 3961 GAGGTGTGTGTGGAGTAATAATATATATATATATATATATATATATATATATATATAT 4015

RESULT 5
PCT-US02-33146-19
Sequence 19, Application PC/TUS0233146
GENERAL INFORMATION:
APPLICANT: University of Rochester Medical Center
APPLICANT: Rowley, Peter
TITLE OF INVENTION: Telomerase Interference
FILE REFERENCE: FP-71506-2/RFT/SRN
CURRENT APPLICATION NUMBER: PCT/US02/33146
CURRENT FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-33146-19

Query Match 99.1%; Score 3969; DB 1; Length 4015;
Best Local Similarity 99.1%; Pred. No. 3.9e-111;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

Qy 8 GCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 67
Db 1 GCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Qy 68 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 127
Db 61 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Qy 128 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187
Db 121 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Qy 188 GGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
Db 181 GGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Qy 248 ACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 307
Db 241 ACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Qy 308 CCGAGTGTGTGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 367
Db 301 CCGAGTGTGTGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Qy 368 GCTGCTGAG 427
Db 361 GCTGCTGAG 420
Qy 428 CCTGCCAACAAGGTGAG 487
Db 421 CCTGCCAACAAGGTGAG 480
Qy 488 CCGGCTGAG 547
Db 481 CCGGCTGAG 540
Qy 548 GGTCTCCAGCTGAGCTTCAAG 607
Db 541 GGTCTCCAGCTGAGCTTCAAG 600
Qy 608 TCAGAGCGGAG 667
Db 601 TCAGAGCGGAG 660

Qy	668	CTGAGACATAGGTCTAGAGAGAGCGCGGGGTCCCCCTGGGCGTGGACAGGCCCGCGGGTCTGAG	722
Dp	661	CTGAGACATATAGGTCTAGAGAGAGCGCGGGGTCCCCCTGGGCGTGGACAGGCCCGCGGGTCTGAG	720
Qy	728	GAGGCGCGGGGGGAGAGGCGACCGCAAGTCTGGCGTCCGCAAGAGGCCAGAGGTGGGCG	787
Dp	721	GAGGCGCGGGGGGAGAGGCGACCGCAAGTCTGGCGTCCGCAAGAGGCCAGAGGTGGGCG	780
Qy	788	TTGCCCCGTGACCCGAGACCGCGATCCGTTGGGCGAGGGGTCTGGGGCCACCCCGGCGAAGAGC	847
Dp	781	TTGCCCCGTGACCCGAGACCGCGATCCGTTGGGCGAGGGGTCTGGGGCCACCCCGGCGAAGAGC	840
Qy	848	GGTGTGACCGAGTGAACGTGGTGTCTGTGTGGTCTCACTGTCCAGACCCGCGCAAGAGC	907
Dp	841	GGTGTGACCGAGTGAACGTGGTGTCTGTGTGGTCTCACTGTCCAGACCCGCGCAAGAGC	900
Qy	908	CACCTCTTTTGAAGGGTGGCGCTCTCTGTGGCAAGCGGCACACTTCCACCCATCCGTGGAGCGCCA	967
Dp	901	CACCTCTTTTGAAGGGTGGCGCTCTCTGTGGCAAGCGGCACACTTCCACCCATCCGTGGAGCGCCA	960
Qy	968	GCACACGACGCGGGCCGCCCATCATATCGCGGCGACACAGTCCCTGGGAGACAGCCTTGTCG	1022
Dp	961	GCACACGACGCGGGCCGCCCATCATATCGCGGCGACACAGTCCCTGGGAGACAGCCTTGTCG	1020
Qy	1028	CCGCGGTGATGAGCCGAGACCAAGCACTTCTCTACTACCCAGAGGCGAAGAGAGAGAGCGTGGC	1087
Dp	1021	CCGCGGTGATGAGCCGAGACCAAGCACTTCTCTACTACCCAGAGGCGAAGAGAGAGAGCGTGGC	1080
Qy	1088	GGCGTCCCTCTACTACAGTCTGTGAGAGGCGCAAGCGTCACTGTGGCGTGGAGAGGCTCGTGGAG	1147
Dp	1081	GGCGTCCCTCTACTACAGTCTGTGAGAGGCGCAAGCGTCACTGTGGCGTGGAGAGGCTCGTGGAG	1140
Qy	1148	GACATCATCTTCTGTGGGTGTGCAAGGCCCTGTGATGTGCAGAGGACATCCCGCAGAGTTGGCCGCGCT	1207
Dp	1141	GACATCATCTTCTGTGGGTGTGCAAGGCCCTGTGATGTGTGCAAGGACATCCCGCAGAGTTGGCCGCGCT	1200
Qy	1208	GGCCCAAGCGCTACTGGCAATATGGGGCCCTGTTTCTGTGAGAGCTGCTTGGGAACACAGCGCA	1267
Dp	1201	GGCCCAAGCGCTACTGGCAATATGGGGCCCTGTTTCTGTGAGAGCTGCTTGGGAACACAGCGCA	1260
Qy	1268	GTGGCCCTCTACGGGGGTCTCTCTCAAGACGACACTGCCCTCTCGAGCTGGGATCACCCACAC	1327
Dp	1261	GTGGCCCTCTACGGGGGTCTCTCTCAAGACGACACTGCCCTCTCGAGCTGGGATCACCCACAC	1320
Qy	1328	AACCGGTTCTGTGGCCCGGAGGAAGGCCACGAGGCGTGTGTGGCGGGCCCGCGAGAGAGAGA	1387
Dp	1321	AACCGGTTCTGTGGCCCGGAGGAAGGCCACGAGGCGTGTGTGGCGGGCCCGCGAGAGAGAGA	1380
Qy	1388	CACAACACCCCGTGGCGCTGTGTGACAGTGTCTCCGACACACAGAGAGCCCTGACAGGTGTA	1447
Dp	1381	CACAACACCCCGTGGCGCTGTGTGACAGTGTCTCCGACACACAGAGAGCCCTGACAGGTGTA	1440
Qy	1448	CGCGTTGGTGGCGGCGCTGCTGCGCGCGGCGTGGTGGCCCGCAGAGGCTGTGGGGTCTCAAGGA	1507
Dp	1441	CGCGTTGGTGGCGGCGCTGCTGCGCGCGGCGTGGTGGCCCGCAGAGGCTGTGGGGTCTCAAGGA	1500
Qy	1508	CAGAGAACGGCGGTTCTCTCAGAGAAACCAAGAAAGTCAATCTCCGTGGGGAAGCATGTGCCAA	1567
Dp	1501	CAGAGAACGGCGGTTCTCTCAGAGAAACCAAGAAAGTCAATCTCCGTGGGGAAGCATGTGCCAA	1560
Qy	1568	GGTCTGCGCTGACAGAGCTGTGAGTGTGAAGATGAGCGTGTGCGGATCTGTGGCTGTGGCGCAG	1627
Dp	1561	GGTCTGCGCTGACAGAGCTGTGAGTGTGAAGATGAGCGTGTGCGGATCTGTGGCTGTGGCGCAG	1620
Qy	1628	GAGCCCAAGGGGTTGGCTGTGTCTCGGCGCCAGAGACCGCTCTCGTGTGAGAGATCTGTGC	1687
Dp	1621	GAGCCCAAGGGGTTGGCTGTGTCTCGGCGCCAGAGACCGCTCTCGTGTGAGAGATCTGTGC	1680
Qy	1688	CAGATTCTCTCACTGTGATGAGTGTGTGACGTGTGTGAGACTGTCTCAGTCTTCTTCTTTTA	1747
Dp	1681	CAGATTCTCTCACTGTGATGAGTGTGTGACGTGTGTGAGACTGTCTCAGTCTTCTTCTTTTA	1740
Qy	1748	TTCTACGAGAACACCAAGTTTCAAAAGAACGGCTCTTTTCTTTTACCGAAGAGCTGTCTGGAG	1807

Db	1741	TGTCAACGAGACCAAGCTTTCAAAAGAAAGAGCGCTCTTTTCTACACGGAAGATGTCGGAG	1800
Oy	1808	CAGATTCGAAGCATTTGAATATCAACAGCATCTTGAAAGAGGTGCAGATCGCGGAGAGCTGTC	1867
Db	1801	CAGATTCGAAGCATTTGAATATCAACAGCATCTTGAAAGAGGTGCAGATCGCGGAGAGCTGTC	1860
Oy	1868	GGAAACAGAGGTGAGGCAGCATCGGGAAAGCCAGGCGCCGCTCTGTCAGCTCAAGACTCCG	1927
Db	1861	GGAAACAGAGGTGAGGCAGCATCGGGAAAGCCAGGCGCCGCTCTGTCAGCTCAAGACTCCG	1920
Oy	1928	CTTTCATCCCAAGCTGACGAGGGCTCGCGGCGATTTGTAAACATGACATAGCTGTGGAGAC	1987
Db	1921	CTTTCATCCCAAGCTGACGAGGGCTCGCGGCGATTTGTAAACATGACATAGCTGTGGAGAC	1980
Oy	1988	CAGAAAGCTTCGCGAGAGAAAGAGAGGCCAGAGGTCCTACCTCCAGAGGTGAAGAGCACTGTT	2047
Db	1981	CAGAAAGCTTCGCGAGAGAAAGAGAGGCCAGAGGTCCTACCTCCAGAGGTGAAGAGCACTGTT	2040
Oy	2048	CAGCGCTGTCAACTACAGAGAGCGGGGCGCGGCGCCCGGCTCTGAGGGGCTCTGTGCTGGG	2107
Db	2041	CAGCGCTGTCAACTACAGAGAGCGGGGCGCGGCGCCCGGCTCTGAGGGGCTCTGTGCTGGG	2100
Oy	2108	CCGTGAGCATATTCACAGAGGAGCCTGGCGACACTTTCGTGTCGTGCTGTCGGAGGCCAGAGACC	2167
Db	2101	CCGTGAGCATATTCACAGAGGAGCCTGGCGACACTTTCGTGTCGTGCTGTCGGAGGCCAGAGACC	2160
Oy	2168	GGCGGCTGAGCTGTTA-----CAATCCCA	2191
Db	2161	GGCGGCTGAGCTGTTA-----CAATCCCA	2220
Oy	2192	GGACAGGCTCACGAGAGATCATCGCAGACATCATAAACCCAGAACAGTACTGCTGCG	2251
Db	2221	GGACAGGCTCACGAGAGATCATCGCAGACATCATAAACCCAGAACAGTACTGCTGCG	2280
Oy	2252	TCGGATACCGGTGCTCAGAAAGGCCGCCATGGGACGCTCCGACAGAGGCCCTTCAAGAGCCA	2311
Db	2281	TCGGATACCGGTGCTCAGAAAGGCCGCCATGGGACGCTCCGACAGAGGCCCTTCAAGAGCCA	2340
Oy	2312	CGTCTCTACCTTACAGACATCTCCAGCCGATACATATGCGAGACATTTGTGGCTACCTCGAGGA	2371
Db	2341	CGTCTCTACCTTACAGACATCTCCAGCCGATACATATGCGAGACATTTGTGGCTACCTCGAGGA	2400
Oy	2372	GACACAGCCCGCTAGAGGATGCGCGTGCATCTCAGAGAGAGTCTCTCCCTGAATGAGGCTCAG	2431
Db	2401	GACACAGCCCGCTAGAGGATGCGCGTGCATCTCAGAGAGAGTCTCTCCCTGAATGAGGCTCAG	2460
Oy	2432	CAGTGGCCCTCTGAGAGCTTCTTCACACTTCAATGTCACACAGCCGCGTGGCCATCAGAGGG	2491
Db	2461	CAGTGGCCCTCTGAGAGCTTCTTCACACTTCAATGTCACACAGCCGCGTGGCCATCAGAGGG	2520
Oy	2492	CAGATTCACAGTGCACATGCGACAGGGGATCCCGAGAGGGCCCATCTCTCCACGCTGCTGTC	2551
Db	2521	CAGATTCACAGTGCACATGCGACAGGGGATCCCGAGAGGGCCCATCTCTCCACGCTGCTGTC	2580
Oy	2552	CAGCGCTGCTACAGGAGCATGAGAGAAACAGTGTTTGGGGGATTTCCGCGGAGAGGGCT	2611
Db	2581	CAGCGCTGCTACAGGAGCATGAGAGAAACAGTGTTTGGGGGATTTCCGCGGAGAGGGCT	2640
Oy	2612	GCTCTCGCTTTGGTGGATGATTTCTTTGTTGGTACACTCACCTACCCACAGCGGAAAC	2671
Db	2641	GCTCTCGCTTTGGTGGATGATTTCTTTGTTGGTACACTCACCTACCCACAGCGGAAAC	2700
Oy	2672	CTTTCCTCAGAGACCTTGTCAGAGGTGCCCTGAGTATGCGTGGCTGGTGGTGAACCTTGGGAA	2731
Db	2701	CTTTCCTCAGAGACCTTGTCAGAGGTGCCCTGAGTATGCGTGGCTGGTGGTGAACCTTGGGAA	2760
Oy	2732	GACAGTGGTGAACCTTCCCTGTAGAAAGACAGAGGCCCTGAGGTGGACAGGCTTTTGTTCAGAT	2791
Db	2761	GACAGTGGTGAACCTTCCCTGTAGAAAGACAGAGGCCCTGAGGTGGACAGGCTTTTGTTCAGAT	2820
Oy	2792	GGCGGCGCCAGAGGCTATTCCTCCCTGTGGCGGAGCTGTGCTGTGATATCCCGAGCCCTGAGAGGT	2851

NAME/REV: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hprt"
/note= "human telomerase reverse
transcriptase (hprt) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-721-456-1
Query Match 99.1%; Score 3969; DB 6; Length 4015;
Best Local Similarity 99.1%; Pred. No. 3..9e-111;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;
QY 8 GCAGGCGTGCCTCTGCTGCGACAGTGGAGAGCCCTGGCCCCGACCCCGGAGATGCC 67
DB 1 GCAGGCGTGCCTCTGCTGCGACAGTGGAGAGCCCTGGCCCCGACCCCGGAGATGCC 60
QY 68 GCGGCTGCCCCGCTGCGAGAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 127
DB 61 GCGGCTGCCCCGCTGCGAGACCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 128 GCGGCTGCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187
DB 121 GCGGCTGCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 188 GCACCCGCGGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
DB 181 GCACCCGCGGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 248 AGCGCCGCGCCCGCCCGCCCGCTTCCGCAAGTCTCCTGCTGCTGCTGCTGCTGCTGCTGCT 307
DB 241 AGCGCCGCGCCCGCCCGCCCGCTTCCGCAAGTCTCCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 308 CCGAGTGTGCGAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
DB 301 CCGAGTGTGCGAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 368 GCTGCTGAGAGCGAGCG 427
DB 361 GCTGCTGAGAGCGAGCG 420
QY 428 CCTGCGCCAAACGGGTGACGACGACACTGCGGGGAGCGGGGCGTGGGGCTGCTGCTGCTGCT 487
DB 421 CCTGCGCCAAACGGGTGACGACGACACTGCGGGGAGCGGGGCGTGGGGCTGCTGCTGCTGCT 480
QY 488 CCGGCTGGGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
DB 481 CCGGCTGGGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 548 GCGTCCGACGCTGGGCTTACCAAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
DB 541 GCGTCCGACGCTGGGCTTACCAAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 608 TCGAGCCCGCGCCCGCGCACACGCTAGTGAACCCCGAAGGCGTCTGGAGTGGAGAGCGGCG 667
DB 601 TCGAGCCCGCGCCCGCGCACACGCTAGTGAACCCCGAAGGCGTCTGGAGTGGAGAGCGGCG 660
QY 668 CTGGAACCATAGCGTCAGGAGAGCGGGGCTCCCTTGGGCTTCCAGCCCGCGGGTGGAG 727
DB 661 CTGGAACCATAGCGTCAGGAGAGCGGGGCTCCCTTGGGCTTCCAGCCCGCGGGTGGAG 720
QY 728 GAGGCGCGGCGGAGTGTGCGAGCGGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 787
DB 721 GAGGCGCGGCGGAGTGTGCGAGCGGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 788 TCGCCCTAGCGCGGAGCGACCGCTTGGGAGAGGCTCTGCGGCCCAACCGGGGAGAGAC 847
DB 781 TCGCCCTAGCGCGGAGCGACCGCTTGGGAGAGGCTCTGCGGCCCAACCGGGGAGAGAC 840
QY 848 GCGTGGAGCGAGTGAAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 907
DB 841 GCGTGGAGCGAGTGAAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900

QY 908 CACCTCTTTTGAAGGCTGCGCTCTGTGGACGCGCACCTCCACCCATCCGTGGGCGCGCA 967
DB 901 CACCTCTTTTGAAGGCTGCGCTCTGTGGACGCGCACCTCCACCCATCCGTGGGCGCGCA 960
QY 968 GCACACGCGGCGGCGCCCGCCATCCATCCATCCGCGCGCACGATGCCCTGGGACAGCGCTGTCC 1027
DB 961 GCACACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1020
QY 1028 CCGGCTGTACGCGGAGGACGACACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1087
DB 1021 CCGGCTGTACGCGGAGGACGACACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
QY 1088 GCGCT 1147
DB 1081 GCGCT 1140
QY 1148 GACCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1207
DB 1141 GACCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1208 GCGCCAGCGCTACTGCGCAATGCGCGCCCTGTTTCTGAGCTGCTTGGGAAACACGCGCA 1267
DB 1201 GCGCCAGCGCTACTGCGCAATGCGCGCCCTGTTTCTGAGCTGCTTGGGAAACACGCGCA 1260
QY 1268 GTGCGCCCTACGCGGCTCTCTCTCAAGAGCGCACTGCGCTGCGAGCTGCGGTCAACCCAGC 1327
DB 1261 GTGCGCCCTACGCGGCTCTCTCTCAAGAGCGCACTGCGCTGCGAGCTGCGGTCAACCCAGC 1320
QY 1328 AGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1387
DB 1321 AGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
QY 1388 CACAGAGCCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1447
DB 1381 CACAGAGCCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1448 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1507
DB 1441 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
QY 1508 CAAGAGAGCGCGCTTCTCTAGAGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCGCAA 1567
DB 1501 CAAGAGAGCGCGCTTCTCTAGAGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCGCAA 1560
QY 1568 GCTGCTGCTGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1627
DB 1561 GCTGCTGCTGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1628 GAGCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1687
DB 1621 GAGCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY 1688 CAACTTCTCTCACTGCTGATGATGTGTACGTGCTGAGCTGCTCAAGTCTCTCTCTCTCT 1747
DB 1681 CAACTTCTCTCACTGCTGATGATGTGTACGTGCTGAGCTGCTCAAGTCTCTCTCTCTCTCT 1740
QY 1748 TGTACGAGAGCACCTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGAG 1807
DB 1741 TGTACGAGAGCACCTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGAG 1800
QY 1808 CAACTTCAAAAGCATTTGAGATGACAGACCTTGAAGAGGCTGCGAGCTGCGGGAGCTGTC 1867
DB 1801 CAACTTCAAAAGCATTTGAGATGACAGACCTTGAAGAGGCTGCGAGCTGCGGGAGCTGTC 1860
QY 1868 GGAAGAGAGAGTGAAGCAGCATGCGGAAAGCGAGGCGCGCTGCTGAGCTGCGAGCTGCG 1927
DB 1861 GGAAGAGAGAGTGAAGCAGCATGCGGAAAGCGAGGCGCGCTGCTGAGCTGCGAGCTGCG 1920
QY 1928 CTTGATCCCAAGCTGAGAGGCTGCGGCGGATTTGGAACATGAGCATGAGCTGCGGGAGC 1987
DB 1921 CTTGATCCCAAGCTGAGAGGCTGCGGCGGATTTGGAACATGAGCATGAGCTGCGGGAGC 1980
QY 1988 CAGAAGCTTCCGAGAGAAAGAGGCGCGAGCTTCACTGAGAGGTGAAGGACACTGTT 2047


```

? PRIOR APPLICATION NUMBER: 60/241,755
? PRIOR FILING DATE: 2000-10-20
? PRIOR APPLICATION NUMBER: 60/237,768
? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: fastseq for Windows Version 4.0
? SEQ ID NO 455
? LENGTH: 4015
? TYPE: DNA
? ORGANISM: Human
? US-09-949-016-455

```

Query Match	Similarity	Score	DB	Length
Best Local Similarity	99.1%	3969	7	4015
Best Local Similarity	99.1%	Pred. No. 3.9e-11		
Matches	3979	Conservative	0	Mismatches
			0	Indels
			36	Gaps
QY	8	GCAGCGCTGCTCCCTGCTGCGCAGTGGGAAGCCCTGCCCCGGGACACCCCGGGAGTGC	67	
Db	1	GCAGCGCTGCTCCCTGCTGCGCAGTGGGAAGCCCTGCCCCGGGACACCCCGGGAGTGC	60	
QY	68	GGGCGCTCCCGCTGCGGAGACCGTGGCTCCCTGCTGCGCAGTCACTACCGGAGAGTCT	127	
Db	61	GGGCGCTCCCGCTGCGGAGACCGTGGCTCCCTGCTGCGCAGTCACTACCGGAGAGTCT	120	
QY	128	GCCCTGCGCAGTTCGTGTGCGGCGCTGGGGCCCAAGGCTGGCGGCTGTGTCAAGCGGG	187	
Db	121	GCGCGTGGCAGTTCGTGTGCGGCGCTGGGGCCCAAGGCTGGCGGCTGTGTCAAGCGGG	180	
QY	188	GGACCCGCGCGCTTTCGCGCGCTGGTGGCCCAAGTGCCTGTGTGCTGCTCCCTGGGAGCG	247	
Db	181	GGACCCGCGCGCTTTCGCGCGCTGGTGGCCCAAGTGCCTGTGTGCTGCTCCCTGGGAGCG	240	
QY	248	ACGGCGCGCCCGCGCCGCCCTCTCTTCGCGAGGTGTCTGCTGATAGAGACTGTGTGC	307	
Db	241	ACGGCGCGCCCGCGCCGCCCTCTCTTCGCGAGGTGTCTGCTGATAGAGACTGTGTGC	300	
QY	308	CCGAGTGTGTGACAGAGCTGTGTGACGAGCGGCGGCAAGAAAGTCTGCTTGCTTGCTGCG	367	
Db	301	CCGAGTGTGTGACAGAGCTGTGTGACGAGCGGCGGCAAGAAAGTCTGCTTGCTTGCTGCG	360	
QY	368	GGTGTGTGACGAGGAGCGCGGGGGGGCCCCCGGAGGCGCTTACACAGCAGGTGTGAGCTA	427	
Db	361	GGTGTGTGACGAGGAGCGCGGGGGGGCCCCCGGAGGCGCTTACACAGCAGGTGTGAGCTA	420	
QY	428	CCGTGCGCAACAGGTGTGTGACGAGCAGTGTGGGGGAGAGGGGGCTGTGTGTCTGTGCG	487	
Db	421	CCGTGCGCAACAGGTGTGTGACGAGCAGTGTGGGGGAGAGGGGGCTGTGTGTCTGTGCG	480	
QY	488	CCGCGTGGGCGAGAGCTGTGTGCTTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	547	
Db	481	CCGCGTGGGCGAGAGCTGTGTGCTTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	540	
QY	548	GGCTTCCAGCTGCGCTTACCAAGTGTGTGGGGCGCGCTGTACACACTGGGCGTGCAC	607	
Db	541	GGCTTCCAGCTGCGCTTACCAAGTGTGTGGGGCGCGCTGTACACACTGGGCGTGCAC	600	
QY	608	TCAGAGCCCGGCGCCCGCGACACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	667	
Db	601	TCAGAGCCCGGCGCCCGCGACACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	660	
QY	668	CTGGAACCATGTAGCTGT	727	
Db	661	CTGGAACCATGTAGCTGT	720	
QY	728	GAGGGGGGGGGGGGAGT	787	
Db	721	GAGGGGGGGGGGGGAGT	780	
QY	788	TGCGCTTGAAGCGGAGCGGAGCGCGCTTGTGGGAGGGGTCTGTGGGCCACCGGGGAGAG	847	
Db	781	TGCGCTTGAAGCGGAGCGGAGCGCGCTTGTGGGAGGGGTCTGTGGGCCACCGGGGAGAG	840	

Qy	848	GGTGGACACGAGTACACGGCTTTCTGTGTGTGACACGTCCACACCCCGCCAAAC	907
Db	841	GGTGGACGAGTACACGGCTTTCTGTGTGTGACACGTCCACACCCCGCCAAAC	900
Qy	908	CACCTTTTGGAGGGGGGCTCTGTGTGTGACACGGCTCCACACCCCGCCGCA	967
Db	901	CACCTTTTGGAGGGGGGCTCTGTGTGTGACACGGCTCCACACCCCGCCGCA	960
Qy	968	GCACACGCGGGGCCCCCATTCACATCTGGGGCACACGTCCTGGGACACGCTTGTCC	1027
Db	961	GCACACGCGGGGCCCCCATTCACATCTGGGGCACACGTCCTGGGACACGCTTGTCC	1020
Qy	1028	CCCGGTGTACGCCGAGACCAAGCACTTCTTACTCTCCAGCGACAGAGGACGTGCG	1087
Db	1021	CCCGGTGTACGCCGAGACCAAGCACTTCTTACTCTCCAGCGACAGAGGACGTGCG	1080
Qy	1088	GGCCCTCTTCTTACTTACTCTCTGTGAGGGCCAGCCTTACATGGGGCTTCGAGGCTCTGTGA	1147
Db	1081	GGCCCTCTTCTTACTTACTTACTCTGTGAGGGCCAGCCTTACATGGGGGGCTCTGTGA	1140
Qy	1148	GACCATCTTCTTGTGGTTTCCAGGCCCCGTGGATGCGACAGGACATCCCGCAGTGTGGCCGCT	1207
Db	1141	GACCATCTTCTTGTGGTTTCCAGGCCCCGTGGATGCGACAGGACATCCCGCAGTGTGGCCGCT	1200
Qy	1208	GGCCACGCGTACTGTGCAAAATGCGGGCCCTGTTTCTGTGACATGTCTTGGGAAACACCGCA	1267
Db	1201	GGCCACGCGTACTGTGCAAAATGCGGGCCCTGTTTCTGTGACATGTCTTGGGAAACACCGCA	1260
Qy	1268	GTGGCCCCACAGGGGGGTGTCCTCAAGACGACATCGCCCTGTGACGCTGGGTCACCCGAC	1327
Db	1261	GTGGCCCCACAGGGGGGTGTCCTCAAGACGACATCGCCCTGTGACGCTGGGTCACCCGAC	1320
Qy	1328	ACCGGGGTGTGTGGCCCGGGAGAAAGCCCCAGGGGCTGTGGGGGGCCCCGAGGAGGAGA	1387
Db	1321	ACCGGGGTGTGTGGCCCGGGAGAAAGCCCCAGGGGCTGTGGGGGGCCCCGAGGAGGAGA	1380
Qy	1388	CACACACCCCCGTGGCTGTGGTACGCTGTCCGGACACAGACGCTTGGAGGTGTGA	1447
Db	1381	CACACACCCCCGTGGCTGTGGTACGCTGTCCGGACACAGACGCTTGGAGGTGTGA	1440
Qy	1448	CGGCTTGTGTGGGGGCTGTGCTGGCGCGGCTGGTGTGCCCCAGGCTCTTGGGGCTTCAGGCA	1507
Db	1441	CGGCTTGTGTGGGGGCTGTGCTGGCGCGGCTGGTGTGCCCCAGGCTCTTGGGGCTTCAGGCA	1500
Qy	1508	CACAGAACGCGGCTTCTCTCAGGAACACACAGAAAGTTATCTCCCTGGGGAAGCATGCNA	1567
Db	1501	CACAGAACGCGGCTTCTCTCAGGAACACACAGAAAGTTATCTCCCTGGGGAAGCATGCNA	1560
Qy	1568	GCTCTCGCTCAGAGACGTGAGTGAAGATGAGCGTGGGATCTCGCTTGGTCGGCAG	1627
Db	1561	GCTCTCGCTCAGAGACGTGAGTGAAGATGAGCGTGGGATCTCGCTTGGTCGGCAG	1620
Qy	1628	GAGCCACAGGGGTGTGCTGTGTCCGGCCCAAGACACGTCGTCGAGAGGAGATCTGGC	1687
Db	1621	GAGCCACAGGGGTGTGCTGTGTCCGGCCCAAGACACGTCGTCGAGAGGAGATCTGGC	1680
Qy	1688	CAGTGTCTCATGTGCTGATGATGTGTACGTGTGACATGTCTCAGTCTTCTTTTGA	1747
Db	1681	CAGTGTCTCATGTGCTGATGATGTGTACGTGTGACATGTCTCAGTCTTCTTTTGA	1740
Qy	1748	TGTACGAGAACACGTTTTCAAAAGAAAGGCTTTTTTCTACCGAAGATGTGTGAG	1807
Db	1741	TGTACGAGAACACGTTTTCAAAAGAAAGGCTTTTTTCTACCGAAGATGTGTGAG	1800
Qy	1808	CAGGTCCAAAGATTTGAAATACAGACAGCATTTGAAGAGGTGTCAAGTCGGACGTTC	1867
Db	1801	CAGGTCCAAAGATTTGAAATACAGACCATTTGAAGAGGTGTCAAGTCGGAGCTGTTC	1860
Qy	1868	GGAGCAGAGGTCAGGCACATGTGGAGGCCAGGCCCTGTCTGACATCTCAAGTCTCG	1927
Db	1861	GGAGCAGAGGTCAGGCACATGTGGAGGCCAGGCCCTGTCTGACATCTCAAGTCTCG	1920

Thu Apr 17 08:21:57 2003

us-09-424-686b-1del.rnpn

Page 21

Oy	3812	ACGTGAGACCCCGAAGAAAGACCCCTGGAGACCTTGGGAAATGAGATGACCAAGGCTG	3873
Db	3841	AGGTGAGACCCCGAAGAAAGACCCCTGGAGACCTTGGGAAATGAGATGACCAAGGCTG	3900
Oy	3872	CCCTGTACACAGCCGAGGACCCCTGACACCTGATGATGGGGTCCCTGTGGCTCAATGGGG	3933
Db	3901	CCCTGTACACAGCCGAGGACCCCTGACACCTGATGATGGGGTCCCTGTGGCTCAATGGGG	3966
Oy	3932	GAGGTGCTGTGGGAGTAATAATCTGATATATGAGCTTTTCACTTTTGAAAAAA	3986
Db	3961	GAGGTGCTGTGGGAGTAATAATCTGATATATGAGCTTTTCACTTTTGAAAAAA	4015

```

RESULT 10
US-10-208-243-1
Sequence 1, Application US/10208243
GENERAL INFORMATION:
APPLICANT: Gaeta, Federico A.
APPLICANT: Geron Corporation
TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
FILE REFERENCE: 015389-003500PC
CURRENT FILING DATE: 2002-07-30
PRIORITY APPLICATION NUMBER: US/10/208,243
PRIORITY FILING DATE: 2000-09-28
PRIORITY APPLICATION NUMBER: US 60/112,006
PRIORITY FILING DATE: 1998-03-31
PRIORITY APPLICATION NUMBER: WO PCT/US99/06898
PRIORITY FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (36)..(3454)
OTHER INFORMATION: human telomerase reverse transcriptase (hTRT)
US-10-208-243-1

```

	Query Match Similarity	99.1% Best local similarity	Score 3969	DB 9	Length 4015
	Matches 3979	Conservative	0	Mismatches	0
				Indels	36
				Gaps	1
QY	8	GCAGGCGTGGCTGCTGCTGGCGACGTTGGAGAACCTTGAGCCCGGACACCCCGGAGATGC	67		
Db	1	GACGCGCTGCTGCTGCTGCTGGCGACGTTGGAGAACCTTGAGCCCGGACACCCCGGAGATGC	60		
QY	68	GCGCGCTCCCGGCTGCGGACCGCTGCGCTCCCTGCTGGGACGACCTACCGGAGTGTCT	127		
Db	61	GCGCGCTCCCGGCTGCGGACCGCTGCGCTCCCTGCTGGGACGACCTACCGGAGTGTCT	120		
QY	128	GCGCGTGGCGACGTTGCGTGGCGGCGCGCTGGGGCCCGAGGCGTGGCGGCTGTTGACAGCGG	187		
Db	121	GCGCGTGGCGACGTTGCGTGGCGGCGCGCTGGGGCCCGAGGCGTGGCGGCTGTTGACAGCGG	180		
QY	188	GGACCGCGGAGCTTTCGCGCGCTGCTGGTGCCGACGTGCTGGTGGTGCTCCCTGGGAGCG	247		
Db	181	GGACCGCGGAGCTTTCGCGCGCTGCTGGTGCCGACGTGCTGGTGGTGCTCCCTGGGAGCG	240		
QY	248	ACGGCGCGCCCGCGCCGCCCTCTCTTCGCGGAGTGTCGCGCTGAAGAGTCTGTGGCG	307		
Db	241	ACGGCGCGCCCGCGCCGCCCTCTCTTCGCGGAGTGTCGCGCTGAAGAGTCTGTGGCG	300		
QY	308	CCGAGTGTGCGAGAGGTGTGGCGAGGGGGGGCGGAGAAAGCTGCTGGCTTGGGTTGGC	367		
Db	301	CCGAGTGTGCGAGAGGTGTGGCGAGGGGGGGCGGAGAAAGCTGCTTGGGTTGGC	360		
QY	368	GCTGCTGGACGGGGCGCGCGGGGGCCCGCGGAGGCTTTCACCAACGAGCTGCGACGTCA	427		

[illegible]

Db	3661	GAGTGTCCACACACCTGCGCTTCACCTTCCCAACAGCGTGCGCGTCCACCCCA	3720
Qy	3692	GGGCGAGCTTTTCTCTACACAGAGACCGGCTTCACACGCCACATAGAAATAGTCATCC	3751
Db	3721	GGGCGAGCTTTTCTCTACACAGAGACCGGCTTCACACGCCACATAGAAATAGTCATCC	3780
Qy	3752	CCAGATTCGGCATTGTTCACCCCTCGCCCTCGCCCTCTTGTGCTTCACCCCAACATCC	3811
Db	3781	CCAGATTCGGCATTGTTCACCCCTCGCCCTCGCCCTCTTGTGCTTCACCCCAACATCC	3840
Qy	3812	ACGTGAGACCCCTGAGAAAGACCCCTGGAGCTCTGGAAATTTTGGAAATGACCAAGCTGTG	3871
Db	3841	ACGTGAGACCCCTGAGAAAGACCCCTGGAGCTCTGGAAATTTTGGAAATGACCAAGCTGTG	3900
Qy	3872	CCCTGTACACAGGACGAGACCTCTGCACCTGTGATGGGGGCTCCCTGTGGGTCAATTAATGGGG	3931
Db	3901	CCCTGTACACAGGACGAGACCTCTGCACCTGTGATGGGGGCTCCCTGTGGGTCAATTAATGGGG	3960
Qy	3932	GAGGTCTCTGTGGAGTAAATTACTGAATATAGTATTTTTCAGTTTGTGAAAAAA	3986
Db	3961	GAGGTCTCTGTGGAGTAAATTACTGAATATAGTATTTTTCAGTTTGTGAAAAAA	4015

RESULT 11
 US-10-325-810-1
 : Sequence 1, Application US/10325810
 GENERAL INFORMATION:
 APPLICANT: Cecch, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 633
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/325, 810
 FILING DATE: 20-Dec-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/402,181
 FILING DATE: 29-Sep-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 23-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17885

[illegible]

QY	668	CTGAAACCATATACGCTCAGAGGAGCCGGGGTCCCTCTGGGCTTGCACGCTCCGGGTGAG	727
Db	661	CTTGGAACCATATACGCTCAGAGGAGCCGGGGTCCCTCTGGGCTTGCACGCTCCGGGTGAG	720
QY	728	GAGGCGGGGGGCAATGTCACGCGAAGTCGCTTCCCAAGAGGCCACAGGGTGGGGC	787
Db	721	GAGGCGGGGGGCAATGTCACGCGAAGTCGCTTCCCAAGAGGCCACAGGGTGGGGC	780
QY	788	TGCCTCTGAGCCGAGCGAGCGAGCCCGTGGGGCAGGGGTCTGGAGCCACCCGGGAGAGC	847
Db	781	TGCCTCTGAGCCGAGCGAGCGAGCCCGTGGGGCAGGGGTCTGGAGCCACCCGGGAGAGC	840
QY	848	CGGTGAGCCAGATGACCTGGTTTCTGTGTGTGTCTACCTGGCAGACCCGCGAAGAGC	907
Db	841	CGGTGAGCCAGATGACCTGGTTTCTGTGTGTGTCTACCTGGCAGACCCGCGAAGAGC	900
QY	908	CACCTCTTTGAGAGGGTGGGGCTCTGTGGCAGCGGCATCTCCACCCATCCGTGGGCGCCA	967
Db	901	CACCTCTTTGAGAGGGTGGGGCTCTGTGGCAGCGGCATCTCCACCCATCCGTGGGCGCCA	960
QY	968	GCACACAGCGGGGCCCCCATCATGCGGGCACACGTCCTGGGAGACCGGCTTGTGC	102
Db	961	GCACACAGCGGGGCCCCCATCATGCGGGCACACGTCCTGGGAGACCGGCTTGTGC	102
QY	1028	CCCGGTGTAGCCGCGAGACCAAGCACTTCTCTACTCTCTAGGGAGACAGGAGCAGCTGG	108
Db	1021	CCCGGTGTAGCCGCGAGACCAAGCACTTCTCTACTCTCTAGGGAGACAGGAGCAGCTGG	108
QY	1088	GCCCTCTTCTCTACTCAGAGCTCTGAGGGCCAGCGCTGACCTGAGGGGTCTGTGGA	1144
Db	1081	GCCCTCTTCTCTACTCAGAGCTCTGAGGGCCAGCGCTGACCTGAGGGGTCTGTGGA	1144
QY	1148	GACCATCTTTCTGGGTTTCAGAGCCCTGATGAGCCAGGAGACTCCCGAGGTGGCCCGGCT	120
Db	1141	GACCATCTTTCTGGGTTTCAGAGCCCTGATGAGCCAGGAGACTCCCGAGGTGGCCCGGCT	120
QY	1208	GCCCCAGCGCTACTGAGCAATGGGGCCCTGTGTTCTGTGAGACTGCTTGGGAACCAAGCGCA	126
Db	1201	GCCCCAGCGCTACTGAGCAATGGGGCCCTGTGTTCTGTGAGACTGCTTGGGAACCAAGCGCA	126
QY	1268	GTGGCCCTTAGGGGGTGGCTCCAGAGAGCACTCCGCTGGGAGCTGGGGTCAACCCAGC	132
Db	1261	GTGGCCCTTAGGGGGTGGCTCCAGAGAGCACTCCGCTGGGAGCTGGGGTCAACCCAGC	132
QY	1328	AGCCGCTGTCTGTCCCGGGGAGAAAGCCCAAGGCTCTGTGGCGGCCCGGAGAGAGAGA	138
Db	1321	AGCCGCTGTCTGTCCCGGGGAGAAAGCCCAAGGCTCTGTGGCGGCCCGGAGAGAGAGA	138
QY	1388	CACAGACCCCGCGTGCCTGGTGACAGTGTCTCGCCACAGCACAGCAAGCCCTGTGCAGGTGA	144
Db	1381	CACAGACCCCGCGTGCCTGGTGACAGTGTCTCGCCACAGCACAGCAAGCCCTGTGCAGGTGA	144
QY	1448	CGGGTGTGTGGGGGCTGGCTCGGGCGGGCGGGTGGGGCCCAAGGCTTGGGGTCCAGAGCA	150
Db	1441	CGGGTGTGTGGGGGCTGGCTCGGGCGGGCGGGTGGGGCCCAAGGCTTGGGGTCCAGAGCA	150
QY	1508	CAACGAAGCGCGCTTCTCTCAGAGAAACACAAGAGTTTATCTCCCTGGGGAACATGAGCA	156
Db	1501	CAACGAAGCGCGCTTCTCTCAGAGAAACACAAGAGTTTATCTCCCTGGGGAACATGAGCA	156
QY	1568	GCTCTCGCTGCAAGAGCTGACGCTGTGGAAGATGACCGTGGCGGAGCTGGCTTGGCTCGGCA	162
Db	1561	GCTCTCGCTGCAAGAGCTGACGCTGTGGAAGATGACCGTGGCGGAGCTGGCTTGGCTCGGCA	162
QY	1628	GAGCCCAAGGGGTTGGCTGTCTCCGGGCGGAGAGCAAGCTGTGGGAGAGAAATCTGTGC	168
Db	1621	GAGCCCAAGGGGTTGGCTGTCTCCGGGCGGAGAGCAAGCTGTGGGAGAGAAATCTGTGC	168
QY	1688	CAAGTTCTCTGACACTGTGATGTGATGTGTACGTCGTCGAGAGCTCAGTCTTTCTTTTA	174
Db	1681	CAAGTTCTCTGACACTGTGATGTGATGTGTACGTCGTCGAGAGCTCAGTCTTTCTTTTA	174
QY	1748	TGTACAGGAGACACGTTTCAAAAGAACAGGCTCTTTTCTTACCGGAGAGAGTGTCTGAG	180

Db	1741	TCATCAGGAGACACAGTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAAGAGTGTGAG	1800
Qy	1808	CAAGTTGCAAGACATGGAAATCACAACAGCACTTGAAGAGGTGCACCTGGGAGCTGC	1867
Db	1801	CAAGTTGCAAGACATGGAAATCACAACAGCACTTGAAGAGGTGCACCTGGGAGCTGC	1866
Qy	1868	GGAAACAGAGGTCAAGGCGAGCTGCGGAAGACAGGCGCGCTCTGACGTCCAGACTCCG	1927
Db	1861	GGAAACAGAGGTCAAGGCGAGCTGCGGAAGACAGGCGCGCTCTGACGTCCAGACTCCG	1926
Qy	1928	CTTCATCCCCAAGCCCTGACGGGCTGCGGCGGATTTGTGAACATGAGTACGTGTGGAGC	1987
Db	1921	CTTCATCCCCAAGCCCTGACGGGCTGCGGCGGATTTGTGAACATGAGTACGTGTGGAGC	1986
Qy	1988	CAGAACGTTCCCGCAGAGAAAAAGAGGCGCAGCGCTCTCACTCGAGGCTGAAGCACTGTT	2047
Db	1981	CAGAACGTTCCCGCAGAGAAAAAGAGGCGCAGCGCTCTCACTCGAGGCTGAAGCACTGTT	2046
Qy	2048	CAGCGTGTCAACTACGAGCGGGGCGGGGCGCCCGGCTCTGTGGGGCGCTGTGTGTGG	2107
Db	2041	CAGCGTGTCAACTACGAGCGGGGCGGGGCGCCCGGCTCTGTGGGGCGCTGTGTGTGG	2106
Qy	2108	CCTGACAGATATCCACAGAGGCGTGGCCACCTTCGTCTGTGCTGCTGCGGGCCAGAGACC	2167
Db	2101	CCTGACAGATATCCACAGAGGCGTGGCCACCTTCGTCTGTGCTGCTGCGGGCCAGAGACC	2166
Qy	2168	GCCGCTACGCTGA-----CATCCCCA	2199
Db	2161	GCCGCTACGCTGA-----CATCCCCA	2220
Qy	2192	GGACAGGCTCAAGAGGTCATCGCACATCATCAAAACCCAGAACAGCTACGTGGGTGG	2255
Db	2221	GGACAGGCTCAAGAGGTCATCGCACATCATCAAAACCCAGAACAGCTACGTGGGTGG	2288
Qy	2252	TCGGTATGCGCTGGTCCAGAAAGGCGGCCATGSGGCACTGCCAGAGCCCTTCAAGAGCA	2311
Db	2281	TCGGTATGCGCTGGTCCAGAAAGGCGGCCATGSGGCACTGCCAGAGCCCTTCAAGAGCA	2340
Qy	2312	CGTCTACTCTTGAACAGACCTCCAGCGCGTACATGCAACAGTGTGTCACCTCGACAGA	2377
Db	2341	CGTCTACTCTTGAACAGACCTCCAGCGCGTACATGCAACAGTGTGTCACCTCGACAGA	2400
Qy	2372	GACCAGCGCGGTGAGGGATGCGCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG	2433
Db	2401	GACCAGCGCGGTGAGGGATGCGCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG	2466
Qy	2432	CAGTGGCCCTTCGACGCTCTTCCTACGCTTCATGTGCCACACGCGCTGCGCATAGGGG	2499
Db	2461	CAGTGGCCCTTCGACGCTCTTCCTACGCTTCATGTGCCACACGCGCTGCGCATAGGGG	2522
Qy	2492	CAAGTCTACGTCAGTGCAGTGCAGAGGGGATCCGCGAGGGCTCCATCTCTCTCAGCGTCTG	2555
Db	2521	CAAGTCTACGTCAGTGCAGTGCAGAGGGGATCCGCGAGGGCTCCATCTCTCTCAGCGTCTG	2588
Qy	2552	CAGCGTGTGCTACGCGCAACATGGAAGAAAGCTGTTGCGGGGAAATTCGCGGAGGCGCT	2611
Db	2581	CAGCGTGTGCTACGCGCAACATGGAAGAAAGCTGTTGCGGGGAAATTCGCGGAGGCGCT	2640
Qy	2612	GCTCCTGCGTTGGTGGATGATTTCTTGTGTGACACCTCACTCAACCAGCGAANAAC	2671
Db	2641	GCTCCTGCGTTGGTGGATGATTTCTTGTGTGACACCTCACTCAACCAGCGAANAAC	2700
Qy	2672	CTTCCTCAGAACCTCGTCCGAGAGTCCCTCGAGTATGAGCTCGGTGGAACCTTCCGAA	2731
Db	2701	CTTCCTCAGAACCTCGTCCGAGAGTCCCTCGAGTATGAGCTCGGTGGAACCTTCCGAA	2760
Qy	2732	GACAGTGTGAACCTCCCTCTAGAAACAGAGCGCCGTGGGTGCACAGGCTTTTGTTCAGAT	2791
Db	2761	GACAGTGTGAACCTCCCTCTAGAAACAGAGCGCCGTGGGTGCACAGGCTTTTGTTCAGAT	2820
Qy	2792	GCGGCGCACAGGCGCTATTTCCCTGCGGTGCGGCGCTGCTGATACCGGAGCCTTGAGCT	2851

Db 2821 GCCGCCCCACGGCCTATTCCTGCTGCGGCTGCTGCTGATACCCGGAGCCCTGGAGT 2880
Qy 2852 GCAGAGCGACTACTCCAGCTATGCTCCGAGCTCCTCAGAGCAGCTGCTGACCTTAACCG 2911
Db 2881 GACAGCGGCTACTCTCCAGCTATGCTCCGAGCTCCTCAGAGCAGCTGCTGACCTTAACCG 2940
Qy 2912 CGGCTTCAAGGCTGGAGGAGCAATGCTGCGCAACTCTTTGGGCTCTGCGGCTAGAGT 2971
Db 2941 CGGCTTCAAGGCTGGAGGAGCAATGCTGCGCAACTCTTTGGGCTCTGCGGCTAGAGT 3000
Qy 2972 TCACAGCCTGTTTCTGATTTGAGAGTGAACAGCTCCAGAGGCTGAGCAACATCTA 3031
Db 3001 TCACAGCCTGTTTCTGATTTGAGAGTGAACAGCTCCAGAGGCTGAGCAACATCTA 3060
Qy 3032 CAGATCTCCCTGCTGCGAGGCTGACAGGTTTCAAGCTGATGCTGCTGAGCTCCATTTCA 3091
Db 3061 CAGATCTCCCTGCTGCGAGGCTGACAGGTTTCAAGCTGATGCTGCTGAGCTCCATTTCA 3120
Qy 3092 TCAGCAAGTTTGGAGAAACCCACATTTTCTGCGGCTGCTGCTGAGAGGCTGCTGCT 3151
Db 3121 TCAGCAAGTTTGGAGAAACCCACATTTTCTGCGGCTGCTGCTGAGAGGCTGCTGCT 3180
Qy 3152 CTGCTACTCTGCTGAGAAACCCAGAAACCCAGAGATGCTGCTGAGAGGCTGCTGCTGCT 3211
Db 3181 CTGCTACTCTGCTGAGAAACCCAGAAACCCAGAGATGCTGCTGAGAGGCTGCTGCTGCT 3240
Qy 3212 CGGCTCTGCTGCTGCGAGGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3271
Db 3241 CGGCTCTGCTGCTGCGAGGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
Qy 3272 GACTGACACCGCTGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3331
Db 3301 GACTGACACCGCTGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
Qy 3332 GCTGAGTCCGAAAGCTCCCGGGGAGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3391
Db 3361 GCTGAGTCCGAAAGCTCCCGGGGAGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
Qy 3392 ACTGCCCTGAGCTTCAAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3451
Db 3421 ACTGCCCTGAGCTTCAAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
Qy 3452 GAGCAGACACCGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3511
Db 3481 GAGCAGACACCGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
Qy 3512 CACACCCAGGCGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3571
Db 3541 CACACCCAGGCGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
Qy 3572 CATGTCGGCTGAGAGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3631
Db 3601 CATGTCGGCTGAGAGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
Qy 3632 GAGTGTCCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3691
Db 3661 GAGTGTCCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
Qy 3692 GGGCCAGCTTCTCTCAACAGAGCCGGCTTCACTCCACATAGAAATAGTGCATCC 3751
Db 3721 GGGCCAGCTTCTCTCAACAGAGCCGGCTTCACTCCACATAGAAATAGTGCATCC 3780
Qy 3752 CCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3811
Db 3781 CCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
Qy 3812 AGGTGAGAGCCCTGAGAGAGCCCTGAGAGCTGCTGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 3871
Db 3841 AGGTGAGAGCCCTGAGAGAGCCCTGAGAGCTGCTGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 3900
Qy 3872 CCCTGTACACAGGAGAGCCCTGACCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 3931
Db 3901 CCCTGTACACAGGAGAGCCCTGACCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 3960

Qy 3932 GAGGTGCTGTGGAGTAAATCTGAATATATGAGTTTTCAGTTTGAAGAAAAA 3986
Db 3961 GAGGTGCTGTGGAGTAAATCTGAATATATGAGTTTTCAGTTTGAAGAAAAA 4015

RESULT 12
US-10-170-235-38656
; Sequence 38656, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPARING A MAJORITY OF HU
; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
; FILE REFERENCE: C1001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; NUMBER OF SEQ. ID NOS.: 42514
; SEQ. ID NO. 38656
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-38656

Query Match 99.08; Score 3967.4; DB 8; Length 4015;
Best Local Similarity 99.18; Pred. No. 4,4e-111;
Matches 3978; Conservative 0; Mismatches 1; Indels 36; Gaps 1;

Qy 8 GCAGGCT 67
Db 1 GCAGGCT 60
Qy 68 GCGGCTCTCCCGCTGCGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 127
Db 61 GCGGCTCTCCCGCTGCGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Qy 128 GCGGCTGCGACGTTGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCG 187
Db 121 GCGGCTGCGACGTTGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCG 180
Qy 188 GGAACCGGCGCTTCCGCGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCT 247
Db 181 GGAACCGGCGCTTCCGCGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCT 240
Qy 248 AGGCG 307
Db 241 AGGCG 300
Qy 308 CCGAGTGTGACAGAGCTGTGAGAGCGGCGCGAGAGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 367
Db 301 CCGAGTGTGACAGAGCTGTGAGAGCGGCGCGAGAGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Qy 368 GCTGTGAGAGGCG 427
Db 361 GCTGTGAGAGGCG 420
Qy 428 CCTGCGCAACAGGCTGACAGCAGCTGCGGCGAGCGGCGGCGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCT 487
Db 421 CCTGCGCAACAGGCTGACAGCAGCTGCGGCGAGCGGCGGCGGCGCTGCGGCGCTGCTGCTGCTGCTGCTGCT 480
Qy 488 CCGGCTGGGCGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
Db 481 CCGGCTGGGCGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Qy 548 GGGCTCCAGCTGCGCT 607
Db 541 GGGCTCCAGCTGCGCT 600
Qy 608 TCAGGCGCGGCG 667
Db 601 TCAGGCGCGGCG 660
Qy 668 CTGGAACCATAGCGCTGAGAGGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGGAG 727

QY 2852 GCAGAGCCACTACTCCAGCTATGCCCCGACCTCCATAGAGCCAGTCTACCTTCACCG 2911
DB 2881 GACAGACCACTACTAGCTATGCCCCGACCTCCATAGAGCCAGTCTACCTTCACCG 2940
QY 2912 CGGCTTCAGAGCTGGAGAGAACATGCTGCGCAACTCTTTGGGGTCTTTCGAGCTGAAGTG 2971
DB 2941 CGGCTTCAGAGCTGGAGAGAACATGCTGCGCAACTCTTTGGGGTCTTTCGAGCTGAAGTG 3000
QY 2972 TCACAGCCTGTTTCTGATTTGAGAGTGAACAGCTCCAGACGCTGTCACCAACATCTA 3031
DB 3001 TCACAGCCTGTTTCTGATTTGAGAGTGAACAGCTCCAGACGCTGTCACCAACATCTA 3060
QY 3032 CAAGATCTCTGCTGAGAGCTGACAGTTCACGATGTGTCTGCTCAGCTCCATTTCA 3091
DB 3061 CAAGATCTCTGCTGAGAGCTGACAGTTCACGATGTGTCTGCTCAGCTCCATTTCA 3120
QY 3092 TCAGCAGTGTGGAGAGAACCCCATTTTCTGCTGGGTATCTGACAGGCGCTGCT 3151
DB 3121 TCAGCAGTGTGGAGAGAACCCCATTTTCTGCTGGGTATCTGACAGGCGCTGCT 3180
QY 3152 CTGCTACTCTCTGCTGAGAGAACCCAGAGAGATGCTGCTGGGGCCAGAGGCGCTGCT 3211
DB 3181 CTGCTACTCTCTGCTGAGAGAACCCAGAGAGATGCTGCTGGGGCCAGAGGCGCTGCT 3240
QY 3212 CGGCTTCAGAGCTGGAGAGAACATGCTGCGCAACTCTTTGGGGTCTTTCGAGCTGAAGTG 3271
DB 3241 CGGCTTCAGAGCTGGAGAGAACATGCTGCGCAACTCTTTGGGGTCTTTCGAGCTGAAGTG 3300
QY 3272 GACCTGACACCGTGTCTACCTAGCTGACACTCTGCGGTCACTGAGAGACGCCAGAGCGCA 3331
DB 3301 GACCTGACACCGTGTCTACCTAGCTGACACTCTGCGGTCACTGAGAGACGCCAGAGCGCA 3360
QY 3332 GCTGAGTGGAGAGCTCCCGGGGAGAGAGCTGACTGCTGAGAGGCGCGAGCAACCCGCG 3391
DB 3361 GCTGAGTGGAGAGCTCCCGGGGAGAGAGCTGACTGCTGAGAGGCGCGAGCAACCCGCG 3420
QY 3392 ACTGCGCTCAACACTCTCAAGACATCTGAGAGTGAATGAGCGCAACCCGCGAGAGCGCGCA 3451
DB 3421 ACTGCGCTCAACACTCTCAAGACATCTGAGAGTGAATGAGCGCAACCCGCGAGAGCGCGCA 3480
QY 3452 GAGCAGACACAGAGCGCTGCTGAGAGCGGGCTGCTAGTCTCCAGAGAGAGAGAGCGCGCG 3511
DB 3481 GAGCAGACACAGAGCGCTGCTGAGAGCGGGCTGCTAGTCTCCAGAGAGAGAGAGCGCGCG 3540
QY 3512 CACACCCAGAGCGCGAGCGCTGAGAGTGAAGCTGAGTGTGTTTGCGAGAGCGCTG 3571
DB 3541 CACACCCAGAGCGCGAGCGCTGAGAGTGAAGCTGAGTGTGTTTGCGAGAGCGCTG 3600
QY 3572 CATGTCGGCTGAAGAGCTGAGTCTCGGCTGAGAGCTGAGAGTGTCCAGCCAGAGGCT 3631
DB 3601 CATGTCGGCTGAAGAGCTGAGTCTCGGCTGAGAGCTGAGAGTGTCCAGCCAGAGGCT 3660
QY 3632 GAGTGTCCAGACACCTGCGCTTCTACTTCCCAAGAGCTGCGCTCCAGCCCA 3691
DB 3661 GAGTGTCCAGACACCTGCGCTTCTACTTCCCAAGAGCTGCGCTCCAGCCCA 3720
QY 3692 GGGCAGGCTTTTCTCTACAGAGAGCGGCTTCCACTCCCAATAGAAATAGTCCATCC 3751
DB 3721 GGGCAGGCTTTTCTCTACAGAGAGCGGCTTCCACTCCCAATAGAAATAGTCCATCC 3780
QY 3752 CCAGATTCGCAATGTTCAACCTCGCTGCGCTGCTTGTGCTTCCAGCCCAACATCC 3811
DB 3781 CCAGATTCGCAATGTTCAACCTCGCTGCGCTGCTTGTGCTTCCAGCCCAACATCC 3840
QY 3812 AGGTGAGAACCTTGAAGAGACCTGAGAGCTGGAGATTTGAGATGAGCAAAAGTGTG 3871
DB 3841 AGGTGAGAACCTTGAAGAGACCTGAGAGCTGGAGATTTGAGATGAGCAAAAGTGTG 3900
QY 3872 CCTGTACACAGGAGAGAGACCTGAGACCTGAGATGGGGTCCCTGTGGGTCAATAGGGGG 3931
DB 3901 CCTGTACACAGGAGAGAGACCTGAGACCTGAGATGGGGTCCCTGTGGGTCAATAGGGGG 3960
QY 3932 GAGGTGCTGTGGAGTAATAATCTGAATATATGATTTTTCAGTTTGAAGAAAAA 3986

DB 3961 GAGGTGCTGTGGAGTAATAATCTGAATATATGATTTTTCAGTTTGAAGAAAAA 4015

RESULT 13
US-09-949-016-5841
; Sequence 5841, Application US/09949016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ. ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ. ID NO 5841
; LENGTH: 4016
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5841

Query Match 98.7%; Score 3954.2; DB 7; Length 4016;
Best Local Similarity 99.0%; Pred. No. 1.1e-110;
Matches 3976; Conservative 0; Mismatches 3; Indels 37; Gaps 2;

QY 8 GCAGAGCTGAGCTCTCTCTGACAGCTGAGAGAGCTGAGCGCCGCGACACCCCGAGAGCGC 67
DB 1 GCAGAGCTGAGCTCTCTCTGACAGCTGAGAGAGCTGAGCGCCGCGACACCCCGAGAGCGC 60
QY 68 GCGGCTGCGCGCGCGCGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 127
DB 61 GCGGCTGCGCGCGCGCGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 128 GCGGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187
DB 121 GCGGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 188 GAGCCGCGCGCGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
DB 181 GAGCCGCGCGCGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 248 ACGGCGCGCGCGCGCGCGCGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 307
DB 241 ACGGCGCGCGCGCGCGCGCGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 308 CCGAGTGTGAGAGAGCTGTGAGAGCGGAGCGAGAAAGTGTGAGAGAGTGTGAGAGAGTGTGAG 367
DB 301 CCGAGTGTGAGAGAGCTGTGAGAGCGGAGCGAGAAAGTGTGAGAGAGTGTGAGAGAGTGTGAG 360
QY 368 GCTGTGAGAGAGAGCGCGCGCGCGCGCGCGCGCTTTCACACACAGAGCTGTGAGAGAGTGTGAG 427
DB 361 GCTGTGAGAGAGAGCGCGCGCGCGCGCGCGCGCTTTCACACACAGAGCTGTGAGAGAGTGTGAG 420
QY 428 CCGTGTGAG 487
DB 421 CCGTGTGAG 480
QY 488 CCGGCTGAG 547
DB 481 CCGGCTGAG 540
QY 548 GAGTGTGAG 607
DB 541 GAGTGTGAG 600
QY 608 TCAGGCGCGCGCGCGCGCGCGAG 667

|||||
Db 601 TCAGGCCGCGCCCGCCACACGCTAGTGACCCCGAAGGGCTGGATCGCAACGGGC 660
QY 668 CTGGAACATATGCTCAGAGGAGGCGGGGGTCCCTGGGCTGGCAGCCCGGGTGGAG 727
Db 661 CTGGAACATATGCTCAGAGGAGGCGGGGGTCCCTGGGCTGGCAGCCCGGGTGGAG 720
QY 728 GAGCGGGGGGGGAGTGGCCAGCGAAGTCTGCGCTTGCCAAAGAGGCGCCAGTGGCGC 787
Db 721 GAGCGGGGGGGGAGTGGCCAGCGAAGTCTGCGCTTGCCAAAGAGGCGCCAGTGGCGC 780
QY 788 TGCCCCGAGCGGAGGAGGAGCCGTTGGGAGGGGCTGGGCGCCAGCCCGGGGAGAGC 847
Db 781 TGCCCCGAGCGGAGGAGGAGCCGTTGGGAGGGGCTGGGCGCCAGCCCGGGGAGAGC 840
QY 848 GCGTGAACCGAGTACCGTGTGTTCTGTGTGTGTCACCTCCAGACCCCGCGAAGAAC 907
Db 841 GCGTGAACCGAGTACCGTGTGTTCTGTGTGTGTCACCTCCAGACCCCGCGAAGAAC 900
QY 908 CACCTCTTTGGAGGGTGGCTCTGTGGCAGCGCCACTCCCAACCCATCCGTGGCGCCCA 967
Db 901 CACCTCTTTGGAGGGTGGCTCTGTGGCAGCGCCACTCCCAACCCATCCGTGGCGCCCA 960
QY 968 GCACACAGCGGGCGCCCGCATCCATCGCGGCGACAGGCTCGGAGAGCGCTGTGCC 1027
Db 961 GCACACAGCGGGCGCCCGCATCCATCGCGGCGACAGGCTCGGAGAGCGCTGTGCC 1020
QY 1028 CCCGGTGTACGCGAGAACCAACACATTCCTCTACTCTCAGGCGCAACAGAGACGCTGCG 1087
Db 1021 CCCGGTGTACGCGAGAACCAACACATTCCTCTACTCTCAGGCGCAACAGAGACGCTGCG 1080
QY 1088 GCCCTCTCTCTACTACTAGCTCTGTAGAGCCAGCGCTACTGCGCTCGGAGGCTGTGGA 1147
Db 1081 GCCCTCTCTCTCTACTACTAGCTCTGTAGAGCCAGCGCTACTGCGCTCGGAGGCTGTGGA 1140
QY 1148 GACCATCTTTCTGGGTTCCAGGCGCTGGATGCAAGGAGCTCCCGGAGAGTTGCCCGGCT 1207
Db 1141 GACCATCTTTCTGGGTTCCAGGCGCTGGATGCAAGGAGCTCCCGGAGAGTTGCCCGGCT 1200
QY 1208 GCCCAGCGCTACTGCAAAATGCGGCCCTTTTCTGTGAGCTGCTTGGGAACACAGCGCA 1267
Db 1201 GCCCAGCGCTACTGCAAAATGCGGCCCTTTTCTGTGAGCTGCTTGGGAACACAGCGCA 1260
QY 1268 GTGCCCTCTAGGGGGTGTCTCTCAAGAGGACACTGCCGCTGGAGAGTGGGGTCAACCCAGC 1327
Db 1261 GTGCCCTCTAGGGGGTGTCTCTCAAGAGGACACTGCCGCTGGAGAGTGGGGTCAACCCAGC 1320
QY 1328 AGCGGTTGTGTGTGCGCGGAGAAAGCCCAAGGGCTGTGTGGCGGCGCCGAGAGAGAGA 1387
Db 1321 AGCGGTTGTGTGTGCGCGGAGAAAGCCCAAGGGCTGTGTGGCGGCGCCGAGAGAGAGA 1380
QY 1388 CACAGACCCCGTGCCTGTGTGAGCTGTCGCCAGCAGCAGACAGCCCGTGGCAGGTGA 1447
Db 1381 CACAGACCCCGTGCCTGTGTGAGCTGTCGCCAGCAGCAGACAGCCCGTGGCAGGTGA 1440
QY 1448 CGGTTGTGTGGGGGCTGCGCCGCGCGGCTGTGTGGCGGCTCTGAGGCTCAAGGCA 1507
Db 1441 CGGTTGTGTGGGGGCTGCGCCGCGCGGCTGTGTGGCGGCTCTGAGGCTCAAGGCA 1500
QY 1508 CAAGGAACGCGCTTCTCTCAGAGAACCAACAAAGTTATCTCCCTGGGGAAGATGCCAA 1567
Db 1501 CAAGGAACGCGCTTCTCTCAGAGAACCAACAAAGTTATCTCCCTGGGGAAGATGCCAA 1560
QY 1568 GCTTCTGCTGAGAGGCTGAGCTGTGAAGATGAGCGTGGGAGATGCGCTTGGCTGGCAG 1627
Db 1561 GCTTCTGCTGAGAGGCTGAGCTGTGAAGATGAGCGTGGGAGATGCGCTTGGCTGGCAG 1620
QY 1628 GAGCCCAAGGGGTGGCTGTGTGTCGGCGCGCAGAGACCGTGTGGTGAAGATCTGGC 1687
Db 1621 GAGCCCAAGGGGTGGCTGTGTGTCGGCGCGCAGAGACCGTGTGGTGAAGATCTGGC 1680
QY 1688 CAAGTCTGCTGAGTGGGATGAGTGTAGTGTGAGTGTGCTCAGGTCTTTCTTTTA 1747
|||||

Db 1681 CAAGTCTGCTGAGTGGGATGAGTGTGTAGTGTGAGTGTGCTCAGGTCTTTCTTTTA 1740
QY 1748 TGTACGAGAGACCAAGTTTCAAAAGACAGGCTCTTTTCTACCGGAAGAGTGTGTGAG 1807
Db 1741 TGTACGAGAGACCAAGTTTCAAAAGACAGGCTCTTTTCTACCGGAAGAGTGTGTGAG 1800
QY 1808 CAAGTTGCAAAAGCATTTGATTCAGACAGCACTTGAAGGGTGCAGCTGGCGGAGCTGTG 1867
Db 1801 CAAGTTGCAAAAGCATTTGATTCAGACAGCACTTGAAGGGTGCAGCTGGCGGAGCTGTG 1860
QY 1868 GGAAGCAGAGGTCAGGCGAGCATTCGAGGAAGCGAGGCGCCGCTGTGTGAGTGTGAGCTGCG 1927
Db 1861 GGAAGCAGAGGTCAGGCGAGCATTCGAGGAAGCGAGGCGCCGCTGTGTGAGTGTGAGCTGCG 1920
QY 1928 CTTATCCCAAGCGCTGACGGGCTGCGCGCGATTGTGAACATGAGACTAGTGTGGAGC 1987
Db 1921 CTTATCCCAAGCGCTGACGGGCTGCGCGCGATTGTGAACATGAGACTAGTGTGGAGC 1980
QY 1988 CAGAACGTTCCGCGAGAGAAAAGAGGGCGGAGGCTCTACCTTCGAGAGGTGAAGCACTGTT 2047
Db 1981 CAGAACGTTCCGCGAGAGAAAAGAGGGCGGAGGCTCTACCTTCGAGAGGTGAAGCACTGTT 2040
QY 2048 CAGCGTGTCAACTACGAGAGGGGCGGCGCGCGCGCTCTGAGGCGCTGTGTGTGG 2107
Db 2041 CAGCGTGTCAACTACGAGAGGGGCGGCGCGCGCGCGCTCTGAGGCGCTGTGTGTGG 2100
QY 2108 CCGGAGCATATTCACAGAGGGCTTGGCGCACCTTGTGTGTGTGGCGGCCAGAGACC 2167
Db 2101 CCGGAGCATATTCACAGAGGGCTTGGCGCACCTTGTGTGTGTGGCGGCCAGAGACC 2160
QY 2168 GCCCGCTGAGCTGTA-----CATCCGCCA 2191
Db 2161 GCCCGCTGAGCTGTA-----CATCCGCCA 2220
QY 2192 GGACAGGCTCAGGAGGTATCGCCAGCATATCAAAACCCAGAAACAGTACTGCTGCG 2251
Db 2221 GGACAGGCTCAGGAGGTATCGCCAGCATATCAAAACCCAGAAACAGTACTGCTGCG 2280
QY 2252 TCGGTATGCGTGTGTCAGAAAGCGCCGCGCATGAGGCGCTCGCAAGGCTTCAAGAGCA 2311
Db 2281 TCGGTATGCGTGTGTCAGAAAGCGCCGCGCATGAGGCGCTCGCAAGGCTTCAAGAGCA 2340
QY 2312 GGTCTACTACTTGAAGAGCTTCAGCGCTTACATGAGTGTGAGTGTGCTGCTGCTGAGGCA 2371
Db 2341 GGTCTACTACTTGAAGAGCTTCAGCGCTTACATGAGTGTGAGTGTGCTGCTGCTGAGGCA 2400
QY 2372 GACCAAGCCGCTGAGAGGATGCGCTGTGTATGAGAGAGAGCTCTCCCTGAATGAGGCGCAG 2431
Db 2401 GACCAAGCCGCTGAGAGGATGCGCTGTGTATGAGAGAGAGCTCTCCCTGAATGAGGCGCAG 2460
QY 2432 CAGTGGCTCTTTCAGAGTCTTCTACGCTTATGCTATGCTGACCAAGCGCTGCGCATCAGGGG 2491
Db 2461 CAGTGGCTCTTTCAGAGTCTTCTACGCTTATGCTATGCTGACCAAGCGCTGCGCATCAGGGG 2520
QY 2492 CAAGTCTTACGTCAGTTCGAGGGGATCCGCAAGGGCTCAATCCGCTGCTCAGCGCTGTG 2551
Db 2521 CAAGTCTTACGTCAGTTCGAGGGGATCCGCAAGGGCTCAATCCGCTGCTCAGCGCTGTG 2580
QY 2552 CAGCCTGTGTACGCGCAGATGAGAACAGCTGTTTGGGGGATTCGCGCGGAGCGGCT 2611
Db 2581 CAGCCTGTGTACGCGCAGATGAGAACAGCTGTTTGGGGGATTCGCGCGGAGCGGCT 2640
QY 2612 GCTCTCGCGTTTGTGTGATATTTCTTGTGTGTGACACTCCTACCTCAGCGCAAAAC 2671
Db 2641 GCTCTCGCGTTTGTGTGATATTTCTTGTGTGTGACACTCCTCAGCGCAAAAC 2700
QY 2672 CTTCTCTAGAACCTTGTGTGAGGATGTCCTGAGATGAGTGTGCGGTGAGTGTGCGGAA 2731
Db 2701 CTTCTCTAGAACCTTGTGTGAGGATGTCCTGAGATGAGTGTGCGGTGAGTGTGCGGAA 2760
QY 2732 GACAGTGTGAACTTCCCTGTAGAAAGAGAGGCGCTGTGTGAGAGGCTTGTGTGAGAT 2791
Db 2761 GACAGTGTGAACTTCCCTGTAGAAAGAGAGGCGCTGTGTGAGAGGCTTGTGTGAGAT 2820

Qy	2792	GGGGCCCGAGGGCTATTTCCTCCGTGGGGGCGCTGTGTGATATACCGGAGACCCGGAGGT	2811
Db	2821	GGCGGCCCGAGGGCTATTTCCTCCGTGGGGGCGCTGTGTGATATACCGGAGACCCGGAGGT	2880
Qy	2852	GGAGAGGGACTACTCCAGCTATGCCCCGAGCTTCATAGAGCCAGTCTCAGCTTCAACCG	29111
Db	2881	GGAGAGGGACTACTCCAGCTATGCCCCGAGCTTCATAGAGCCAGTCTCAGCTTCAACCG	29400
Qy	2912	CGGCTTCAGGGCTGGAGGAACATGCTGCGCAACTCTTTGGGGGTCTTGGCGGTGAAGTG	29711
Db	2941	CGGCTTCAGGGCTGGAGGAACATGCTGCGCAACTCTTTGGGGGTCTTGGCGGTGAAGTG	30000
Qy	2972	TCACAGCCCTTTCTGATTTGCAAGCTGAGCAAGCTTCACAGCGGTGTGCACAACTCTA	30311
Db	3001	TCACAGCCCTTTCTGATTTGCAAGCTGAGCAAGCTTCACAGCGGTGTGCACAACTCTA	30600
Qy	3032	CAGATCCCTCTCTGCAAGGGGTGCAAGTTTACGCAATGTTGTCTGCAAGTCCCATTTCA	30911
Db	3061	CAGATCCCTCTCTGCAAGGGGTGCAAGTTTACGCAATGTTGTCTGCAAGTCCCATTTCA	31200
Qy	3092	TCAGCAAGTTTGGAGAAGACCCCAATTTTCTCGTGGGTATCTCGACAGCGCTCCCT	31511
Db	3121	TCAGCAAGTTTGGAGAAGACCCCAATTTTCTCGTGGGTATCTCGACAGCGCTCCCT	31800
Qy	3152	CTGCTACTCCATCTGGAAGCAAGCAAGCAAGGATGTGCTGTGGGGGCCAAGAGGCCCGC	32111
Db	3181	CTGCTACTCCATCTGGAAGCAAGCAAGCAAGGATGTGCTGTGGGGGCCAAGAGGCCCGC	32400
Qy	3212	CGGCGCTCTGCGCTCCGAGGCGCTGCAGTGGGTGTGCCACCAAGCATTTCTGCTCAAGCT	32711
Db	3241	CGGCGCTCTGCGCTCCGAGGCGCTGCAGTGGGTGTGCCACCAAGCATTTCTGCTCAAGCT	33000
Qy	3272	GACTCGACACCGGTGTACCTTACGTGCGACTCTGTGGGGTCACTAGAGACGCCAG-AGCG	33300
Db	3301	GACTCGACACCGGTGTACCTTACGTGCGACTCTGTGGGGTCACTAGAGACGCCAGTACGC	33600
Qy	3331	AGCTGAGTGGGAAGCTCCCGGGGACGACGTACGTGCGCTCGAGAGCGGACCAACCCGG	33900
Db	3361	AGCTGAGTGGGAAGCTCCCGGGGACGACGTACGTGCGCTCGAGAGCGGACCAACCCGG	34200
Qy	3391	CAGTGCCTCAGACTTCAAGACATCTCTGATGATATGGCACCCGCGACAGCAGCGCG	34500
Db	3421	CAGTGCCTCAGACTTCAAGACATCTCTGATGATATGGCACCCGCGACAGCAGCGCG	34800
Qy	3451	AAGAGACACACAGACAGCCGTGTACGCCGGGCTCTACGTCCAGAGGAGGAGGGCGCG	35100
Db	3481	AAGAGACACACAGACAGCCGTGTGTACGCCGGGCTCTACGTCCAGAGGAGGAGGGCGCG	35400
Qy	3511	CCACACCCAGGCCCGACCGCTGGGAGTGTAGGCGTCGATAGTGTGTTGGCCGAGGCGCT	35700
Db	3541	CCACACCCAGGCCCGACCGCTGGGAGTGTAGGCGTCGATAGTGTGTTGGCCGAGGCGCT	36000
Qy	3571	GGATGTCCGGCTGAAGGTGTAGTGTCCGGCTGAGGCTGAGAGCAATGTCCACGCAAGGCG	36300
Db	3601	GGATGTCCGGCTGAAGGTGTAGTGTCCGGCTGAGGCTGAGAGCAATGTCCACGCAAGGCG	36600
Qy	3631	TGAGGTTCACAGACACCTGCGTGTACCTTCCACAGGCTGTGGCTGCGGCTCACGCC	36900
Db	3661	TGAGGTTCACAGACACCTGCGTGTGTACCTTCCACAGGCTGTGGCTGCGGCTCACGCC	37200
Qy	3691	AGGGCAGACTTTCTCTCACAGAGAGCCCGGCTTCCACTCCCAATAGAGAAATGTCCATC	37500
Db	3721	AGGGCAGACTTTCTCTCACAGAGAGCCCGGCTTCCACTCCCAATAGAGAAATGTCCATC	37800
Qy	3751	CCGAGATTGCGCATTTGTTCACCCCTGCGCTCCCTCTTGTGCTTCCACCCCGACCATC	38100
Db	3781	CCGAGATTGCGCATTTGTTCACCCCTGCGCTCCCTCTTGTGCTTCCACCCCGACCATC	38400
Qy	3811	CAGGTGAGAGCCCTGAGAAGAGACCTGTGGAGTCTGGGAATTTTGGAGAGACAAAGTGT	38700
Db	3841	CAGGTGAGAGCCCTGAGAAGAGACCTGTGGAGTCTGGGAATTTTGGAGAGACAAAGTGT	39000

[illegible]

QY	2847	GAGGTGACAGAGAGACTACTCTCCAGCTATGCCGGAACTCTCATGAGGACGATCTACCTTC	2906
Db	2821	GAGGTGACAGAGAGACTACTCTCCAGCTATGCCGGAACTCTCATGAGGACGATCTACCTTC	2880
QY	2907	AACGGGCGCTTCAAGGCTGGGAGGAACATGGGTGCAAAATCTCTTGGGGCTTTGGGGTG	2966
Db	2881	AACGGGCGCTTCAAGGCTGGGAGGAACATGGGTGCAAAATCTCTTGGGGCTTTGGGGTG	2940
QY	2967	AAGGTGACAGGCTCTTCTTGATTTGGATTTGGAGGTGAACAGCTCTCAAGGCTGTGACCAAC	3026
Db	2941	AAGGTGACAGGCTCTTCTTGATTTGGATTTGGAGGTGAACAGCTCTCAAGGCTGTGACCAAC	3000
QY	3027	ATCTACAAGATCTCTCTCTGTCTGACAGGCTACAGGTTTTCAGCGATGTGTCTGTGACCTCCA	3086
Db	3001	ATCTACAAGATCTCTCTCTGTCTGACAGGCTACAGGTTTTCAGCGATGTGTCTGTGACCTCCA	3060
QY	3087	TTTCATCAGCAAGTTTGGAGAAACCCCACTATTTTTCCTGGGCGCTATCTGTGACAGGCG	3146
Db	3061	TTTCATCAGCAAGTTTGGAGAAACCCCACTATTTTTCCTGGGCGCTATCTGTGACAGGCG	3120
QY	3147	TCCCTCTGTACTCCATCTGTAAAGCAAGAACAGAGGATGTCCCTGGGGGCGCAAGGGCC	3206
Db	3121	TCCCTCTGTACTCCATCTGTAAAGCAAGAACAGAGGATGTCCCTGGGGGCGCAAGGGCC	3180
QY	3207	GCCGCGCGCCCTCTCTCCCTCCGAGGCGCGTGAAGTGGCTGTGGCCACAAGCATTCCTGTCTC	3266
Db	3181	GCCGCGCGCCCTCTCTCCCTCCGAGGCGCGTGAAGTGGCTGTGGCCACAAGCATTCCTGTCTC	3240
QY	3267	AAGCTGACTGACACCGTGTACTCTAGTGCACACTCTGGGGGCACTGAGACAGGCCAG	3326
Db	3241	AAGCTGACTGACACCGTGTACTCTAGTGCACACTCTGGGGGCACTGAGACAGGCCAG	3300
QY	3327	ACGCGAGTGTGTGGAGAACTCCGGGGGAGAGGCTGACTCCCTGAGAGCGGACAGCAAC	3386
Db	3301	ACGCGAGTGTGTGGAGAACTCCGGGGGAGAGGCTGACTCCCTGAGAGCGGACAGCAAC	3360
QY	3387	CCGGCACTGTCCCMCAGATTTCAAGACATCCGCGATGATGGGCAACCGGCCACACAGC	3446
Db	3361	CCGGCACTGTCCCMCAGATTTCAAGACATCCGCGATGATGGGCAACCGGCCACACAGC	3420
QY	3447	GCCGAGAGCAGACACCAGACGCCCTGTCAAGCGCGGGCTCTAGCTCCCAAGGGAGGGGG	3506
Db	3421	GCCGAGAGCAGACACCAGACGCCCTGTCAAGCGCGGGCTCTAGCTCCCAAGGGAGGGGG	3480
QY	3507	CGGCGCCACACCAAGGCGCCGACCGGCTGGGAGTCTGAGGCGCTGAGTGTTTTGGCCGAG	3566
Db	3481	CGGCGCCACACCAAGGCGCCGACCGGCTGGGAGTCTGAGGCGCTGAGTGTTTTGGCCGAG	3540
QY	3567	GCTGCTATGTCCGGCTGAAGGCTGATGTTCGGGCTGAGGCGCTGAGCGATGTCTCACCCAA	3626
Db	3541	GCTGCTATGTCCGGCTGAAGGCTGATGTTCGGGCTGAGGCGCTGAGCGATGTCTCACCCAA	3600
QY	3627	GAGGCTGATGTCTCACACACACTCGCTCTTCACTTCCCAACAGGCTGGGCGCTCGGCTCCA	3686
Db	3601	GAGGCTGATGTCTCACACACACTCGCTCTTCACTTCCCAACAGGCTGGGCGCTCGGCTCCA	3660
QY	3687	CCCCAGGCGCAGTTTTTCTGTACACAGAACCGGGCTTTCACACTGCCCAATATGAAATATGTC	3746
Db	3661	CCCCAGGCGCAGTTTTTCTGTACACAGAACCGGGCTTTCACACTGCCCAATATGAAATATGTC	3720
QY	3747	CATCCCGAATTTGGCAATTTGTATGACCCCTGGCGCTCGGCTCCCTTGGCTGTCAACCCCAAC	3806
Db	3721	CATCCCGAATTTGGCAATTTGTATGACCCCTGGCGCTCGGCTCCCTTGGCTGTCAACCCCAAC	3780
QY	3807	CATCCAGTGTGAGAACCCCTGAGAAAGAACCTGGGAGCTCTTGGAAATTTGGAGTGAACCAAG	3866
Db	3781	CATCCAGTGTGAGAACCCCTGAGAAAGAACCTGGGAGCTCTTGGAAATTTGGAGTGAACCAAG	3840
QY	3867	GTGTGCTCTGTACACAGGCGAGGACCTTCACTCACTGTGATGGGGGTCCCTGTGGCTCAATT	3926
Db	3841	GTGTGCTCTGTGTACACAGGCGAGGACCTTCACTCACTGTGATGGGGGTCCCTGTGTGGCTCAATT	3900

[illegible]

```
|||||
Db 601 CGGGCTGGAACCATAGCTAGAGGAGGCCGGGGTCCCCCTGGGCTGCGCCAGCCCGGGT 660
Qy 723 GCGAGAGGGGGGGGAGTGGCCAGCGAGTCTGCGTTGGCCAGAGGCCAGGGCT 782
Db 661 GCGAGAGGGGGGGGAGTGGCCAGCGAGTCTGCGTTGGCCAGAGGCCAGGGCT 720
Qy 783 GGGCTGCCCCGTGAGCCGAGCGAGCGGCCCTTGGGAGGGGCTTGGGCCACCCGGG 842
Db 721 GGGCTGCCCCGTGAGCCGAGCGAGCGGCCCTTGGGAGGGGCTTGGGCCACCCGGG 780
Qy 843 AGGACGCTGGAGCCAGTGAACCTGTTCTGTGTGTGACCTGCCAGACCCCGGAA 902
Db 781 AGGACGCTGGAGCCAGTGAACCTGTTCTGTGTGTGACCTGCCAGACCCCGGAA 840
Qy 903 GAACCCACCTTTGAGGGGGGGCTCTGAGGAGCGGCCCTCCAGCCCATCCGTTGGG 962
Db 841 GAACCCACCTTTGAGGGGGGGCTCTGAGGAGCGGCCCTCCAGCCCATCCGTTGGG 900
Qy 963 GCGCAGACACACGCGGGGCCCCCATCCATCGCGGCCACGACGTCCTGGAGACGCT 1022
Db 901 GCGCAGACACACGCGGGGCCCCCATCCATCGCGGCCACGACGTCCTGGAGACGCT 960
Qy 1023 TGTCCCCGGGTGAGCGCGAGACCAAGACTTCTTACTCTCAGCGGCAAGAGAGAG 1082
Db 961 TGTCCCCGGGTGAGCGCGAGACCAAGACTTCTTACTCTCAGCGGCAAGAGAGAG 1020
Qy 1083 CTGGGGCCCTCTCTACTAGCTCTGTAGGCGCCAGCCGACTGGCGGCTGGAGGCTC 1142
Db 1021 CTGGGGCCCTCTCTACTAGCTCTGTAGGCGCCAGCCGACTGGCGGCTGGAGGCTC 1080
Qy 1143 GTGAGAGACATCTTCTGGGTTCCAGGCGCTGATGCGAGGAGTCCCGCAGGTTGCC 1202
Db 1081 GTGAGAGACATCTTCTGGGTTCCAGGCGCTGATGCGAGGAGTCCCGCAGGTTGCC 1140
Qy 1203 GCGCTGCCCCAGCGCTTACTGGCAATGCGGCCCTGTTTCTGAGCTGTTGGAGCCAC 1262
Db 1141 GCGCTGCCCCAGCGCTTACTGGCAATGCGGCCCTGTTTCTGAGCTGTTGGAGCCAC 1200
Qy 1263 GCGCAGTGGCCCTTACGGGGGTCTCTCAAGAGCAGTCCCGCGAGCTGGCGTACC 1322
Db 1201 GCGCAGTGGCCCTTACGGGGGTCTCTCAAGAGCAGTCCCGCGAGCTGGCGTACC 1260
Qy 1323 CCAGCAGCGGGTGTCTGTGCGGGAGAAAGCCAGGGCTGTGTGGCGCCCGAGAG 1382
Db 1261 CCAGCAGCGGGTGTCTGTGCGGGAGAAAGCCAGGGCTGTGTGGCGCCCGAGAG 1320
Qy 1383 GAGGACACAGACCCCGCTGCGCTGAGTGTCTCGCCAGCAGAGCCCTGTGAG 1442
Db 1321 GAGGACACAGACCCCGCTGCGCTGAGTGTCTCGCCAGCAGAGCCCTGTGAG 1380
Qy 1443 GTGTACGGCTTCTGTGCGGGGTCTGCGCGGGCTGTGTGCCAGGCTTGGGGCTCC 1502
Db 1381 GTGTACGGCTTCTGTGCGGGGTCTGCGCGGGCTGTGTGCCAGGCTTGGGGCTCC 1440
Qy 1503 AGGACACAAGACCGCGCTCTCAGAGAACCAAGAAATTCACTCCCTGGGAAAGCAT 1562
Db 1441 AGGACACAAGACCGCGCTCTCAGAGAACCAAGAAATTCACTCCCTGGGAAAGCAT 1500
Qy 1563 GCCAAGCTCTGCTGAGAGAGCTAGTGAAGATGAGCGGAGCGGAGCTGGGCTGGCTG 1622
Db 1501 GCCAAGCTCTGCTGAGAGAGCTAGTGAAGATGAGCGGAGCGGAGCTGGGCTGGCTG 1560
Qy 1623 CCGAGAGACCCAGGGGTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGAGAGATC 1682
Db 1561 CCGAGAGACCCAGGGGTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGAGAGATC 1620
Qy 1683 CTGGCCAAAGTTCTGCACTGGCTATGATGTATGCTGTGAGCTGCTAGGCTTTTTC 1742
Db 1621 CTGGCCAAAGTTCTGCACTGGCTATGATGTATGCTGTGAGCTGCTAGGCTTTTTC 1680
Qy 1743 TTTTATGTCAGAGAGACCACTTCAAAAGAACAGGCTTTTCTTACCGGAAGTGTCTC 1802
|||||

Db 1681 TTTTATGTCAGAGAGACCACTTCAAAAGAACAGGCTTTTCTTACCGGAAGTGTCTC 1740
Qy 1803 TGGAGCAAGTTGCAAGACATTTGAATCAGACAGCACTTTGAAGAGGTGTGACCTGGAG 1862
Db 1741 TGGAGCAAGTTGCAAGACATTTGAATCAGACAGCACTTTGAAGAGGTGTGACCTGGAG 1800
Qy 1863 CTGTGGAAGCAGAGGTGAGGACATTCGGAAGCCAGGCCGCTGTGACGTCCAGA 1922
Db 1801 CTGTGGAAGCAGAGGTGAGGACATTCGGAAGCCAGGCCGCTGTGACGTCCAGA 1860
Qy 1923 CTCCGCTTCATCCCAAGCCTGAGGGGTGGGGCCGANTTGTGAACATGATAGTGTGTG 1982
Db 1861 CTCCGCTTCATCCCAAGCCTGAGGGGTGGGGCCGANTTGTGAACATGATAGTGTGTG 1920
Qy 1983 GGAGCCAGAAAGTTCCGAGAGAAAGAGGSCCAGAGCTCTACCTCGAGGGTGAAGCA 2042
Db 1921 GGAGCCAGAAAGTTCCGAGAGAAAGAGGSCCAGAGCTCTACCTCGAGGGTGAAGCA 1980
Qy 2043 CTGTTCAAGCTGTCAATACAGAGCGGGGCGGGGCCCGGCTCTGAGCGCTGTGTG 2102
Db 1981 CTGTTCAAGCTGTCAATACAGAGCGGGGCGGGGCCCGGCTCTGAGCGCTGTGTG 2040
Qy 2103 CTGGGCTTGGAGCATATTCACAGGGGCTGGCGACCTTTCGTGCTGCTGGGGCCAG 2162
Db 2041 CTGGGCTTGGAGCATATTCACAGGGGCTGGCGACCTTTCGTGCTGCTGGGGCCAG 2100
Qy 2163 GACCGCGCGCTGAGCTGTA-----CATC 2186
Db 2101 GACCGCGCGCTGAGCTGTA-----CATC 2160
Qy 2187 CCCCAGAGCAGGCTACAGGAGGTATCGCCAGCATCATCAAAACCCAGAAACAGTACTGC 2246
Db 2161 CCCCAGAGCAGGCTACAGGAGGTATCGCCAGCATCATCAAAACCCAGAAACAGTACTGC 2220
Qy 2247 GTGGCTGGGTATGCGCGTGTGTCAGAAAGCCCGCCATGGGCGACGTCGGAAGGCTTAA 2306
Db 2221 GTGGCTGGGTATGCGCGTGTGTCAGAAAGCCCGCCATGGGCGACGTCGGAAGGCTTAA 2280
Qy 2307 AGCCAGCTCTTACTTGAACAGACCTCCAGCGTACATGAGCAGATTCGTGGCTACCTG 2366
Db 2281 AGCCAGCTCTTACTTGAACAGACCTCCAGCGTACATGAGCAGATTCGTGGCTACCTG 2340
Qy 2367 CAGAGACACAGCCCGCTGAGGGATGCGGTGTATTCAGACAGAGCTCTCCTGAATGAG 2426
Db 2341 CAGAGACACAGCCCGCTGAGGGATGCGGTGTATTCAGACAGAGCTCTCCTGAATGAG 2400
Qy 2427 GCGACAGATGCGCTTTCGAGGCTCTTCCTACGTTCAATGTGCGACAGCGCGTGCATC 2486
Db 2401 GCGACAGATGCGCTTTCGAGGCTCTTCCTACGTTCAATGTGCGACAGCGCGTGCATC 2460
Qy 2487 AGGGCAAGTCTCTACGTCAGTGCAGGGATGCCAGGGATCCGACGGCTCATCTCCAGCGTG 2546
Db 2461 AGGGCAAGTCTCTACGTCAGTGCAGGGATGCCAGGGATCCGACGGCTCATCTCCAGCGTG 2520
Qy 2547 CTCTGCAAGCTGTGCTTACGGCGACATGAGAAACAAGCTGTTGGGGGATTCGGCGGGAC 2606
Db 2521 CTCTGCAAGCTGTGCTTACGGCGACATGAGAAACAAGCTGTTGGGGGATTCGGCGGGAC 2580
Qy 2607 GGGCGTGTCTGCGCTTGGTGGATGATTTCTTGTGGAGACACCTCAACCTCACCGACGCG 2666
Db 2581 GGGCGTGTCTGCGCTTGGTGGATGATTTCTTGTGGAGACACCTCAACCTCACCGACGCG 2640
Qy 2667 AAAACCTTCTCAGAGACCTGTGTCGAGAGTGTCCCTGAGTATGGCTGCGTGTGAACCTTG 2726
Db 2641 AAAACCTTCTCAGAGACCTGTGTCGAGAGTGTCCCTGAGTATGGCTGCGTGTGAACCTTG 2700
Qy 2727 CCGAAGACAGTGTGAACCTTCCCTGTAGAGACAGAGCCCTGGGTGGCAGGGCTTTTGT 2786
Db 2701 CCGAAGACAGTGTGAACCTTCCCTGTAGAGACAGAGCCCTGGGTGGCAGGGCTTTTGT 2760
Qy 2787 CAGATGCGGGCCAGCGGCTTTCCTCGTGGGCGGCGCTGTGAGTATACCGGACCTGT 2846
Db 2761 CAGATGCGGGCCAGCGGCTTTCCTCGTGGGCGGCTGTGAGTATACCGGACCTGT 2820
|||||
```

```
QY 2847 GAGGTGAGAGCGACTACTCCAGCTATGCCGAGCTCCATGAGGCCAGTCTCACCTTC 2906
    |||||||
Db 2821 GAGGTGAGAGCGACTACTCCAGCTATGCCGAGCTCCATGAGGCCAGTCTCACCTTC 2880
QY 2907 AACCGGGCTTCAAGGCTGGAGAGACATGCTGCGCAAACTTTGGGGCTTGGCGCTG 2966
Db 2881 AACCGGGCTTCAAGGCTGGAGAGACATGCTGCGCAAACTTTGGGGCTTGGCGCTG 2940
QY 2967 AAGTGTACAGCCTGTTTCTGATTTGTCAGGTGAACAGCCTCCAGACGGTGTGACCAAC 3026
    |||||||
Db 2941 AAGTGTACAGCCTGTTTCTGATTTGTCAGGTGAACAGCCTCCAGACGGTGTGACCAAC 3000
QY 3027 ATCTACAAGATCCCTGCTGCTGAGCGCTACAGGTTTCACGATGTGTGCTGCAAGTCCCA 3086
    |||||||
Db 3001 ATCTACAAGATCCCTGCTGCTGAGCGCTACAGGTTTCACGATGTGTGCTGCAAGTCCCA 3060
QY 3087 TTTCAATGAGCAAGTTTGGAAAGACCCACATTTTTCGCGGTATCTGACACGGCC 3146
    |||||||
Db 3061 TTTCAATGAGCAAGTTTGGAAAGACCCACATTTTTCGCGGTATCTGACACGGCC 3120
QY 3147 TCCTCTGCTACTCCATCTCTGAAAGCCAAAGACGAGGGATGTGCTGAGGGCCCAAGGGC 3206
    |||||||
Db 3121 TCCTCTGCTACTCCATCTCTGAAAGCCAAAGACGAGGGATGTGCTGAGGGCCCAAGGGC 3180
QY 3207 GCGCGGGCCCTCTGCTCCCTCCGAGGCCGTGCAATGGCTGTGCAACCAAGCATTTCTGCTC 3266
    |||||||
Db 3181 GCGCGGGCCCTCTGCTCCCTCCGAGGCCGTGCAATGGCTGTGCAACCAAGCATTTCTGCTC 3240
QY 3267 AAGCTGACTGACACCGGTGTCACCTACGTGCACTCTGCGGTCACTGAGACAGCCACG 3326
    |||||||
Db 3241 AAGCTGACTGACACCGGTGTCACCTACGTGCACTCTGCGGTCACTGAGACAGCCACG 3300
QY 3327 ACGGAGCTGAGTGGAGAGCTCCCGGGGAGCAGCCTGACTGCCCCTGAGAGCCGACGCCAAC 3386
    |||||||
Db 3301 ACGGAGCTGAGTGGAGAGCTCCCGGGGAGCAGCCTGACTGCCCCTGAGAGCCGACGCCAAC 3360
QY 3387 CCGGCACTGCCCTCAGACTTCAAGACCATCTGACTGATGAGCGCACCCGCCACAGCCAG 3446
    |||||||
Db 3361 CCGGCACTGCCCTCAGACTTCAAGACCATCTGACTGATGAGCGCACCCGCCACAGCCAG 3420
QY 3447 GCCGAGAGCGAGACACGAGGCCCTGTACAGCCGGGCTCTACGTCCAGGGAGGGAGGGG 3506
    |||||||
Db 3421 GCCGAGAGCGAGACACGAGGCCCTGTACAGCCGGGCTCTACGTCCAGGGAGGGAGGGG 3480
QY 3507 CGGGCCACACCCAGCGCCGCGACCGCTGGAGTCTGAGGGCTGAGTGAATGTTGGCCGAG 3566
    |||||||
Db 3481 CGGGCCACACCCAGCGCCGCGACCGCTGGAGTCTGAGGGCTGAGTGAATGTTGGCCGAG 3540
QY 3567 GCTTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAA 3626
    |||||||
Db 3541 GCTTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAA 3600
QY 3627 GGGCTGAGTGTCCAGACACCTGCCGCTTCTACTTCCCCACAGGCTGGGCTGCCA 3686
    |||||||
Db 3601 GGGCTGAGTGTCCAGACACCTGCCGCTTCTACTTCCCCACAGGCTGGGCTGCCA 3660
QY 3687 CCCCAGGGCCAGCTTTCCTCACCAGAGGCCGGCTTCCACTCCCCACATAGGATATAGTC 3746
    |||||||
Db 3661 CCCCAGGGCCAGCTTTCCTCACCAGAGGCCGGCTTCCACTCCCCACATAGGATATAGTC 3720
QY 3747 CATCCCCAGATTGGCATTGTTCACCCCTGCGCTGCTCTTGGCTTCCACCCCCAC 3806
    |||||||
Db 3721 CATCCCCAGATTGGCATTGTTCACCCCTGCGCTGCTCTTGGCTTCCACCCCCAC 3780
QY 3807 CATCCAGTGGAGACCTGTAGAGAGACCTGGAGGCTGGGAATTTGAGTGAACCAAG 3866
    |||||||
Db 3781 CATCCAGTGGAGACCTGTAGAGAGACCTGGAGGCTGGGAATTTGAGTGAACCAAG 3840
QY 3867 GTGTGCCCTGTACAGAGGGAGAGACCTGACACTGATGGGGTCCCTGTGTGGTCAAAATT 3926
    |||||||
Db 3841 GTGTGCCCTGTACAGAGGGAGAGACCTGACACTGATGGGGTCCCTGTGTGGTCAAAATT 3900
```

```
QY 3927 GGGGAGAGTCTGCTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAAAAAA 3986
    |||||||
Db 3901 GGGGAGAGTCTGCTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAAAAAA 3960
QY 3987 AAAA 3990
    ||||
Db 3961 AAAA 3964
```

Search completed: April 17, 2003, 05:14:37
Job time : 2828 secs

Page 1

Db	241	GTGGCCCGAGTCTGTCAGAGGCGTGTGCAGAGCGCGGCGCCAAAGACTGTGGCTTCGGCC	300
Qy	363	TTTCGCGCTCTGAGAGGGGGCCCGCGGGGGCCCGCCGAGGCTTCACACACAGCTGGCC	422
Db	301	TTTCGCGCTCTGAGAGGGGGCCCGCGGGGGCCCGCCGAGGCTTCACACACAGCTGGCC	360
Qy	423	AGTACCTGCGCCAAACAGGATGAGACGACGACATCGGAGGGGAGCGGGGGCTGGGGGGTGTG	482
Db	361	AGTACCTGCGCCAAACAGGATGAGACGACGACATCGGAGGGGAGCGGGGGCTGGGGGGTGTG	420
Qy	483	CTGGCGCGGGTGGGGAGAGAGCGTGGTGTACCTGCTGGAGACGCTGGCGCTTTTGG	542
Db	421	CTGGCGCGGGTGGGGAGAGAGCGTGGTGTACCTGCTGGAGACGCTGGCGCTTTTGG	480
Qy	543	CTGGTGGCTTCCAGCTGCGCTTACAGGTGTGCGGGCGCGCGCTTACAGCTGGCGCT	602
Db	481	CTGGTGGCTTCCAGCTGCGCTTACAGGTGTGCGGGCGCGCGCTTACAGCTGGCGCT	540
Qy	603	GCACACTAGAGCCCGGCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGAGTGGAA	662
Db	541	GCACACTAGAGCCCGGCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGAGTGGAA	600
Qy	663	CGGGCCCTGGAAACATAGCGTACAGGAGGCGGGGCTCCCTGGGCTCTCCAGCCCGGGT	722
Db	601	CGGGCCCTGGAAACATAGCGTACAGGAGGCGGGGCTCCCTGGGCTCTCCAGCCCGGGT	660
Qy	723	GCAGAGAGCGCGGGGGGAGCTGCGACCGCAAGTGTGCGCTGCCCAAGAGGCGACGAGCT	782
Db	661	GCAGAGAGCGCGGGGGGAGCTGCGACCGCAAGTGTGCGCTGCCCAAGAGGCGACGAGCT	720
Qy	783	GGGCTGTCCCTCGACCGGAGGCGGAGCGCCCGTGGAGGAGGGGCTGGGCGCACCCGGGC	842
Db	721	GGGCTGTCCCTCGACCGGAGGCGGAGCGCCCGTGGAGGAGGGGCTGGGCGCACCCGGGC	780
Qy	843	AGGAGCGGTGGAGCGAGTGAACGCTGGTTTCTGTGGTGTGCACCTGGCAAGCCGCGGAA	902
Db	781	AGGAGCGGTGGAGCGAGTGAACGCTGGTTTCTGTGGTGTGCACCTGGCAAGCCGCGGAA	840
Qy	903	GAAAGCACTCTTTTGGAGGGTGGCGCTCTGGGACGGGCGACATCCGCAACCCATCGGTGGC	962
Db	841	GAAAGCACTCTTTTGGAGGGTGGCGCTCTGGGACGGGCGACATCCGCAACCCATCGGTGGC	900
Qy	963	CGCCAGACCAACGCGGGGGCCCCCATCATCATGCGGCGACACAGTCTCTGGAGACAGCTT	1022
Db	901	CGCCAGACCAACGCGGGGGCCCCCATCATCATGCGGCGACACAGTCTCTGGAGACAGCTT	960
Qy	1023	TGTCCCCCGGTGTACGCGCGAGAACAGCACTTCTCTACTCTGAGGCGAAGAGAGCAG	1082
Db	961	TGTCCCCCGGTGTACGCGCGAGAACCACTTCTCTACTCTGAGGCGAAGAGAGCAG	1020
Qy	1083	CTGGGAGCCCTCTTCTACTACCTCTCTGAGGGCCAGGCTGACATGCGGCGCTCGGAGAGCTC	1142
Db	1021	CTGGGAGCCCTCTTCTACTACCTCTCTGAGGGCCAGGCTGACATGCGGCGCTCGGAGAGCTC	1080
Qy	1143	GTTGAGAGCACTTTTCTGTGGTTCAGGCGCTGAGATGCGAAGGAGCTCCCGAGATTTGGCC	1202
Db	1081	GTTGAGAGCACTTTTCTGTGGTTCAGGCGCTGAGATGCGAAGGAGCTCCCGAGATTTGGCC	1140
Qy	1203	CGGCTGCCCAACGCTATGTGGCAAAATGCGGGCCCGTGTCTTGGAGACTCTTGGGAACAC	1262
Db	1141	CGGCTGCCCAACGCTATGTGGCAAAATGCGGGCCCGTGTCTTGGAGACTCTTGGGAACAC	1200
Qy	1263	GGGAGTGGCCCTACGGGGTGGTGCCTCAAGAGAGACATGGCCGCTGCGAGCTGGGGTACAC	1322
Db	1201	GGGAGTGGCCCTACGGGGTGGTGCCTCAAGAGAGACATGGCCGCTGCGAGCTGGGGTACAC	1260
Qy	1323	CGAGCAACGGGTGTCTGTGTGCCGGGAGAAAGCCCAAGGGCTCTGTGTGGCGGCCCGCCAGAG	1382
Db	1261	CGAGCAACGGGTGTGTGTGTGCCGGGAGAAAGCCCAAGGGCTCTGTGTGGCGGCCCGCCAGAG	1320
Qy	1383	GAGGACACAGACCCCGGTGTGTGTGTGACGTCTCGGCTGACAGCAGCAGCCCTCTGGCAG	1442


```

OY 3603 AGGCTGAGCGAGTGTCCAGCCAGGCGTGAATGTCTCAGACACACCTCCGTTCTTCACTTC 3662
    |||||||
Db 3541 AGGCTGAGCGAGTGTCCAGCCAGGCGTGAATGTCTCAGACACACCTCCGTTCTTCACTTC 3600
OY 3663 CCCACAGGCTGAGCGTCCAGCCAGGCGAGCTTTTCTCACCAGAGACCCCGGCT 3722
    |||||||
Db 3601 CCCACAGGCTGAGCGTCCAGCCAGGCGAGCTTTTCTCACCAGAGACCCCGGCT 3660
OY 3723 TCCACATCCCATATGAGATATGTCATCCCAATTCGCAATGTCTGACCCCTGCGCCGTG 3782
    |||||||
Db 3661 TCCATCTCCCATATGAGATATGTCATCCCAATTCGCAATGTCTGACCCCTGCGCCGTG 3720
OY 3783 CCCCTCTTGGCCCTTCCACACCCCAATCCAGTGAAGACCCCTGAGAGACCCCTGGAGAC 3842
    |||||||
Db 3721 CCCCTCTTGGCCCTTCCACACCCCAATCCAGTGAAGACCCCTGAGAGACCCCTGGAGAC 3780
OY 3843 TCTGGGAATTTGAGATGACCAAGATGTGCGCTGTACACAGGCGAGACCCCTGACCTGG 3902
    |||||||
Db 3781 TCTGGGAATTTGAGATGACCAAGATGTGCGCTGTACACAGGCGAGACCCCTGACCTGG 3840
OY 3903 ATGGGGGTCCTCTGTGCTCAAAATTTGGGGGAGTGTCTGGAGTAAATTAATTAATA 3962
    |||||||
Db 3841 ATGGGGGTCCTCTGTGCTCAAAATTTGGGGGAGTGTCTGGAGTAAATTAATTAATA 3900
OY 3963 TGAATTTTCAATTTGA 3980
    |||||||
Db 3901 TGAATTTTCAATTTGA 3918

RESULT 2
us-09-108-401a-75
Query Match          97.4%; Score 3900; DB 2; Length 4022;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 3913; Conservative 0; Mismatches 5; Indels 104; Gaps 1;

```

```

Db 541 ACAGAGCTGCTGCTTCACTGCTGTGACAGGCTGCGCGCTCTTGTGCTGTGGCTCCAGCT 600
    |||||||
OY 559 GCGCTACAGAGTGTGCGGGGCGCGGCTGTACACAGTGGGCGCTGCGCACTACAGAGCCGAG 618
    |||||||
Db 601 GCGCTACAGAGTGTGCGGGGCGCGGCTGTACACAGTGGGCGCTGCGCACTACAGAGCCGAG 660
OY 619 CCCGGCACAGCTATGTGAGACCCGGAAGGCGTGTGGATGTGGAACGGGCGCTGGAACCTA 678
    |||||||
Db 661 CCCGGCACAGCTATGTGAGACCCGGAAGGCGTGTGGATGTGGAACGGGCGCTGGAACCTA 720
OY 679 GCGTACAGAGAGGCGCGGGGTCCTCCGCGCTGCGACGCGCGGGTGTGAGAGAGGCGCGGG 738
    |||||||
Db 721 GCGTACAGAGAGGCGCGGGGTCCTCCGCGCTGCGACGCGCGGGTGTGAGAGAGGCGCGGG 780
OY 739 GCAATGCGACGCGGAAGTGTGCGCTGTGCGCAAGAGCCAGCGCTGTGCGCTGCGAGC 798
    |||||||
Db 781 GCAATGCGACGCGGAAGTGTGCGCTGTGCGCAAGAGGCGCGAGCGCTGTGCGCTGCGAGC 840
OY 799 CGAGCGGACGCGCGTTGGGCGAGGGGTCCTGGGCGCCACCGGGGCGAGACGCGTGGACGA 858
    |||||||
Db 841 CGAGCGGACGCGCGTTGGGCGAGGGGTCCTGGGCGCCACCGGGGCGAGACGCGTGGACGA 900
OY 859 GTGACCGTGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 918
    |||||||
Db 901 GTGACCGTGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
OY 919 AGGATGCGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 978
    |||||||
Db 961 AGGATGCGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
OY 979 GCCCCCATTCACATGCGGGGCGACACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1038
    |||||||
Db 1021 GCCCCCATTCACATGCGGGGCGACACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
OY 1039 CCGGAGACCAAGACTTCTCTTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1098
    |||||||
Db 1081 CCGGAGACCAAGACTTCTCTTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
OY 1099 TACTCAAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1158
    |||||||
Db 1141 TACTCAAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
OY 1159 TGGGTTTCAAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1218
    |||||||
Db 1201 TGGGTTTCAAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
OY 1219 ACTGGGAATATGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1278
    |||||||
Db 1261 ACTGGGAATATGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
OY 1279 GGGTGTCTCTCAAGACGACATGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1338
    |||||||
Db 1321 GGGTGTCTCTCAAGACGACATGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
OY 1339 GTGCGCGGAGAGAGCCCGAGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1398
    |||||||
Db 1381 GTGCGCGGAGAGAGCCCGAGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
OY 1399 GTGCGCGGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1458
    |||||||
Db 1441 GTGCGCGGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
OY 1459 GGGGCTGTGCTGTGCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1518
    |||||||
Db 1501 GGGGCTGTGCTGTGCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560
OY 1519 GCTTCTCAAGAGAACCAAGAAATCTTCTCTGGGGAACCAATGCTGTGCTGTGCTGCT 1578
    |||||||
Db 1561 GCTTCTCAAGAGAACCAAGAAATCTTCTCTGGGGAACCAATGCTGTGCTGTGCTGCT 1620
OY 1579 AGAAGCTGACGTGGAAGATGAGCTGTGCGGAGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1638
    |||||||

```

Db 1621 AGGAGCTGACGTGGAAAGATGAGCGTGGGAGCTGCCCTTGCGTCCGAGAGGCCAGGGG 1680
 QY 1639 TTGGCTGTGTTCGGCGCGGAGAGACACCGTCTGGCTGAGAGATCTGGCCAACTTCTCG 1698
 Db 1681 TTGGCTGTGTTCGGCGCGGAGAGACACCGTCTGGCTGAGAGATCTGGCCAACTTCTCG 1740
 QY 1699 ACTGGCTGATGATGTGTGTACGTGTGAGCTGTCAAGTCTTTTATGTATGTCAGGAGA 1758
 Db 1741 ACTGGCTGATGATGT 1800
 QY 1759 CCAGCTTTAAAGAAAGACAGCGCTTTTCTTACCGGAAAGTGTGTGTGTGTGTGTGTGTGT 1818
 Db 1801 CCAGCTTTAAAGAAAGACAGCGCTTTTCTTACCGGAAAGTGTGTGTGTGTGTGTGTGTGT 1860
 QY 1819 GCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGGCGGAGCTGTGCGGAAGCAGAG 1878
 Db 1861 GCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGGCGGAGCTGTGCGGAAGCAGAG 1920
 QY 1879 TCAGGCAACATCGGGAAGCCAGGCGCCCTGTGACGTCCAGACTCCGCTTATCCCA 1938
 Db 1921 TCAGGCAACATCGGGAAGCCAGGCGCCCTGTGACGTCCAGACTCCGCTTATCCCA 1980
 QY 1939 AGCCTGACGGGCTGGGCGCGATTTGTGACATGAGTACGTCGTCGTCGTCGTCGTCGTCGTC 1998
 Db 1981 AGCCTGACGGGCTGGGCGCGATTTGTGACATGAGTACGTCGTCGTCGTCGTCGTCGTCGTC 2040
 QY 1999 GCAGAGAAAAAGAGGGCGGAGCGTCTCAGCTCAGAGGTGAAGGCACTGTTCAGCGTCTCA 2058
 Db 2041 GCAGAGAAAAAGAGGGCGGAGCGTCTCAGCTCAGAGGTGAAGGCACTGTTCAGCGTCTCA 2100
 QY 2059 ACTACAGAGGGGCGGCG 2118
 Db 2101 ACTACAGAGGGGCGGCG 2160
 QY 2119 TTCACAGGGGCTGGGCGCACCTTGTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2178
 Db 2161 TTCACAGGGGCTGGGCGCACCTTGTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2220
 QY 2179 TGTACATCCCGCAGAGACAGCTTCACGAGTATCCAGCATCATCAAAACCCAGAAACA 2238
 Db 2221 TGTACATCCCGCAGAGACAGCTTCACGAGTATCCAGCATCATCAAAACCCAGAAACA 2280
 QY 2239 CGTACTGCGT 2298
 Db 2281 CGTACTGCGT 2340
 QY 2299 CCTTCAAGGCCAGCTCTTACCTTGACAGACTCCAGCGCTTCAGTCCAGCAAGTGTGTGT 2358
 Db 2341 CCTTCAAGGCCAGCTCTTACCTTGACAGACTCCAGCGCTTCAGTCCAGCAAGTGTGTGT 2400
 QY 2359 CTCACCTGACAGAGACAGCCCGCTGAGGAGTCCGTCGTATCGAGAGAGTCTCTCC 2418
 Db 2401 CTCACCTGACAGAGACAGCCCGCTGAGGAGTCCGTCGTATCGAGAGAGTCTCTCC 2460
 QY 2419 TGAATGAGCCAGCACTGT 2478
 Db 2461 TGAATGAGCCAGCACTGT 2520
 QY 2479 TGGGATCAAGGGGCAAGTCTTACGTCAGTCCAGGAGTCCCGGAGGGGCTCCATCTCT 2538
 Db 2521 TGGGATCAAGGGGCAAGTCTTACGTCAGTCCAGGAGTCCCGGAGGGGCTCCATCTCT 2580
 QY 2539 CCACGCTGCTTCGACACCTGT 2598
 Db 2581 CCACGCTGCTTCGACACCTGT 2640
 QY 2599 GGGGGAGCGGGCTGCTGT 2658
 Db 2641 GGGGGAGCGGGCTGCTGT 2700
 QY 2659 CCACAGCGAAACCTTCGACAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2718
 Db 2701 CCACAGCGAAACCTTCGACAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2760

QY 2719 TGAATTTGGGAGAGACAGT 2778
 Db 2761 TGAATTTGGGAGAGACAGT 2820
 QY 2779 CTTTGTTCAGATGCGGCGCCACGGCTATTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2838
 Db 2821 CTTTGTTCAGATGCGGCGCCACGGCTATTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2880
 QY 2839 GGACCTTGAGGTGTGAGAGGAGTACTCCAGTATGACCGGAGCTTCATCAGAGCCAGTTC 2898
 Db 2881 GGACCTTGAGGTGTGAGAGGAGTACTCCAGTATGACCGGAGCTTCATCAGAGCCAGTTC 2940
 QY 2899 TCACCTTCAACCGCGCTTCAGGCTGGAGGAATGCGTGCAGAACTTTTGGGGTCT 2958
 Db 2941 TCACCTTCAACCGCGCTTCAGGCTGGAGGAATGCGTGCAGAACTTTTGGGGTCT 3000
 QY 2959 TGGGCTGAAGTGTACACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3018
 Db 3001 TGGGCTGAAGTGTACACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3060
 QY 3019 GCACCAACATCTCAAGATTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3078
 Db 3061 GCACCAACATCTCAAGATTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3120
 QY 3079 AGCTCCATTTTCATCAGCAAGTTTGGAGAACCCCAATTTTCTGCGCGTATCTGTG 3138
 Db 3121 AGCTCCATTTTCATCAGCAAGTTTGGAGAACCCCAATTTTCTGCGCGTATCTGTG 3180
 QY 3139 ACACGGGCTCCCT 3198
 Db 3181 ACACGGGCTCCCT 3240
 QY 3199 CCAAGGGCGCGCGCGCGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3258
 Db 3241 CCAAGGGCGCGCGCGCGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3300
 QY 3259 TCTGTCTCAAGT 3318
 Db 3301 TCTGTCTCAAGT 3360
 QY 3319 CAGCCAGACGACGT 3378
 Db 3361 CAGCCAGACGACGT 3420
 QY 3379 CAGCCAGACGACGT 3438
 Db 3421 CAGCCAGACGACGT 3480
 QY 3439 ACAGCCAGGCGGAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 3498
 Db 3481 ACAGCCAGGCGGAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 3540
 QY 3499 GGGAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 3558
 Db 3541 GGGAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 3600
 QY 3559 TGGGCGAGGCTGT 3618
 Db 3601 TGGGCGAGGCTGT 3660
 QY 3619 CCAGCCAAAGGGGTGAGT 3678
 Db 3661 CCAGCCAAAGGGGTGAGT 3720
 QY 3679 CGGCTCACCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 3738
 Db 3721 CGGCTCACCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 3780
 QY 3739 GAATAGTCCATCCCGAGATTTGGCATTTGTACCCCTGCGCGCTCTCTTGTGCTTCC 3798
 Db 3781 GAATAGTCCATCCCGAGATTTGGCATTTGTACCCCTGCGCGCTCTCTTGTGCTTCC 3840

OY	3799	ACCCCAACATCCAGGTGGAGACCCCTGAGAGACCCCTGGAGCTCTGGAAATTTGGAGT	3858
Db	3841	ACCCCAACATCCAGGTGGAGACCCCTGAGAGACCCCTGGAGCTCTGGAAATTTGGAGT	3900
OY	3859	GACCAAAAGTGTGCTGTACACAGGCGAGGACCTGCACCTGATGAGGCTCCCTGTGG	3918
Db	3901	GACCAAAAGTGTGCTGTACACAGGCGAGGACCTGCACCTGATGAGGCTCCCTGTGG	3960
OY	3919	GTCAAATTTGGGGGAGTGTCTGTGGAGTAAATACTGAATATATAGATTTCAGTTT	3978
Db	3961	GTCAAATTTGGGGGAGTGTCTGTGGAGTAAATACTGAATATATAGATTTCAGTTT	4020
OY	3979	GA 3980	
Db	4021	GA 4022	

Search completed: April 17, 2003, 16:37:50
Job time : 21 secs

THIS PAGE BLANK (USPTO)

Thu Apr 17 16:44:05 2003

align_p_n

PROTEIN

Page 1

splice variant SEQ1, 2184-2215

GenCore version 5.1.4-P5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 17, 2003, 16:41:18 ; Search time 4 seconds

(without alignments)
2.243 Million cell updates/sec in "401"

Title: us-09-108-401a-46
Perfect score: 5882
Sequence: 1 MPRAPRCRAVRSILRSHYRE.....TALEAANPALPSDFKTLID 1120

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 1 segs, 4006 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 0%

Listing first 1 summaries

Command line parameters:
-MODEL-frame+p2n-model -DEV-soft -O-us-09-108-401a-46 -DB-walicka686.seq
-SUFFIX-prot -OUT-align_p_n -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0 -UNITS-bits
-START=1 -END=1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=1 -DOCCALIGN=200
-THR SCORE=prot -THR MAX=100 -THR MIN=0 -ALIGN=1 -MODE-LOCAL -OUTFMT-prot
-NOR-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO_XIPX
-MGC SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FAROP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database: walicka686.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	5882	99.7	4006 1	US-09-424-686B-1del

ALIGNMENTS

RESULT 1
US-09-424-686B-1del
Sequence 1, Application US/09424686B
GENERAL INFORMATION:
APPLICANT: Hagen, Gustav
APPLICANT: Siegmund, Hans
APPLICANT: Weichelt, Walter
APPLICANT: Wicher, Maressa
APPLICANT: Zdobov, Dmitry
TITLE OF INVENTION: Human Catalytic Telomerase Sub-unit and its Diagnostic and
FILE REFERENCE: Human Patent Use
CURRENT APPLICATION NUMBER: US/09/424,686B
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/EP98/03468
PRIOR FILING DATE: 1998-06-03

NUMBER OF SEQ ID NOS: 7
SOFTWARE: Microsoft Word
SEQ ID NO 1
LENGTH: 4042
TYPE: DNA
ORGANISM: Homo sapiens
US-09-424-686B-1del

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
0	5882.00	4006	1117
Percent Similarity:	99.82%	Conservative:	1
Best Local Similarity:	99.73%	Mismatches:	2
Query Match:	99.73%	Indels:	0
DB:	1	Gaps:	0

us-09-108-401a-46 (1-1120) x US-09-424-686B-1del (1-4006)

QY	1	MECHPRAAGALAPROAGCYSARGLAVALARGSERLEULEAARGSERHISTYARGILU	20
DB	63	ATGCGCGGCGCTCCCGCGCGAGCGCTCCCTGCTCGCGACGACCTACCGCGAG	122
QY	21	VALLEUPROEUALARHPHEVALARGLEUGLYPROGLNGLYTPARGLEUVALGIN	40
DB	123	GTCGTGCGCTGCGCACCTGCTGCGCGCTGCGCGCGCGAGCGCTGCGCTGCGG	182
QY	41	ARGGLYASPROALALAPHEARGALALEUVALAGLNCYSLEUVALCYVALPROTP	60
DB	183	CGCGGGGACCGCGCGCTTCCGCGCGCTGCGCGCGCTGCGCTGCGCTGCGCTG	242
QY	61	ASPLAARGPROPROALALAPROSERPHEARGLVALISERCYSLEULYSGLULEU	80
DB	243	GACGACG	302
QY	81	VALAARGVALLEUGLARGLEUCYSGLUARGGLYVALALYSASVALLEUALAPHEGLY	100
DB	303	GTCGCGCGAGTGTGCGAGGCTGTGGAGCGCGCGCGCGAGAGCGTGTGCGCG	362
QY	101	PHALALEULEASGLYVALARGGLYLYPROPROGLUALAPHEPHTHRISERVALARG	120
DB	363	TTGCGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	422
QY	121	SERYTRLEUPROASNTHRVALTHRASPALALEUARGGLYSERGLYALATRPGLYLEU	140
DB	423	AGCTACCTGCGCACACGCTGACGACGCTGCGGGGAGCGGGGCGTGGGCGTGG	482
QY	141	LEUARGARGVALGLYASPAVALLEUVALHISLEULEUALARGCYSALEUALAPHEVAL	160
DB	483	CTGCGCGCGCTGCGAGCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	542
QY	161	LEUVALALAPROSECYALATYRGIVALCYSGLYPROPROLEUTYRGINLEUGLYALA	180
DB	543	CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	602
QY	181	ALATHRGINALARGPROPROPROHISALISERGLYPROARGARGARGLEUGLYCYSGLU	200
DB	603	GCCACTCAGGCG	662
QY	201	ARGALATRPASNHISERVALARGGLYVALPROLEUGLYLEUPROALAPROGLY	220
DB	663	CGGCGCTGAGACATAGCGCTCAGGAGCGCGCGCGCGCGCGCGCGCGCGCG	722
QY	221	ALARGARGARGGLYLYSERALASERTRISERLEUPROLEUPROLYASARGPROARG	240
DB	723	CGGAGAGCG	782
QY	241	GLYVALALAPROGLUARGGLYVALARGGLYLYNGLYNGLYSERTPRALHISPROGLY	260
DB	783	GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	842
QY	261	ARGTHARGGLYPROSERASPARGLYPHECYVALVALSERPROALATARGPROALAGLU	280
DB	843	AGGACGCTGAGCGAGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	902

Qy	281	GIUAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300
Db	903	GAAGGACACCTCTTGGAGGGGTGCCTCTCGGCACGGCGCCACCTCCACCCATCCGTGGGAC	962
Qy	301	ArgGlnHisAlaGlyProProSerThrSerArgProProArgProIrrPsrphPro	320
Db	965	CCCGAGACACACGGGGGCCCCCATCCACATCGGGGACACAGTCCCTGGGACAGCGCT	1022
Qy	321	CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyLysPylsGluGln	340
Db	1023	TTCTCCCGGGGTGAGCGCGAGACCAACACACTCTCTACTCTACGAGCGACAAAGAGAGC	1082
Qy	341	LeuArgProSerPheLeuLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgLeu	360
Db	1083	CTGGCGGCCCCCTCTTCTATACAGCTCTAGGCCACGACTGACCTGGCCCTCGAGAGCTC	1142
Qy	361	ValGluThrIlePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro	380
Db	1143	GTGGAGACCACTTTCTTGGGTTCAGGCGCTGGATGCCAGGACTCCCGCAGGTGGCC	1202
Qy	381	ArgLeuProGlnArgTyrTyrPglMetArgProLeuPheLeuGluIleuLeuGlyLysHis	400
Db	1203	CGCCTGCCCGCAGCGCTAGTGGCAATCGGCGCCCTGTCTTGAGAGCTGTGGAAACAC	1262
Qy	401	AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	420
Db	1263	GGCGAGTCCCTCCAGGGGGGTCTCTCAACACCACTGCCCTCGGAGACTCCGTGACC	1322
Qy	421	ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGluGlu	440
Db	1323	CCAGACCGCGGTGTCTGTGCCCGGAGACACCCCAAGGCTGTGGCGGCCCCAGAGAG	1382
Qy	441	GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln	460
Db	1383	GAGGACACAGACCCCGCGCGTGGTGGTACACTCTCGCGACAGACAGACCCCTGGAG	1442
Qy	461	ValTyrGlyPheValAlaGlyAlaCysLeuArgArgLeuValProProGlyLeuTyrPylSer	480
Db	1443	GTGACGGCTTCGTAGCGGGCTGCTGCTCGCGGCTGTGCTCCCGCAGGCTCTGGGGCTCC	1502
Qy	481	ArgHisAsnGluAlaGArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	500
Db	1503	AGCGACACAGACCCCTCTCTCAGGACACCAACAAAGTATATCTCCCTGGGAGAGCAT	1562
Qy	501	AlaLysLeuSerLeuGlnGluLeuThrTyrPylsMetSerValArgAspCysAlaTyrLeu	520
Db	1563	GCGAAGCTCTGCTGAGGAGCTGAGTGGAAATGATAGGTGCGGAGTCCGCTTGGCTG	1622
Qy	521	ArgArgSerProGlyValAlaGlyCysValProAlaAlaGlnHisArgLeuArgGluIle	540
Db	1623	CGCAGGACCCACGGGCTGTGGCTGTGTCCGGCGCGAGACACCGTCTCGTAGAGATGC	1682
Qy	541	LeuAlaLysPheLeuHisTsrPleuMetSerValTyrValGluLeuLeuArgSerPhe	560
Db	1683	CTGGCCAGATTCTGCACTGGCTGATGATGTGTACTGTGTGACACTGTCTAGGCTTTTC	1742
Qy	561	PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	580
Db	1743	TTTTATGTACGAGACACAGCTTCAAAAGAACAGGCTTTTTTTTACCAGGAAAGTGTCT	1802
Qy	581	TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu	600
Db	1803	TGGAGCAAGTTGCAAACATTTGGAATCAGACAGCACTTGAAGAAGGTGCAGCTGGGAG	1862
Qy	601	LeuSerGluAlaGluValAlaArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	620
Db	1863	CTGTGCAAGACAGAGCTCAGACAGCATCGGGAAGCAGGCGCCGCTCTAGACGTCCAGA	1922
Qy	621	LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal	640
Db	1923	CTCCGGCTTACATCCCAAGCTTGACGGGCTGCGCGCATTTGTAAATGAGTACTGCTGTG	1982

[illegible]

2
2
2

being
it is
grass
lateral
like
this


```

Db 3063 CACGCAATGTCCTGCACCTCCATTTCATCAGCAAGTTGGAGAACCCACATTTTC 3122
Oy 1021 LeuArgValIleSerAspThrAlaSerLeuGlyTyrSerIleLeuLysAlaLysAsnAla 1040
Db 3123 CTGCGGCTCATCTCTGACACGGCCCTCCCTCTGCTACTCTCATCTGAAAGCCAGAACGCA 3182
Oy 1041 GlyMetSerLeuGlyAlaLysGlyAlaAlaGlyProLeuProSerGluAlaValGlnTrp 1060
Db 3183 GGGATGTCCCTGGGGGCCAGAGGGGCCGCCCTCTGCCCCCTCCGAGGCCGTGCAGTGG 3242
Oy 1061 LeuGlySerLeuGlyAlaLysGlyAlaAlaGlyProLeuProSerGluAlaValGlnTrp 1080
Db 3243 CTGTGCCACCAAGCATTCCTGCTCAAGCTGACTCGACACCGTGCACCTGACCTGACCTGC 3302
Oy 1081 LeuGlySerLeuArgThrAlaGlnThrGlnLeuSerArgLysLeuProGlyThrThrLeu 1100
Db 3303 CTGGGGTCACTCAGACAGCCAGACGACGAGTGGAGCTCCCGGGGACGACGCTG 3362
Oy 1101 ThrAlaLeuGluAlaAlaAlaAsnProAlaLeuProSerAspPheLysThrIleLeuAsp 1120
Db 3363 ACTGCCCTGGAGGCCGACGACCCGACCTGCCCCCTCAGACTTCAAGACCACATCTGAGAC 3422

```

Search completed: April 17, 2003, 16:41:35
 Job time : 17 secs

THIS PAGE BLANK (USPTO)